



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 29, 2024 – 06:12 PM JST

PDB ID : 8YX9
Title : CD40 in complex with Dacetuzumab Fab
Authors : Caaveiro, J.M.M.; Fernandez-Perez, J.; Tsumoto, K.
Deposited on : 2024-04-02
Resolution : 2.80 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36.2
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

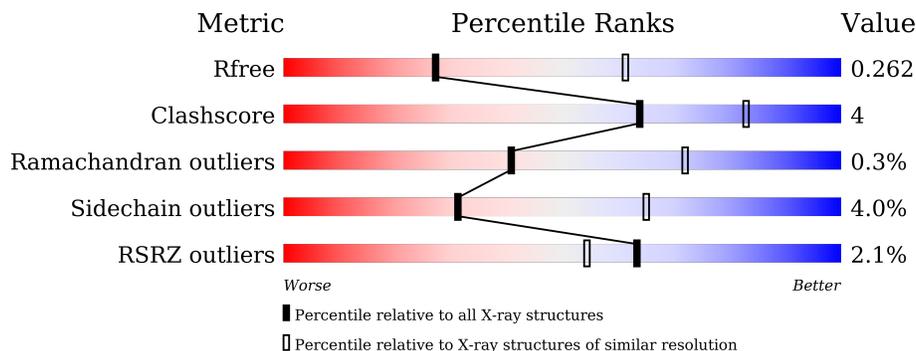
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	B	223	 73% 18% 5%
1	E	223	 80% 13% 5%
1	G	223	 82% 13% 5%
1	H	223	 84% 11% 5%
2	C	219	 89% 10% 5%
2	F	219	 83% 16% 5%

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Mol	Chain	Length	Quality of chain
2	I	219	<p>86% 10% . .</p>
2	L	219	<p>87% 12% .</p>
3	A	179	<p>12% 77% 10% . 12%</p>
3	D	179	<p>3% 59% 6% . 34%</p>
3	J	179	<p>% 37% . 62%</p>
3	K	179	<p>7% 75% . . 20%</p>

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 16889 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Dacetuzumab, Heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	H	212	Total 1587	C 1007	N 269	O 306	S 5	0	0	0
1	B	211	Total 1578	C 1002	N 268	O 303	S 5	0	0	0
1	E	211	Total 1583	C 1005	N 268	O 305	S 5	0	0	0
1	G	211	Total 1583	C 1005	N 268	O 305	S 5	0	0	0

- Molecule 2 is a protein called Dacetuzumab, light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	L	217	Total 1674	C 1048	N 286	O 335	S 5	0	0	0
2	C	217	Total 1674	C 1048	N 286	O 335	S 5	0	0	0
2	F	217	Total 1674	C 1048	N 286	O 335	S 5	0	0	0
2	I	215	Total 1659	C 1040	N 281	O 333	S 5	0	0	0

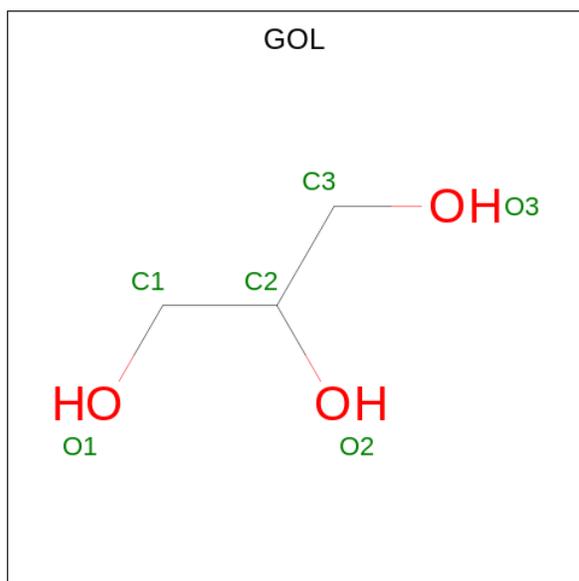
- Molecule 3 is a protein called Tumor necrosis factor receptor superfamily member 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	A	157	Total 1206	C 735	N 206	O 245	S 20	0	1	0
3	D	119	Total 923	C 556	N 161	O 190	S 16	0	1	0
3	J	68	Total 533	C 322	N 91	O 112	S 8	0	0	0
3	K	144	Total 1115	C 683	N 191	O 223	S 18	0	1	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	194	HIS	-	expression tag	UNP P25942
A	195	HIS	-	expression tag	UNP P25942
A	196	HIS	-	expression tag	UNP P25942
A	197	HIS	-	expression tag	UNP P25942
A	198	HIS	-	expression tag	UNP P25942
A	199	HIS	-	expression tag	UNP P25942
D	194	HIS	-	expression tag	UNP P25942
D	195	HIS	-	expression tag	UNP P25942
D	196	HIS	-	expression tag	UNP P25942
D	197	HIS	-	expression tag	UNP P25942
D	198	HIS	-	expression tag	UNP P25942
D	199	HIS	-	expression tag	UNP P25942
J	194	HIS	-	expression tag	UNP P25942
J	195	HIS	-	expression tag	UNP P25942
J	196	HIS	-	expression tag	UNP P25942
J	197	HIS	-	expression tag	UNP P25942
J	198	HIS	-	expression tag	UNP P25942
J	199	HIS	-	expression tag	UNP P25942
K	194	HIS	-	expression tag	UNP P25942
K	195	HIS	-	expression tag	UNP P25942
K	196	HIS	-	expression tag	UNP P25942
K	197	HIS	-	expression tag	UNP P25942
K	198	HIS	-	expression tag	UNP P25942
K	199	HIS	-	expression tag	UNP P25942

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	H	1	Total C O 6 3 3	0	0
4	B	1	Total C O 6 3 3	0	0
4	E	1	Total C O 6 3 3	0	0
4	A	1	Total C O 6 3 3	0	0
4	D	1	Total C O 6 3 3	0	0
4	J	1	Total C O 6 3 3	0	0
4	K	1	Total C O 6 3 3	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	H	5	Total O 5 5	0	0
5	L	8	Total O 8 8	0	0
5	B	2	Total O 2 2	0	0
5	C	7	Total O 7 7	0	0
5	E	5	Total O 5 5	0	0
5	F	10	Total O 10 10	0	0
5	G	2	Total O 2 2	0	0
5	I	6	Total O 6 6	0	0
5	A	5	Total O 5 5	0	0
5	D	3	Total O 3 3	0	0
5	J	2	Total O 2 2	0	0
5	K	3	Total O 3 3	0	0

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

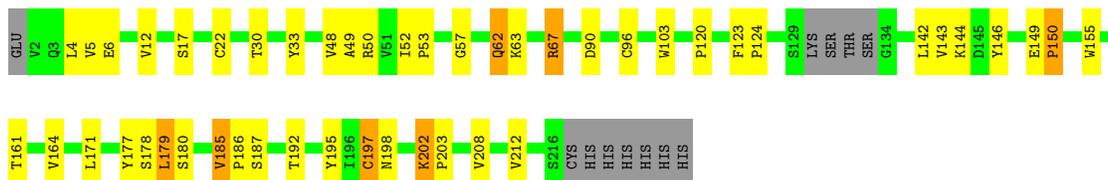
- Molecule 1: Dacetuzumab, Heavy chain

Chain H: 84% 11% 5%



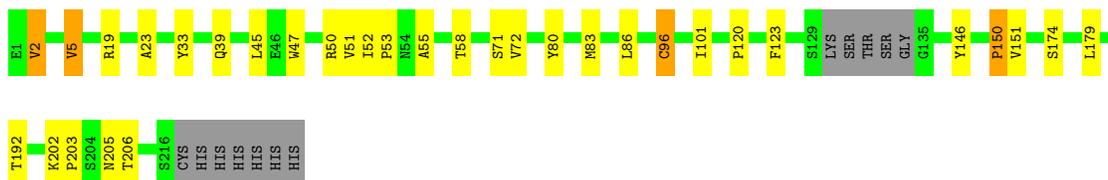
- Molecule 1: Dacetuzumab, Heavy chain

Chain B: 73% 18% 5%



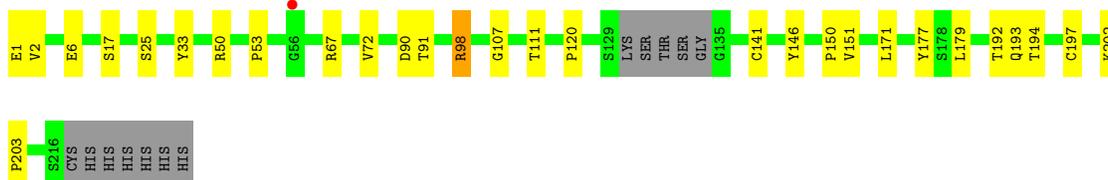
- Molecule 1: Dacetuzumab, Heavy chain

Chain E: 80% 13% 5%



- Molecule 1: Dacetuzumab, Heavy chain

Chain G: 82% 13% 5%



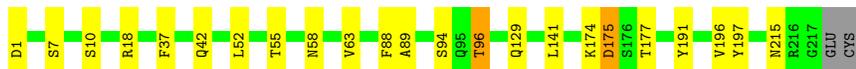
- Molecule 2: Dacetuzumab, light chain

Chain L:  87% 12%



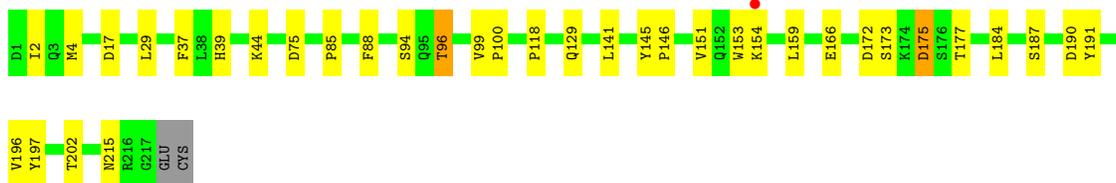
• Molecule 2: Dacetuzumab, light chain

Chain C:  89% 10%



• Molecule 2: Dacetuzumab, light chain

Chain F:  83% 16%



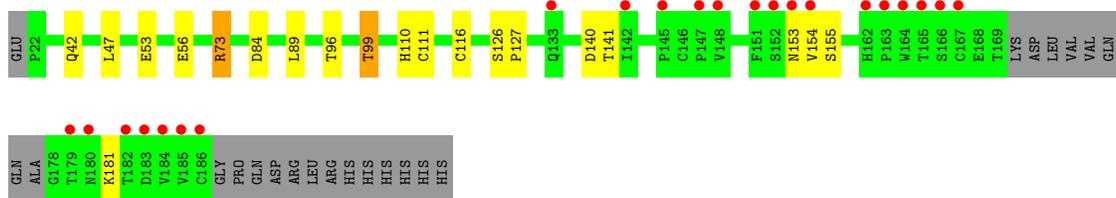
• Molecule 2: Dacetuzumab, light chain

Chain I:  86% 10%



• Molecule 3: Tumor necrosis factor receptor superfamily member 5

Chain A:  77% 10% 12%



• Molecule 3: Tumor necrosis factor receptor superfamily member 5

Chain D:  59% 6% 34%



THR
LYS
ASP
LEU
VAL
VAL
GLN
GLN
ALA
GLY
THR
THR
LYS
LYS
THR
ASP
VAL
VAL
CYS
GLY
PRO
GLN
ASP
ARG
LEU
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HIS
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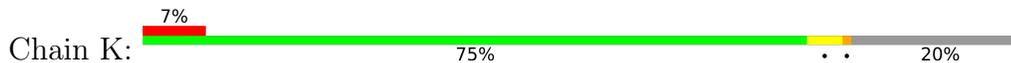
● Molecule 3: Tumor necrosis factor receptor superfamily member 5



GLY
VAL
SER
ASP
THR
ILE
CYS
GLU
PRO
CYS
PRO
VAL
GLY
PHE
PHE
SER
ASN
VAL
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SER
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● Molecule 3: Tumor necrosis factor receptor superfamily member 5



ASP
ARG
LEU
ARG
HIS
HIS
HIS
HIS
HIS

4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	199.19Å 208.17Å 198.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.80 – 2.80 49.80 – 2.80	Depositor EDS
% Data completeness (in resolution range)	100.0 (49.80-2.80) 100.0 (49.80-2.80)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.39 (at 2.81Å)	Xtrriage
Refinement program	REFMAC 5.8.0425	Depositor
R, R_{free}	0.209 , 0.262 0.213 , 0.262	Depositor DCC
R_{free} test set	4995 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	56.9	Xtrriage
Anisotropy	0.477	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 35.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.004 for -k,-h,-l	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	16889	wwPDB-VP
Average B, all atoms (Å ²)	68.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.39% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	B	0.37	0/1618	0.77	1/2205 (0.0%)
1	E	0.37	0/1623	0.77	2/2212 (0.1%)
1	G	0.35	0/1623	0.74	0/2212
1	H	0.37	0/1627	0.78	1/2217 (0.0%)
2	C	0.42	0/1713	0.76	1/2327 (0.0%)
2	F	0.41	0/1713	0.76	1/2327 (0.0%)
2	I	0.38	0/1698	0.74	0/2308
2	L	0.39	0/1713	0.76	0/2327
3	A	0.37	0/1237	0.76	1/1679 (0.1%)
3	D	0.35	0/943	0.73	0/1276
3	J	0.40	0/543	0.78	1/734 (0.1%)
3	K	0.33	0/1147	0.71	0/1558
All	All	0.38	0/17198	0.76	8/23382 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1
1	G	0	1
2	F	0	1
All	All	0	3

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	150	PRO	N-CA-CB	-7.24	94.61	103.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	150	PRO	N-CA-CB	-7.14	94.73	103.30
1	H	150	PRO	N-CA-CB	-6.71	95.21	102.60
3	J	42	GLN	CB-CA-C	-6.34	97.73	110.40
2	F	175	ASP	CB-CA-C	-6.12	98.16	110.40

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	57	GLY	Peptide
2	F	118	PRO	Peptide
1	G	98	ARG	Sidechain

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1578	0	1547	28	0
1	E	1583	0	1553	15	0
1	G	1583	0	1553	13	0
1	H	1587	0	1556	12	0
2	C	1674	0	1625	12	0
2	F	1674	0	1625	23	0
2	I	1659	0	1609	11	0
2	L	1674	0	1625	15	0
3	A	1206	0	1098	8	0
3	D	923	0	842	4	0
3	J	533	0	482	0	0
3	K	1115	0	1013	5	0
4	A	6	0	8	0	0
4	B	6	0	8	1	0
4	D	6	0	8	0	0
4	E	6	0	8	0	0
4	H	6	0	8	0	0
4	J	6	0	8	0	0
4	K	6	0	8	0	0
5	A	5	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	2	0	0	0	0
5	C	7	0	0	0	0
5	D	3	0	0	0	0
5	E	5	0	0	0	0
5	F	10	0	0	0	0
5	G	2	0	0	0	0
5	H	5	0	0	0	0
5	I	6	0	0	0	0
5	J	2	0	0	0	0
5	K	3	0	0	0	0
5	L	8	0	0	0	0
All	All	16889	0	16184	139	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

The worst 5 of 139 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:171:LEU:HD13	1:H:177:TYR:CE1	2.22	0.74
1:B:161:THR:O	1:B:164:VAL:HG12	1.88	0.74
2:C:37:PHE:HB3	2:C:96:THR:HG22	1.76	0.67
1:G:197:CYS:SG	1:G:197:CYS:O	2.54	0.66
1:B:146:TYR:CE2	1:B:177:TYR:HB2	2.32	0.65

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	B	207/223 (93%)	195 (94%)	11 (5%)	1 (0%)	29 61

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	207/223 (93%)	194 (94%)	12 (6%)	1 (0%)	29	61
1	G	207/223 (93%)	188 (91%)	19 (9%)	0	100	100
1	H	208/223 (93%)	194 (93%)	13 (6%)	1 (0%)	29	61
2	C	215/219 (98%)	206 (96%)	9 (4%)	0	100	100
2	F	215/219 (98%)	203 (94%)	12 (6%)	0	100	100
2	I	213/219 (97%)	197 (92%)	14 (7%)	2 (1%)	17	46
2	L	215/219 (98%)	207 (96%)	7 (3%)	1 (0%)	29	61
3	A	154/179 (86%)	145 (94%)	9 (6%)	0	100	100
3	D	116/179 (65%)	110 (95%)	6 (5%)	0	100	100
3	J	64/179 (36%)	57 (89%)	7 (11%)	0	100	100
3	K	143/179 (80%)	131 (92%)	12 (8%)	0	100	100
All	All	2164/2484 (87%)	2027 (94%)	131 (6%)	6 (0%)	41	72

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	I	157	ASN
1	H	174	SER
1	B	192	THR
2	L	216	ARG
1	E	55	ALA

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	173/185 (94%)	160 (92%)	13 (8%)	13	37
1	E	174/185 (94%)	165 (95%)	9 (5%)	23	55
1	G	174/185 (94%)	169 (97%)	5 (3%)	42	76
1	H	174/185 (94%)	168 (97%)	6 (3%)	37	71
2	C	194/196 (99%)	189 (97%)	5 (3%)	46	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	F	194/196 (99%)	190 (98%)	4 (2%)	53	84
2	I	193/196 (98%)	181 (94%)	12 (6%)	18	47
2	L	194/196 (99%)	191 (98%)	3 (2%)	65	89
3	A	144/163 (88%)	137 (95%)	7 (5%)	25	57
3	D	110/163 (68%)	103 (94%)	7 (6%)	17	45
3	J	64/163 (39%)	63 (98%)	1 (2%)	62	88
3	K	132/163 (81%)	127 (96%)	5 (4%)	33	67
All	All	1920/2176 (88%)	1843 (96%)	77 (4%)	31	65

5 of 77 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	47	LEU
3	J	24	THR
3	A	73	ARG
3	D	73	ARG
3	K	139	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
3	A	153	ASN
3	A	34	ASN
1	E	62	GLN
2	I	204	GLN
2	C	215	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

7 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	GOL	E	301	-	5,5,5	0.06	0	5,5,5	0.25	0
4	GOL	H	301	-	5,5,5	0.18	0	5,5,5	0.40	0
4	GOL	J	201	-	5,5,5	0.15	0	5,5,5	0.36	0
4	GOL	A	201	-	5,5,5	0.13	0	5,5,5	0.35	0
4	GOL	D	201	-	5,5,5	0.22	0	5,5,5	0.50	0
4	GOL	K	201	-	5,5,5	0.13	0	5,5,5	0.38	0
4	GOL	B	301	-	5,5,5	0.09	0	5,5,5	0.29	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GOL	E	301	-	-	2/4/4/4	-
4	GOL	H	301	-	-	1/4/4/4	-
4	GOL	J	201	-	-	0/4/4/4	-
4	GOL	A	201	-	-	2/4/4/4	-
4	GOL	D	201	-	-	2/4/4/4	-
4	GOL	K	201	-	-	2/4/4/4	-
4	GOL	B	301	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	201	GOL	C1-C2-C3-O3
4	D	201	GOL	O1-C1-C2-O2
4	D	201	GOL	O1-C1-C2-C3
4	B	301	GOL	O1-C1-C2-O2
4	H	301	GOL	O1-C1-C2-C3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	301	GOL	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	B	211/223 (94%)	-0.19	0 100 100	42, 65, 103, 122	0
1	E	211/223 (94%)	-0.30	0 100 100	42, 64, 90, 126	0
1	G	211/223 (94%)	-0.08	1 (0%) 91 88	46, 77, 112, 129	0
1	H	212/223 (95%)	-0.19	0 100 100	36, 64, 95, 112	0
2	C	217/219 (99%)	-0.27	0 100 100	33, 50, 99, 115	0
2	F	217/219 (99%)	-0.25	1 (0%) 91 88	34, 47, 98, 111	0
2	I	215/219 (98%)	-0.16	2 (0%) 84 80	37, 56, 110, 121	0
2	L	217/219 (99%)	-0.10	1 (0%) 91 88	31, 50, 110, 128	0
3	A	157/179 (87%)	0.28	22 (14%) 2 1	39, 70, 138, 154	0
3	D	119/179 (66%)	-0.16	5 (4%) 36 26	41, 66, 121, 136	0
3	J	68/179 (37%)	-0.05	2 (2%) 51 41	40, 62, 99, 114	0
3	K	144/179 (80%)	0.22	13 (9%) 9 5	50, 89, 126, 141	0
All	All	2199/2484 (88%)	-0.13	47 (2%) 63 54	31, 65, 112, 154	0

The worst 5 of 47 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	A	182	THR	5.8
3	K	164	TRP	5.1
3	A	153	ASN	4.1
3	D	142	ILE	4.1
3	A	152	SER	3.8

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	GOL	A	201	6/6	0.78	0.20	68,75,82,84	0
4	GOL	D	201	6/6	0.87	0.13	63,72,76,78	0
4	GOL	J	201	6/6	0.91	0.11	71,80,84,86	0
4	GOL	H	301	6/6	0.93	0.28	50,59,60,62	0
4	GOL	B	301	6/6	0.93	0.21	62,65,67,67	0
4	GOL	E	301	6/6	0.93	0.26	59,65,66,68	0
4	GOL	K	201	6/6	0.93	0.09	73,80,83,83	0

6.5 Other polymers [i](#)

There are no such residues in this entry.