wwPDB X-ray Structure Validation Summary Report (i)

Oct 23, 2021 – 11:31 AM EDT

PDB ID	:	1JRH
Title	:	COMPLEX (ANTIBODY/ANTIGEN)
Authors	:	Winkler, F.K.; Sogabe, S.
Deposited on	:	1997-09-23
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 (i) symbol.

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

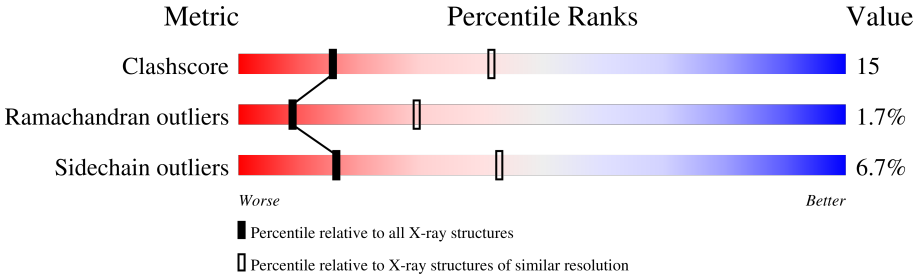
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

1 Overall quality at a glance (i)

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))
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	L	213	51% 24% • 22%
2	H	219	54% 26% • 18%
3	I	108	56% 28% • • 12%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 3465 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 ANTIBODY A6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	L	167	1290	809	211	264	6	0	0	0

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	9	SER	ALA	conflict	PIR S01320
L	11	PHE	LEU	conflict	PIR S01320
L	15	LEU	VAL	conflict	PIR S01320
L	17	ASP	GLU	conflict	PIR S01320
L	18	ARG	SER	conflict	PIR S01320
L	24	LYS	ARG	conflict	PIR S01320
L	28	ASP	ASN	conflict	PIR S01320
L	31	ASN	SER	conflict	PIR S01320
L	32	ARG	ASN	conflict	PIR S01320
L	40	PRO	GLN	conflict	PIR S01320
L	42	ASN	LYS	conflict	PIR S01320
L	43	ALA	SER	conflict	PIR S01320
L	45	ARG	GLN	conflict	PIR S01320
L	48	ILE	VAL	conflict	PIR S01320
L	49	SER	TYR	conflict	PIR S01320
L	50	GLY	VAL	conflict	PIR S01320
L	53	SER	LYS	conflict	PIR S01320
L	55	GLU	VAL	conflict	PIR S01320
L	56	THR	ASP	conflict	PIR S01320
L	57	GLU	GLY	conflict	PIR S01320
L	69	LYS	THR	conflict	PIR S01320
L	70	ASP	GLN	conflict	PIR S01320
L	72	THR	SER	conflict	PIR S01320
L	74	SER	LYS	conflict	PIR S01320
L	76	THR	ASN	conflict	PIR S01320
L	80	THR	SER	conflict	PIR S01320
L	83	VAL	PHE	conflict	PIR S01320

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Chain	Residue	Modelled	Actual	Comment	Reference
L	84	ALA	GLY	conflict	PIR S01320
L	85	THR	SER	conflict	PIR S01320
L	90	GLN	HIS	conflict	PIR S01320
L	91	TYR	PHE	conflict	PIR S01320
L	93	SER	ASP	conflict	PIR S01320
L	?	-	PRO	deletion	PIR S01320
L	96	TRP	PHE	conflict	PIR S01320
L	100	GLY	SER	conflict	PIR S01320
L	106	ILE	MET	conflict	PIR S01320

- Molecule 2 is a protein called ANTIBODY A6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	H	180	1384	881	230	267	6	0	0	0

- Molecule 3 is a protein called INTERFERON-GAMMA RECEPTOR ALPHA CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	I	95	761	485	126	146	4	11	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	105	SER	CYS	engineered mutation	UNP P15260

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	L	9	9	9	0	0
4	H	16	16	16	0	0
4	I	5	5	5	0	0

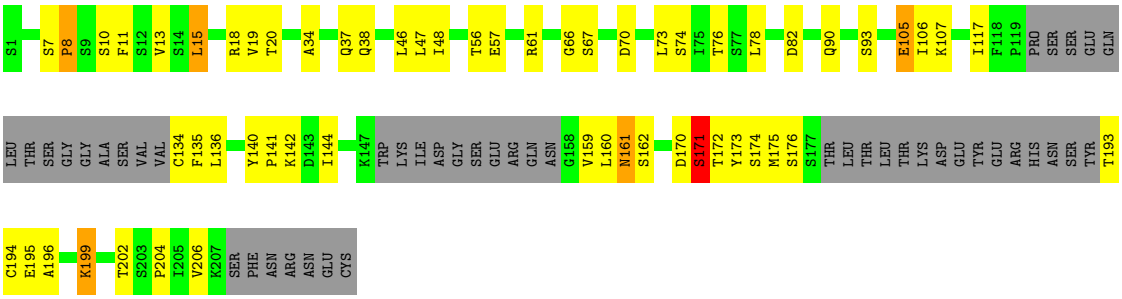
3 Residue-property plots (i)

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. 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. 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.

Note EDS was not executed.

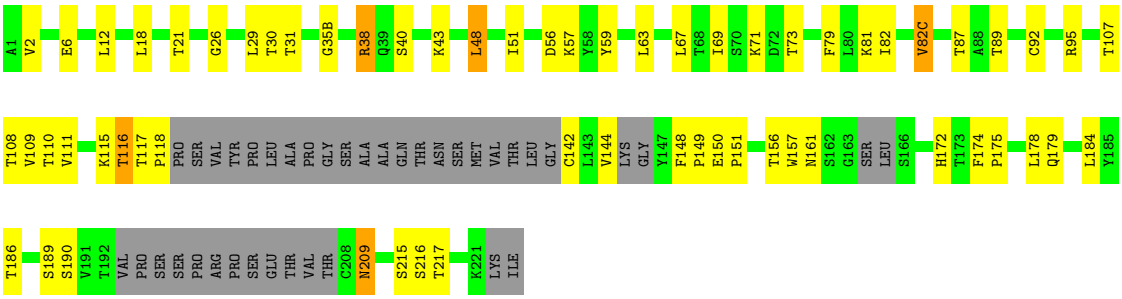
• Molecule 1: ANTIBODY A6

Chain L:



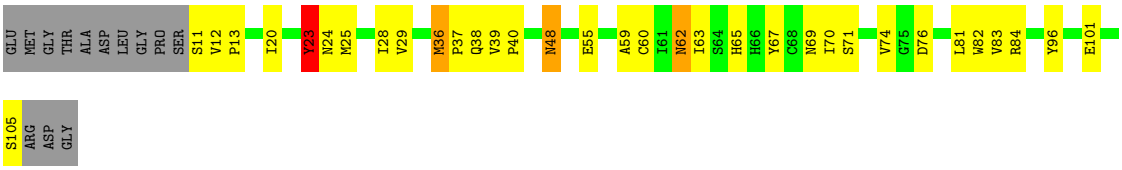
• Molecule 2: ANTIBODY A6

Chain H:



• Molecule 3: INTERFERON-GAMMA RECEPTOR ALPHA CHAIN

Chain I:



4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	85.74Å 90.80Å 101.58Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.80	Depositor
% Data completeness (in resolution range)	99.3 (20.00-2.80)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.246 , 0.314	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3465	wwPDB-VP
Average B, all atoms (Å^2)	62.0	wwPDB-VP

5 Model quality (i)

5.1 Standard geometry (i)

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	L	0.55	0/1317	0.82	0/1787
2	H	0.53	0/1419	0.82	2/1932 (0.1%)
3	I	0.62	1/783 (0.1%)	0.80	1/1071 (0.1%)
All	All	0.56	1/3519 (0.0%)	0.81	3/4790 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	I	11	SER	CB-OG	-5.32	1.35	1.42

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	I	23	TYR	N-CA-C	-5.60	95.88	111.00
2	H	63	LEU	CA-CB-CG	5.14	127.12	115.30
2	H	56	ASP	N-CA-C	-5.07	97.32	111.00

There are no chirality outliers.

There are no planarity outliers.

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	L	1290	0	1239	43	0
2	H	1384	0	1342	41	0
3	I	761	0	724	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	H	16	0	0	2	0
4	I	5	0	0	0	0
4	L	9	0	0	2	0
All	All	3465	0	3305	99	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 15.

The worst 5 of 99 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)
2:H:150:GLU:HG3	2:H:151:PRO:HA	1.47	0.93
1:L:135:PHE:CE2	2:H:190:SER:HB3	2.11	0.85
2:H:30:THR:HG23	2:H:73:THR:HG21	1.60	0.83
1:L:162:SER:HB2	2:H:175:PRO:HG2	1.65	0.77
1:L:141:PRO:HG3	1:L:199:LYS:HD3	1.69	0.73

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	L	159/213 (75%)	142 (89%)	15 (9%)	2 (1%)	12 36
2	H	170/219 (78%)	146 (86%)	21 (12%)	3 (2%)	8 28
3	I	93/108 (86%)	81 (87%)	10 (11%)	2 (2%)	6 22
All	All	422/540 (78%)	369 (87%)	46 (11%)	7 (2%)	9 29

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	L	171	SER
2	H	116	THR
2	H	179	GLN
2	H	216	SER
3	I	62	ASN

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	L	148/190 (78%)	138 (93%)	10 (7%)	16	42
2	H	155/188 (82%)	145 (94%)	10 (6%)	17	44
3	I	87/96 (91%)	81 (93%)	6 (7%)	15	41
All	All	390/474 (82%)	364 (93%)	26 (7%)	16	43

5 of 26 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	81	LYS
2	H	161	ASN
3	I	62	ASN
2	H	95	ARG
2	H	184	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	L	161	ASN
1	L	198	HIS
3	I	66	HIS
3	I	69	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)

There are no ligands in this entry.

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)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.