



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 27, 2014 – 04:16 PM GMT

PDB ID : 2H32
Title : Crystal structure of the pre-B cell receptor
Authors : Bankovich, A.J.
Deposited on : 2006-05-22
Resolution : 2.70 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

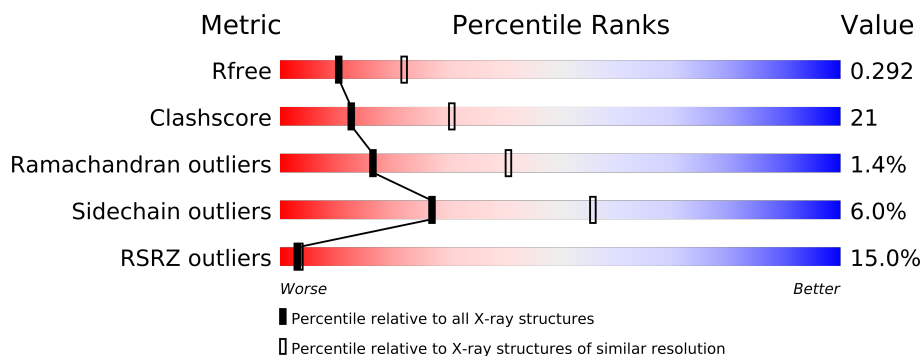
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.70 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}	66092	1557 (2.70-2.70)
Clashscore	79885	1939 (2.70-2.70)
Ramachandran outliers	78287	1905 (2.70-2.70)
Sidechain outliers	78261	1905 (2.70-2.70)
RSRZ outliers	66119	1559 (2.70-2.70)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	126	
2	B	121	
3	H	223	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
4	ZN	A	302	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 3535 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Immunoglobulin iota chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	111	Total	C	N	O	S	14	0	0
			896	557	164	170	5			

- Molecule 2 is a protein called Immunoglobulin omega chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	117	Total	C	N	O	S	20	0	0
			892	560	149	178	5			

- Molecule 3 is a protein called Immunoglobulin heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	H	211	Total	C	N	O	S	26	0	0
			1639	1048	268	314	9			

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	H	1	Total	Zn	0	0
			1	1		
4	A	1	Total	Zn	0	0
			1	1		

- Molecule 5 is water.

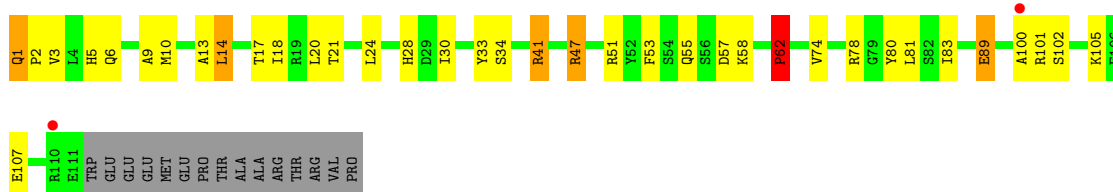
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	28	Total	O	0	0
			28	28		
5	B	24	Total	O	0	0
			24	24		
5	H	54	Total	O	0	0
			54	54		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

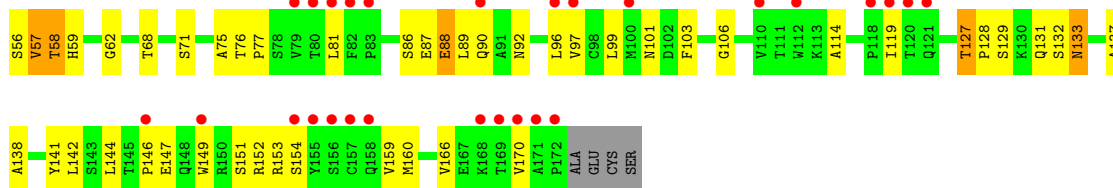
- Molecule 1: Immunoglobulin iota chain

Chain A: 



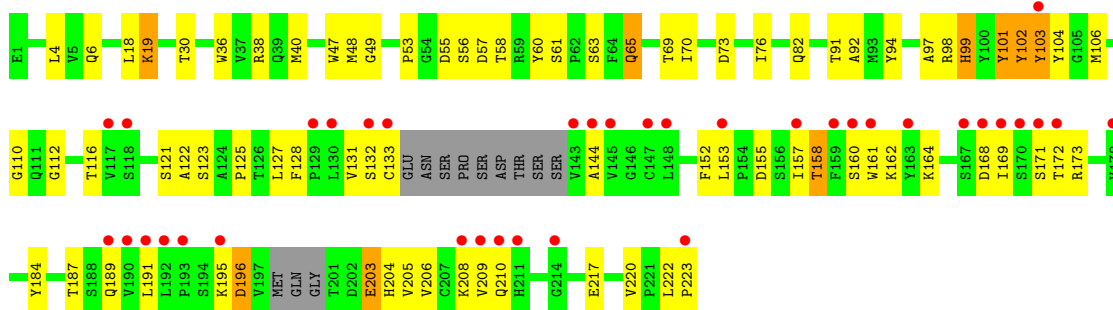
- Molecule 2: Immunoglobulin omega chain

Chain B: 



- Molecule 3: Immunoglobulin heavy chain

Chain H: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	71.50Å 71.50Å 217.93Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.70 59.78 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.7 (20.00-2.70) 99.6 (59.78-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.48 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.267 , 0.295 0.261 , 0.292	Depositor DCC
R_{free} test set	826 reflections (5.34%)	DCC
Wilson B-factor (Å ²)	65.4	Xtriage
Anisotropy	0.600	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 63.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 16299 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	3535	wwPDB-VP
Average B, all atoms (Å ²)	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.06% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

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

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	A	0.81	3/920 (0.3%)	0.76	0/1245
2	B	0.73	3/913 (0.3%)	0.62	0/1247
3	H	0.79	4/1685 (0.2%)	0.67	0/2289
All	All	0.78	10/3518 (0.3%)	0.68	0/4781

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	H	203	GLU	CD-OE1	9.97	1.36	1.25
3	H	203	GLU	CD-OE2	8.47	1.34	1.25
1	A	107	GLU	CB-CG	7.03	1.65	1.52
1	A	89	GLU	CD-OE2	6.83	1.33	1.25
2	B	87	GLU	CD-OE2	6.69	1.33	1.25
1	A	1	GLN	CB-CG	-6.52	1.34	1.52
3	H	168	ASP	CG-OD2	5.83	1.38	1.25
3	H	168	ASP	CG-OD1	5.78	1.38	1.25
2	B	88	GLU	CD-OE1	5.49	1.31	1.25
2	B	144	LEU	CB-CG	5.09	1.67	1.52

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Close contacts

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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the

chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	896	0	859	37	0
2	B	892	0	879	43	0
3	H	1639	0	1583	77	1
4	A	1	0	0	0	0
4	H	1	0	0	0	0
5	A	28	0	0	11	0
5	B	24	0	0	10	0
5	H	54	0	0	15	1
All	All	3535	0	3321	138	1

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 21.

All (138) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:80:TYR:HD1	5:A:319:HOH:O	1.45	1.00
1:A:14:LEU:HD11	2:B:71:SER:HA	1.49	0.94
3:H:102:TYR:O	3:H:104:TYR:N	2.09	0.85
1:A:14:LEU:HD12	1:A:14:LEU:H	1.42	0.84
3:H:57:ASP:HA	5:H:341:HOH:O	1.76	0.84
1:A:24:LEU:HB3	5:A:314:HOH:O	1.77	0.83
3:H:69:THR:HB	5:H:321:HOH:O	1.83	0.79
1:A:6:GLN:HE21	2:B:62:GLY:HA3	1.46	0.79
3:H:158:THR:HG23	3:H:210:GLN:HB2	1.66	0.78
1:A:47:ARG:NH1	5:A:327:HOH:O	2.17	0.77
2:B:129:SER:HB3	5:B:192:HOH:O	1.83	0.77
3:H:103:TYR:O	3:H:104:TYR:HD1	1.68	0.76
3:H:65:GLN:HB3	5:H:348:HOH:O	1.86	0.75
1:A:33:TYR:CE2	1:A:100:ALA:HB2	2.24	0.73
2:B:59:HIS:CE1	3:H:104:TYR:CZ	2.77	0.72
3:H:220:VAL:HG13	5:H:353:HOH:O	1.89	0.72
2:B:96:LEU:HB2	2:B:142:LEU:HB3	1.72	0.71
2:B:132:SER:H	3:H:173:ARG:HH12	1.37	0.70
3:H:99:HIS:CE1	3:H:103:TYR:O	2.45	0.70
1:A:102:SER:O	5:A:307:HOH:O	2.09	0.70
3:H:173:ARG:HG3	5:H:355:HOH:O	1.91	0.69
1:A:13:ALA:HA	5:B:180:HOH:O	1.92	0.69
2:B:59:HIS:CE1	3:H:104:TYR:CE2	2.81	0.68
2:B:103:PHE:CE2	2:B:106:GLY:HA2	2.29	0.67
1:A:78:ARG:HD3	1:A:80:TYR:OH	1.93	0.67

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:41:ARG:HD2	5:A:317:HOH:O	1.94	0.66
3:H:6:GLN:HE21	3:H:110:GLY:HA3	1.60	0.65
1:A:101:ARG:HA	3:H:103:TYR:OH	1.98	0.64
3:H:123:SER:HB3	5:H:317:HOH:O	1.96	0.64
5:B:198:HOH:O	3:H:128:PHE:CB	2.46	0.64
2:B:153:ARG:HH11	2:B:154:SER:HB2	1.61	0.64
2:B:97:VAL:HG12	2:B:99:LEU:CD1	2.29	0.63
2:B:59:HIS:NE2	3:H:104:TYR:CZ	2.67	0.62
1:A:6:GLN:NE2	2:B:62:GLY:HA3	2.13	0.61
3:H:122:ALA:HA	3:H:153:LEU:HB3	1.83	0.61
3:H:6:GLN:NE2	3:H:112:GLY:H	2.00	0.59
3:H:104:TYR:HB2	5:H:347:HOH:O	2.04	0.57
2:B:132:SER:H	3:H:173:ARG:NH1	1.99	0.57
3:H:99:HIS:ND1	3:H:103:TYR:O	2.37	0.57
2:B:86:SER:C	2:B:88:GLU:H	2.09	0.56
2:B:89:LEU:HD11	2:B:149:TRP:HD1	1.71	0.56
3:H:144:ALA:HB2	3:H:191:LEU:HG	1.87	0.56
3:H:101:TYR:CD2	3:H:102:TYR:HD2	2.24	0.55
3:H:38:ARG:HD3	3:H:40:MET:HG3	1.87	0.55
3:H:203:GLU:HA	5:H:310:HOH:O	2.06	0.55
2:B:147:GLU:O	2:B:151:SER:HB3	2.07	0.55
1:A:53:PHE:HB3	1:A:57:ASP:HB3	1.88	0.55
1:A:21:THR:HG23	1:A:80:TYR:CE2	2.42	0.55
3:H:217:GLU:HG2	5:H:330:HOH:O	2.06	0.54
1:A:33:TYR:CD2	1:A:100:ALA:HB2	2.42	0.54
1:A:14:LEU:N	5:B:180:HOH:O	2.40	0.54
3:H:155:ASP:HB2	3:H:184:TYR:CE2	2.42	0.54
3:H:101:TYR:CD2	3:H:102:TYR:CD2	2.96	0.54
3:H:121:SER:HB3	5:H:323:HOH:O	2.07	0.54
2:B:97:VAL:HG11	3:H:187:THR:HG21	1.91	0.53
3:H:40:MET:HG2	3:H:92:ALA:HB2	1.89	0.53
2:B:92:ASN:HA	2:B:146:PRO:HG2	1.90	0.52
2:B:131:GLN:OE1	2:B:137:ALA:HB2	2.09	0.52
3:H:102:TYR:C	3:H:104:TYR:H	2.11	0.52
2:B:96:LEU:O	2:B:141:TYR:HA	2.09	0.52
2:B:81:LEU:HD23	2:B:170:VAL:HG22	1.92	0.51
2:B:59:HIS:NE2	3:H:104:TYR:CE2	2.78	0.51
1:A:9:ALA:O	1:A:10:MET:HG3	2.10	0.51
5:B:196:HOH:O	3:H:173:ARG:HB3	2.10	0.51
3:H:205:VAL:O	3:H:220:VAL:HB	2.10	0.51
3:H:160:SER:OG	3:H:208:LYS:HB2	2.11	0.51
3:H:208:LYS:HG2	3:H:217:GLU:CB	2.41	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:57:VAL:O	2:B:58:THR:O	2.29	0.50
2:B:132:SER:N	3:H:173:ARG:HH12	2.07	0.50
2:B:97:VAL:HG12	2:B:99:LEU:HD11	1.93	0.50
1:A:62:PRO:HD2	5:A:316:HOH:O	2.11	0.50
1:A:33:TYR:CE2	2:B:57:VAL:HG21	2.47	0.50
2:B:131:GLN:HB3	3:H:173:ARG:NH1	2.26	0.49
3:H:161:TRP:HB3	3:H:169:ILE:HD12	1.95	0.49
1:A:30:ILE:HB	5:A:314:HOH:O	2.14	0.48
2:B:75:ALA:CB	5:B:190:HOH:O	2.62	0.48
3:H:47:TRP:HE3	3:H:61:SER:HB2	1.77	0.48
3:H:164:LYS:NZ	3:H:204:HIS:HE1	2.12	0.48
2:B:103:PHE:HE2	2:B:106:GLY:HA2	1.79	0.48
2:B:159:VAL:HB	2:B:166:VAL:CG1	2.44	0.48
1:A:55:GLN:O	1:A:58:LYS:HE3	2.14	0.48
1:A:30:ILE:HD12	5:A:314:HOH:O	2.14	0.47
2:B:58:THR:O	2:B:59:HIS:HB2	2.15	0.47
3:H:169:ILE:HG22	3:H:171:SER:H	1.78	0.47
3:H:6:GLN:HB3	5:H:335:HOH:O	2.14	0.47
2:B:160:MET:HE3	5:B:197:HOH:O	2.15	0.47
3:H:73:ASP:HB3	3:H:76:ILE:HG12	1.96	0.47
3:H:164:LYS:HZ3	3:H:204:HIS:HE1	1.62	0.47
2:B:114:ALA:HB2	2:B:119:ILE:HD11	1.97	0.47
3:H:49:GLY:HA3	3:H:70:ILE:CD1	2.45	0.46
3:H:4:LEU:O	3:H:110:GLY:HA2	2.14	0.46
3:H:131:VAL:HG12	3:H:132:SER:N	2.31	0.46
3:H:63:SER:N	5:H:345:HOH:O	2.49	0.46
1:A:20:LEU:HD12	1:A:20:LEU:N	2.30	0.46
1:A:101:ARG:CA	3:H:103:TYR:OH	2.63	0.46
3:H:196:ASP:HB2	5:H:337:HOH:O	2.15	0.46
2:B:128:PRO:HA	2:B:137:ALA:O	2.16	0.46
1:A:5:HIS:HA	5:A:322:HOH:O	2.15	0.46
1:A:51:ARG:HD3	3:H:102:TYR:CG	2.51	0.45
3:H:161:TRP:CD1	3:H:172:THR:HG21	2.51	0.45
3:H:127:LEU:HD11	3:H:209:VAL:HG22	1.98	0.45
2:B:138:ALA:HA	5:B:178:HOH:O	2.17	0.45
3:H:65:GLN:HB3	3:H:65:GLN:HE21	1.60	0.45
1:A:41:ARG:NH1	5:A:305:HOH:O	2.46	0.45
1:A:28:HIS:ND1	1:A:33:TYR:OH	2.40	0.44
2:B:56:SER:O	5:B:186:HOH:O	2.21	0.44
3:H:102:TYR:C	3:H:104:TYR:N	2.67	0.44
1:A:105:LYS:HE3	1:A:105:LYS:HB2	1.73	0.44
1:A:21:THR:HG23	1:A:80:TYR:HE2	1.81	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:H:38:ARG:HG3	3:H:94:TYR:CE2	2.52	0.44
3:H:60:TYR:HB2	5:H:348:HOH:O	2.18	0.44
3:H:19:LYS:CG	3:H:82:GLN:HG3	2.48	0.44
2:B:127:THR:HG22	2:B:128:PRO:HD2	1.99	0.43
3:H:36:TRP:O	3:H:48:MET:HB2	2.18	0.43
3:H:6:GLN:HE21	3:H:110:GLY:CA	2.27	0.43
1:A:41:ARG:NE	1:A:89:GLU:O	2.50	0.43
3:H:30:THR:HA	3:H:53:PRO:HB2	1.99	0.43
1:A:102:SER:C	5:A:307:HOH:O	2.55	0.43
3:H:208:LYS:HG2	3:H:217:GLU:HB2	2.00	0.43
2:B:59:HIS:CE1	3:H:104:TYR:CE1	3.06	0.43
3:H:82:GLN:HB3	5:H:321:HOH:O	2.19	0.43
3:H:133:CYS:SG	3:H:223:PRO:HB3	2.59	0.43
2:B:57:VAL:O	2:B:58:THR:C	2.57	0.42
1:A:18:ILE:HD13	1:A:20:LEU:HD11	2.01	0.42
2:B:59:HIS:HE1	3:H:104:TYR:CE1	2.37	0.42
3:H:157:ILE:HG13	3:H:210:GLN:O	2.19	0.42
1:A:1:GLN:HA	1:A:2:PRO:HD3	1.91	0.42
2:B:133:ASN:H	3:H:173:ARG:HH22	1.68	0.42
3:H:125:PRO:HA	3:H:152:PHE:HB3	2.01	0.42
1:A:17:THR:HA	1:A:83:ILE:O	2.20	0.41
2:B:76:THR:CG2	2:B:77:PRO:HD2	2.51	0.41
1:A:13:ALA:CA	5:B:180:HOH:O	2.61	0.41
3:H:162:LYS:O	3:H:205:VAL:HG23	2.21	0.41
3:H:91:THR:HG23	3:H:116:THR:HA	2.02	0.41
3:H:162:LYS:HB3	3:H:206:VAL:HB	2.03	0.40
3:H:55:ASP:O	3:H:56:SER:HB2	2.21	0.40
2:B:101:ASN:HB2	2:B:131:GLN:OE1	2.22	0.40
3:H:97:ALA:HB1	3:H:106:MET:HB3	2.03	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:H:58:THR:O	5:H:341:HOH:O[8_555]	2.16	0.04

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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	A	109/126 (86%)	97 (89%)	11 (10%)	1 (1%)	25	55
2	B	115/121 (95%)	98 (85%)	14 (12%)	3 (3%)	8	20
3	H	205/223 (92%)	181 (88%)	22 (11%)	2 (1%)	22	51
All	All	429/470 (91%)	376 (88%)	47 (11%)	6 (1%)	16	41

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	58	THR
3	H	103	TYR
1	A	62	PRO
2	B	57	VAL
3	H	195	LYS
2	B	152	ARG

5.3.2 Protein sidechains ⓘ

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	A	98/111 (88%)	90 (92%)	8 (8%)	17	36
2	B	104/107 (97%)	100 (96%)	4 (4%)	44	76
3	H	181/192 (94%)	170 (94%)	11 (6%)	26	54
All	All	383/410 (93%)	360 (94%)	23 (6%)	27	56

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	VAL
1	A	14	LEU
1	A	34	SER
1	A	41	ARG
1	A	47	ARG
1	A	62	PRO

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Mol	Chain	Res	Type
1	A	74	VAL
1	A	81	LEU
2	B	68	THR
2	B	90	GLN
2	B	127	THR
2	B	133	ASN
3	H	18	LEU
3	H	19	LYS
3	H	65	GLN
3	H	98	ARG
3	H	99	HIS
3	H	101	TYR
3	H	102	TYR
3	H	158	THR
3	H	189	GLN
3	H	196	ASP
3	H	222	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	6	GLN
1	A	44	HIS
2	B	72	GLN
2	B	133	ASN
3	H	6	GLN
3	H	65	GLN
3	H	99	HIS
3	H	189	GLN
3	H	204	HIS
3	H	213	ASN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	A	111/126 (88%)	0.40	2 (1%) 65 71	35, 50, 79, 86	3 (2%)
2	B	117/121 (96%)	1.25	27 (23%) 1 1	39, 94, 110, 115	5 (4%)
3	H	211/223 (94%)	1.00	37 (17%) 2 2	32, 60, 120, 122	4 (1%)
All	All	439/470 (93%)	0.92	66 (15%) 3 3	32, 62, 117, 122	12 (2%)

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	H	143	VAL	13.7
2	B	149	TRP	7.7
3	H	172	THR	7.6
2	B	155	TYR	7.5
3	H	163	TYR	6.3
2	B	81	LEU	5.8
2	B	96	LEU	5.3
2	B	79	VAL	5.0
3	H	191	LEU	4.9
3	H	192	LEU	4.8
2	B	156	SER	4.7
2	B	119	ILE	4.7
3	H	159	PHE	4.6
3	H	147	CYS	4.6
3	H	189	GLN	4.1
2	B	112	TRP	4.1
2	B	172	PRO	4.1
2	B	83	PRO	4.0
2	B	82	PHE	4.0
3	H	144	ALA	4.0
3	H	145	VAL	3.9
3	H	169	ILE	3.9
3	H	214	GLY	3.9

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Mol	Chain	Res	Type	RSRZ
3	H	161	TRP	3.9
3	H	190	VAL	3.8
2	B	80	THR	3.6
2	B	170	VAL	3.6
3	H	209	VAL	3.5
3	H	168	ASP	3.5
3	H	118	SER	3.4
3	H	210	GLN	3.4
3	H	129	PRO	3.3
3	H	133	CYS	3.3
1	A	100	ALA	3.2
3	H	103	TYR	3.2
3	H	208	LYS	3.1
2	B	110	VAL	3.1
3	H	167	SER	3.0
2	B	100	MET	2.9
3	H	211	HIS	2.9
3	H	153	LEU	2.9
3	H	117	VAL	2.6
2	B	121	GLN	2.6
2	B	158	GLN	2.6
3	H	178	VAL	2.6
2	B	120	THR	2.5
3	H	171	SER	2.5
2	B	118	PRO	2.5
2	B	90	GLN	2.5
2	B	97	VAL	2.5
3	H	130	LEU	2.5
3	H	195	LYS	2.4
2	B	157	CYS	2.4
3	H	148	LEU	2.4
2	B	154	SER	2.4
3	H	160	SER	2.4
2	B	171	ALA	2.4
3	H	132	SER	2.3
2	B	168	LYS	2.3
3	H	170	SER	2.2
2	B	146	PRO	2.2
3	H	157	ILE	2.2
2	B	169	THR	2.1
3	H	223	PRO	2.1
1	A	110	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
3	H	193	PRO	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(\AA^2)	Q<0.9
4	ZN	A	302	1/1	0.20	4.86	52,52,52,52	0
4	ZN	H	301	1/1	0.20	-0.32	53,53,53,53	0

6.5 Other polymers ⓘ

There are no such residues in this entry.