



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 4NEF / pdb_00004nef
Title : X-ray structure of human Aquaporin 2
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Deposited on : 2013-10-29
Resolution : 2.75 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

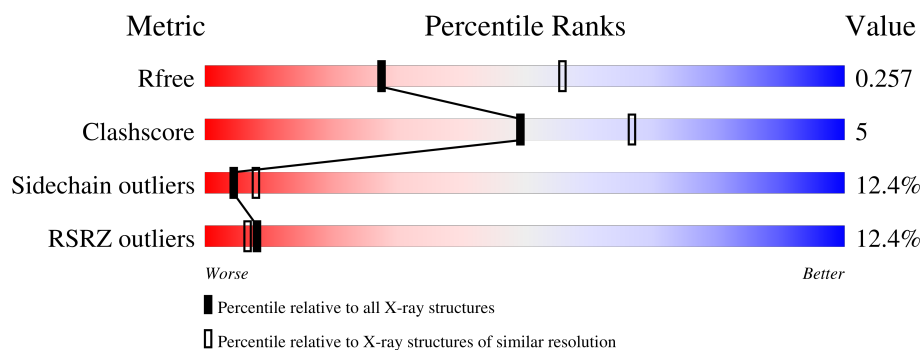
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.75 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}	180053	1009 (2.76-2.76)
Clashscore	190562	1044 (2.76-2.76)
Sidechain outliers	187428	1024 (2.76-2.76)
RSRZ outliers	180081	1009 (2.76-2.76)

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	A	242	8% 84% 14% ..
1	B	242	14% 82% 14% .
1	C	242	10% 83% 14% ..
1	D	242	15% 79% 15% ..

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6986 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 Aquaporin-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	239	Total	C	N	O	S	0	0	0
			1761	1150	296	309	6			
1	B	233	Total	C	N	O	S	0	0	0
			1715	1122	287	300	6			
1	C	236	Total	C	N	O	S	0	0	0
			1736	1135	290	305	6			
1	D	232	Total	C	N	O	S	0	0	0
			1712	1116	288	302	6			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	expression tag	UNP P41181
A	2	SER	-	expression tag	UNP P41181
A	242	PRO	-	expression tag	UNP P41181
B	1	GLY	-	expression tag	UNP P41181
B	2	SER	-	expression tag	UNP P41181
B	242	PRO	-	expression tag	UNP P41181
C	1	GLY	-	expression tag	UNP P41181
C	2	SER	-	expression tag	UNP P41181
C	242	PRO	-	expression tag	UNP P41181
D	1	GLY	-	expression tag	UNP P41181
D	2	SER	-	expression tag	UNP P41181
D	242	PRO	-	expression tag	UNP P41181

- Molecule 2 is CADMIUM ION (CCD ID: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Cd	0	0
			1	1		
2	D	1	Total	Cd	0	0
			1	1		

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total 1	Zn 1	0	0

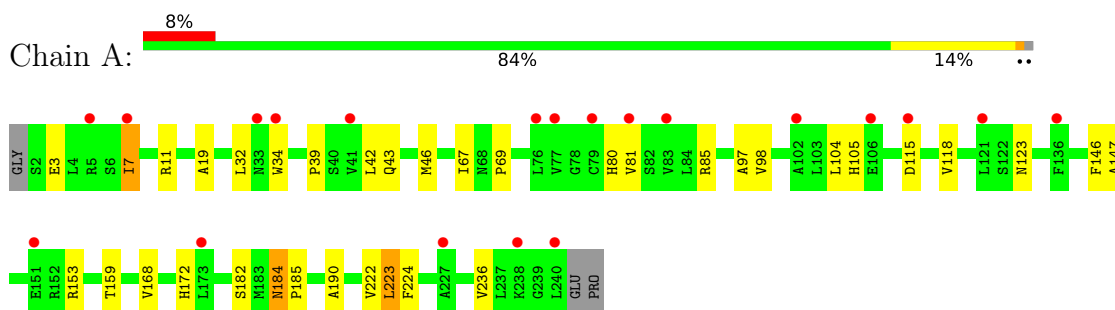
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	19	Total 19	O 19	0	0
4	B	14	Total 14	O 14	0	0
4	C	13	Total 13	O 13	0	0
4	D	13	Total 13	O 13	0	0

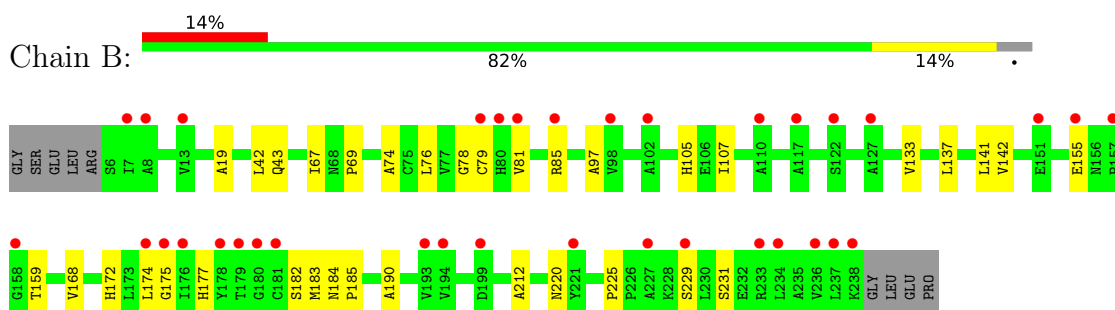
3 Residue-property plots [i](#)

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.

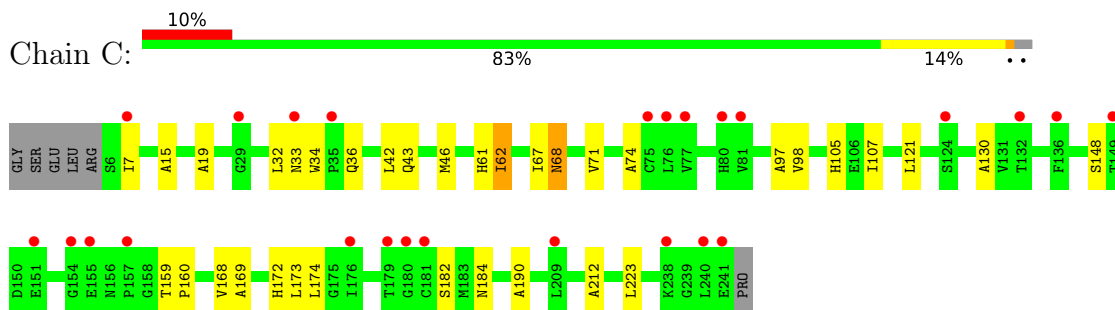
• Molecule 1: Aquaporin-2



• Molecule 1: Aquaporin-2

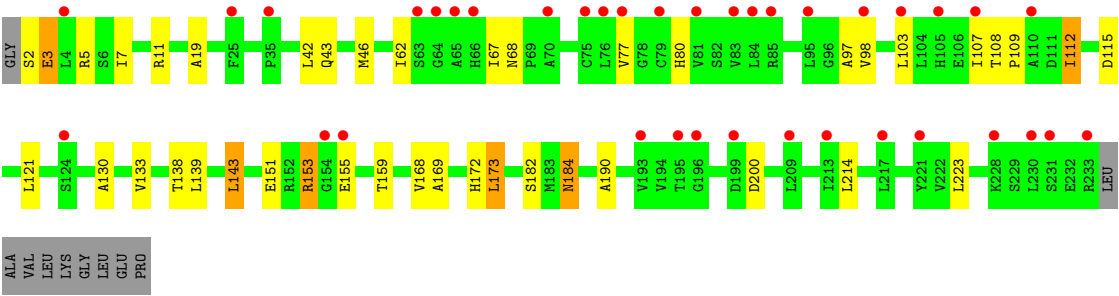


• Molecule 1: Aquaporin-2



• Molecule 1: Aquaporin-2





4 Data and refinement statistics

Property	Value	Source
Space group	P 42	Depositor
Cell constants a, b, c, α , β , γ	119.11Å 119.11Å 90.62Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.96 – 2.75 49.96 – 2.75	Depositor EDS
% Data completeness (in resolution range)	99.8 (49.96-2.75) 99.8 (49.96-2.75)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.51 (at 2.73Å)	Xtriage
Refinement program	BUSTER-TNT, BUSTER 2.10.0	Depositor
R, R_{free}	0.202 , 0.225 (Not available) , 0.257	Depositor DCC
R_{free} test set	1674 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	64.4	Xtriage
Anisotropy	0.067	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 94.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.036 for h,-k,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	6986	wwPDB-VP
Average B, all atoms (Å ²)	91.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.46% 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: CD, 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	0/1802	1.48	10/2463 (0.4%)
1	B	0.83	0/1756	1.49	7/2402 (0.3%)
1	C	0.83	0/1777	1.50	9/2430 (0.4%)
1	D	0.82	0/1753	1.48	8/2397 (0.3%)
All	All	0.82	0/7088	1.49	34/9692 (0.4%)

There are no bond length outliers.

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	184	ASN	CA-CB-CG	6.16	118.76	112.60
1	D	223	LEU	N-CA-C	5.98	117.67	111.03
1	C	223	LEU	N-CA-C	5.83	117.50	111.03
1	D	184	ASN	CA-CB-CG	5.74	118.34	112.60
1	A	223	LEU	N-CA-C	5.64	117.29	111.03
1	C	62	ILE	CB-CA-C	5.57	116.95	110.88
1	C	36	GLN	N-CA-C	-5.55	104.93	112.26
1	C	68	ASN	CA-CB-CG	5.53	118.13	112.60
1	C	105	HIS	CA-C-N	5.49	127.90	120.38
1	C	105	HIS	C-N-CA	5.49	127.90	120.38
1	B	105	HIS	CA-C-N	5.48	127.62	120.28
1	B	105	HIS	C-N-CA	5.48	127.62	120.28
1	A	224	PHE	CA-CB-CG	5.40	119.20	113.80
1	A	105	HIS	CA-C-N	5.39	127.77	120.38
1	A	105	HIS	C-N-CA	5.39	127.77	120.38
1	D	3	GLU	CA-C-N	5.27	127.34	120.28
1	D	3	GLU	C-N-CA	5.27	127.34	120.28
1	D	115	ASP	CA-CB-CG	5.26	117.86	112.60
1	C	159	THR	CB-CA-C	5.26	115.78	109.31
1	A	7	ILE	N-CA-CB	5.25	116.33	110.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	143	LEU	CA-C-N	5.16	127.46	120.44
1	D	143	LEU	C-N-CA	5.16	127.46	120.44
1	C	174	LEU	CA-C-N	5.15	125.69	119.98
1	C	174	LEU	C-N-CA	5.15	125.69	119.98
1	B	174	LEU	CA-C-N	5.12	126.54	120.14
1	B	174	LEU	C-N-CA	5.12	126.54	120.14
1	A	3	GLU	CA-C-N	5.11	127.44	120.54
1	A	3	GLU	C-N-CA	5.11	127.44	120.54
1	B	78	GLY	N-CA-C	5.11	114.86	110.21
1	A	236	VAL	CA-C-N	5.09	127.36	120.38
1	A	236	VAL	C-N-CA	5.09	127.36	120.38
1	B	155	GLU	CA-C-N	5.09	126.45	120.09
1	B	155	GLU	C-N-CA	5.09	126.45	120.09
1	D	68	ASN	CA-CB-CG	5.00	117.61	112.60

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	A	1761	0	1805	25	0
1	B	1715	0	1757	21	0
1	C	1736	0	1775	23	0
1	D	1712	0	1741	21	0
2	A	1	0	0	0	0
2	D	1	0	0	0	0
3	A	1	0	0	0	0
4	A	19	0	0	0	0
4	B	14	0	0	0	0
4	C	13	0	0	0	0
4	D	13	0	0	0	0
All	All	6986	0	7078	75	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 5.

All (75) 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:A:222:VAL:O	1:D:11:ARG:HD3	1.97	0.64
1:C:32:LEU:HD12	1:C:33:ASN:H	1.65	0.61
1:B:42:LEU:HB2	1:C:43:GLN:HG3	1.83	0.60
1:B:69:PRO:HD2	1:B:185:PRO:HD2	1.87	0.57
1:B:81:VAL:HG23	1:B:85:ARG:HD2	1.89	0.54
1:D:112:ILE:O	1:D:112:ILE:HD13	2.08	0.54
1:A:80:HIS:HE1	1:A:146:PHE:HE1	1.56	0.53
1:A:223:LEU:HB3	1:D:62:ILE:HD13	1.91	0.52
1:A:42:LEU:HB2	1:D:43:GLN:HG3	1.92	0.52
1:D:19:ALA:HB1	1:D:67:ILE:HG12	1.93	0.50
1:A:19:ALA:HB1	1:A:67:ILE:HG12	1.93	0.50
1:A:159:THR:HG21	1:D:159:THR:HG22	1.94	0.50
1:B:43:GLN:HG3	1:D:42:LEU:HB2	1.94	0.50
1:B:142:VAL:HG21	1:B:212:ALA:HA	1.94	0.49
1:A:46:MET:HG2	1:C:42:LEU:HD11	1.94	0.49
1:C:34:TRP:CD1	1:C:34:TRP:N	2.79	0.49
1:A:80:HIS:CE1	1:A:146:PHE:HE1	2.31	0.48
1:A:182:SER:C	1:A:184:ASN:H	2.22	0.48
1:D:169:ALA:O	1:D:173:LEU:HD22	2.13	0.48
1:D:168:VAL:O	1:D:172:HIS:HD2	1.96	0.48
1:A:81:VAL:HG13	1:A:85:ARG:HB3	1.95	0.48
1:C:74:ALA:HB2	1:C:212:ALA:HB1	1.96	0.48
1:C:168:VAL:O	1:C:172:HIS:HD2	1.95	0.48
1:B:159:THR:HG22	1:D:159:THR:HG21	1.94	0.48
1:C:34:TRP:CD1	1:C:34:TRP:H	2.32	0.48
1:D:3:GLU:O	1:D:7:ILE:HG13	2.14	0.48
1:B:19:ALA:HB1	1:B:67:ILE:HG12	1.95	0.47
1:B:168:VAL:O	1:B:172:HIS:HD2	1.97	0.47
1:C:19:ALA:HB1	1:C:67:ILE:HG12	1.95	0.47
1:D:2:SER:HB3	1:D:5:ARG:HG3	1.95	0.47
1:A:43:GLN:HG3	1:C:42:LEU:HB2	1.97	0.46
1:A:168:VAL:O	1:A:172:HIS:HD2	1.98	0.46
1:B:74:ALA:HB2	1:B:212:ALA:HB1	1.97	0.46
1:C:61:HIS:H	1:C:61:HIS:CD2	2.33	0.46
1:A:69:PRO:HD2	1:A:185:PRO:HD2	1.98	0.46
1:B:133:VAL:HG22	1:C:107:ILE:HD13	1.96	0.46
1:B:182:SER:C	1:B:184:ASN:H	2.24	0.46
1:C:148:SER:HB3	1:C:160:PRO:HD2	1.98	0.45
1:A:34:TRP:HB3	1:A:39:PRO:HD3	1.99	0.44
1:D:153:ARG:O	1:D:153:ARG:HG3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:220:ASN:O	1:B:225:PRO:HA	2.17	0.44
1:B:137:LEU:HD21	1:B:175:GLY:HA3	1.99	0.44
1:C:98:VAL:HG12	1:C:190:ALA:HA	2.00	0.44
1:C:169:ALA:O	1:C:173:LEU:HD22	2.18	0.44
1:B:42:LEU:HD11	1:C:46:MET:HG2	2.00	0.44
1:A:80:HIS:HE1	1:A:146:PHE:CE1	2.36	0.44
1:B:229:SER:C	1:B:231:SER:H	2.26	0.43
1:A:97:ALA:HB1	1:A:190:ALA:HB2	2.01	0.43
1:A:147:ALA:O	1:A:153:ARG:HD3	2.17	0.43
1:A:115:ASP:HB2	1:A:118:VAL:HG22	2.01	0.43
1:A:32:LEU:HD21	1:A:104:LEU:HD21	2.01	0.43
1:B:177:HIS:CG	1:C:33:ASN:HB3	2.53	0.43
1:C:182:SER:C	1:C:184:ASN:H	2.27	0.43
1:D:121:LEU:HD21	1:D:130:ALA:CB	2.48	0.42
1:A:7:ILE:H	1:A:7:ILE:HG13	1.68	0.42
1:C:121:LEU:HD21	1:C:130:ALA:CB	2.49	0.42
1:B:76:LEU:HA	1:B:81:VAL:CG1	2.50	0.42
1:B:79:CYS:C	1:B:81:VAL:H	2.27	0.42
1:C:121:LEU:HD21	1:C:130:ALA:HB2	2.01	0.42
1:A:98:VAL:HG12	1:A:190:ALA:HA	2.02	0.42
1:A:7:ILE:O	1:A:11:ARG:HG3	2.19	0.42
1:D:121:LEU:HD21	1:D:130:ALA:HB2	2.00	0.42
1:D:182:SER:C	1:D:184:ASN:H	2.27	0.42
1:B:141:LEU:HD22	1:B:183:MET:HE2	2.02	0.41
1:C:15:ALA:HB2	1:C:62:ILE:HD11	2.01	0.41
1:B:107:ILE:HD13	1:D:133:VAL:HG22	2.03	0.41
1:C:7:ILE:H	1:C:7:ILE:HG13	1.74	0.41
1:D:98:VAL:HG12	1:D:190:ALA:HA	2.03	0.41
1:A:80:HIS:CE1	1:A:146:PHE:CE1	3.09	0.41
1:D:97:ALA:HB1	1:D:190:ALA:HB2	2.01	0.41
1:C:68:ASN:HB3	1:C:71:VAL:HB	2.01	0.41
1:B:97:ALA:HB1	1:B:190:ALA:HB2	2.02	0.41
1:C:97:ALA:HB1	1:C:190:ALA:HB2	2.03	0.41
1:A:42:LEU:HD11	1:D:46:MET:HG2	2.02	0.40
1:A:123:ASN:O	1:D:109:PRO:HG3	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

There are no protein backbone outliers to report in this entry.

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	D	121/184 (66%)	106 (88%)	15 (12%)	4 8

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	77	VAL
1	D	80	HIS
1	D	103	LEU
1	D	107	ILE
1	D	108	THR
1	D	112	ILE
1	D	138	THR
1	D	139	LEU
1	D	143	LEU
1	D	151	GLU
1	D	153	ARG
1	D	155	GLU
1	D	173	LEU
1	D	200	ASP
1	D	214	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	D	105	HIS
1	D	119	ASN
1	D	172	HIS

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Mol	Chain	Res	Type
1	D	220	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 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.

No monomer is involved in short contacts.

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

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	239/242 (98%)	0.51	20 (8%) 17 17	38, 88, 142, 183	0
1	B	233/242 (96%)	0.87	35 (15%) 5 5	35, 90, 145, 235	1 (0%)
1	C	236/242 (97%)	0.61	25 (10%) 11 10	43, 81, 124, 193	0
1	D	232/242 (95%)	0.95	37 (15%) 5 4	38, 91, 133, 190	2 (0%)
All	All	940/968 (97%)	0.74	117 (12%) 8 7	35, 88, 137, 235	3 (0%)

All (117) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	79	CYS	14.4
1	B	79	CYS	11.9
1	D	75	CYS	10.8
1	D	64	GLY	6.2
1	C	155	GLU	6.2
1	D	84	LEU	5.9
1	D	66	HIS	5.9
1	B	8	ALA	5.8
1	B	158	GLY	5.8
1	B	175	GLY	5.1
1	A	227	ALA	4.8
1	D	154	GLY	4.6
1	D	85	ARG	4.6
1	B	178	TYR	4.6
1	D	65	ALA	4.5
1	B	81	VAL	4.3
1	D	4	LEU	4.2
1	B	151	GLU	4.2
1	B	181	CYS	4.0
1	B	80	HIS	4.0
1	C	33	ASN	3.9

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Mol	Chain	Res	Type	RSRZ
1	B	233	ARG	3.8
1	B	155	GLU	3.8
1	A	79	CYS	3.7
1	C	157	PRO	3.7
1	B	180	GLY	3.6
1	B	174	LEU	3.6
1	B	179	THR	3.6
1	A	106	GLU	3.5
1	D	193	VAL	3.5
1	A	33	ASN	3.5
1	C	238	LYS	3.5
1	A	240	LEU	3.5
1	C	77	VAL	3.5
1	B	194	VAL	3.4
1	B	234	LEU	3.4
1	C	81	VAL	3.3
1	C	29	GLY	3.2
1	C	154	GLY	3.2
1	B	102	ALA	3.1
1	D	83	VAL	3.1
1	C	149	THR	3.1
1	D	124	SER	3.0
1	D	217	LEU	3.0
1	B	13	VAL	3.0
1	B	176	ILE	3.0
1	D	230	LEU	3.0
1	D	196	GLY	2.9
1	A	7	ILE	2.9
1	D	221	TYR	2.8
1	A	115	ASP	2.8
1	D	103	LEU	2.8
1	A	102	ALA	2.8
1	C	240	LEU	2.8
1	D	155	GLU	2.8
1	D	231	SER	2.8
1	B	199	ASP	2.8
1	D	98	VAL	2.7
1	B	193	VAL	2.7
1	D	77	VAL	2.7
1	B	157	PRO	2.7
1	A	41	VAL	2.6
1	C	76	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	236	VAL	2.6
1	D	107	ILE	2.6
1	D	209	LEU	2.6
1	C	180	GLY	2.5
1	C	80	HIS	2.5
1	A	83	VAL	2.5
1	D	199	ASP	2.5
1	C	179	THR	2.5
1	C	241	GLU	2.5
1	A	77	VAL	2.5
1	C	136	PHE	2.5
1	D	25	PHE	2.5
1	D	228	LYS	2.4
1	A	151	GLU	2.4
1	A	136	PHE	2.4
1	B	117	ALA	2.4
1	D	213	ILE	2.3
1	C	35	PRO	2.3
1	C	181	CYS	2.3
1	B	85	ARG	2.3
1	A	81	VAL	2.3
1	B	7	ILE	2.3
1	B	110	ALA	2.3
1	B	127	ALA	2.2
1	B	98	VAL	2.2
1	D	76	LEU	2.2
1	D	95	LEU	2.2
1	A	238	LYS	2.2
1	B	238	LYS	2.2
1	C	7	ILE	2.2
1	C	176	ILE	2.2
1	B	227	ALA	2.2
1	C	132	THR	2.2
1	D	233	ARG	2.2
1	D	35	PRO	2.2
1	A	173	LEU	2.2
1	C	124	SER	2.2
1	D	110	ALA	2.2
1	A	5	ARG	2.2
1	C	75	CYS	2.2
1	B	221	TYR	2.2
1	D	70	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	229	SER	2.1
1	C	151	GLU	2.1
1	A	121	LEU	2.1
1	B	237	LEU	2.1
1	B	122	SER	2.1
1	D	105	HIS	2.1
1	D	81	VAL	2.1
1	D	195	THR	2.1
1	C	209	LEU	2.1
1	D	63	SER	2.0
1	A	34	TRP	2.0
1	A	76	LEU	2.0

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 oligosaccharides 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($\text{\AA}^2$)	Q<0.9
3	ZN	A	302	1/1	0.92	0.15	77,77,77,77	1
2	CD	D	301	1/1	0.94	0.06	87,87,87,87	1
2	CD	A	301	1/1	0.99	0.04	48,48,48,48	0

6.5 Other polymers [i](#)

There are no such residues in this entry.