



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:59 PM GMT

PDB ID : 4NEF
Title : X-ray structure of human Aquaporin 2
Authors : Frick, A.; Eriksson, U.; Mattia, F.D.; Oberg, F.; Hedfalk, K.; Neutze, R.; Grip, W.D.; Deen, P.M.T.; Tornroth-horsefeld, S.
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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

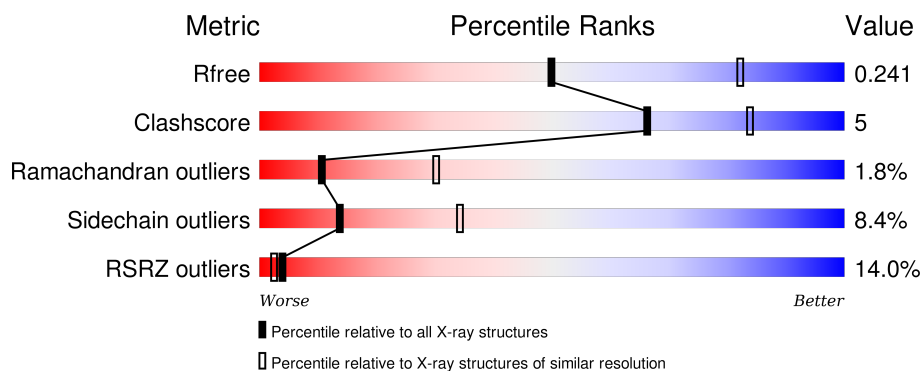
1 Overall quality at a glance

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}	91344	3340 (2.80-2.72)
Clashscore	102246	3829 (2.80-2.72)
Ramachandran outliers	100387	3767 (2.80-2.72)
Sidechain outliers	100360	3770 (2.80-2.72)
RSRZ outliers	91569	3352 (2.80-2.72)

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. 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	<div> <div>11%</div> <div>80% 17% ..</div> </div>
1	B	242	<div> <div>14%</div> <div>81% 15% ..</div> </div>
1	C	242	<div> <div>7%</div> <div>81% 13% ..</div> </div>
1	D	242	<div> <div>23%</div> <div>78% 16% ..</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	CD	A	301	-	-	-	X

2 Entry composition [i](#)

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 (three-letter code: 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 (three-letter code: ZN) (formula: Zn).

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

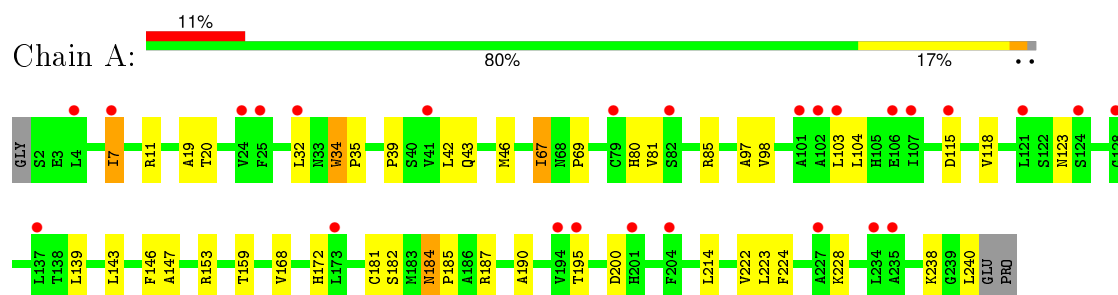
- Molecule 4 is water.

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

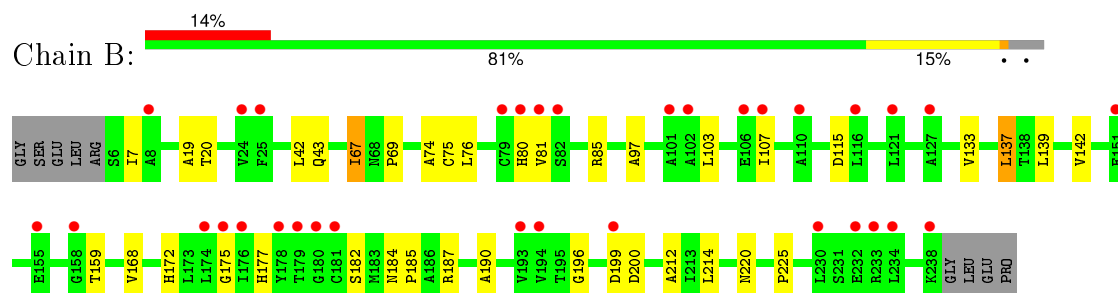
3 Residue-property plots

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.

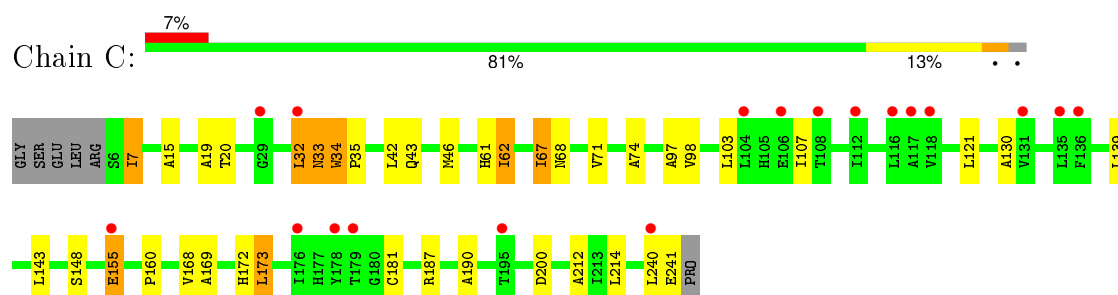
- Molecule 1: Aquaporin-2



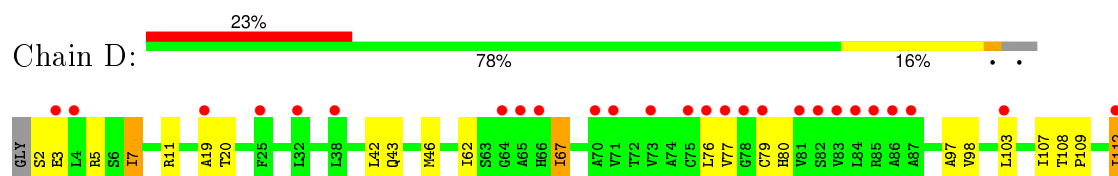
- Molecule 1: Aquaporin-2

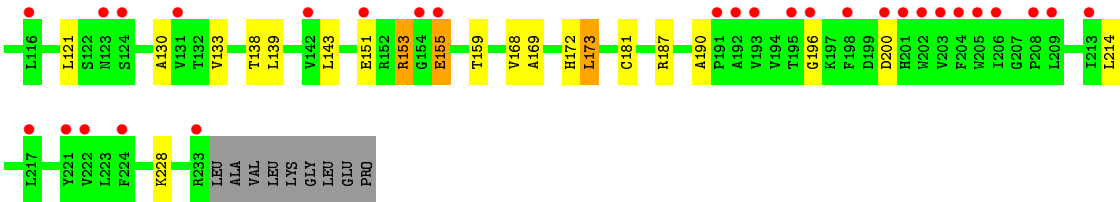


- Molecule 1: Aquaporin-2



- 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 72.12 – 2.75	Depositor EDS
% Data completeness (in resolution range)	99.8 (49.96-2.75) 99.8 (72.12-2.75)	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 2.10.0	Depositor
R, R_{free}	0.202 , 0.225 0.212 , 0.241	Depositor DCC
R_{free} test set	1674 reflections (5.34%)	DCC
Wilson B-factor (Å ²)	64.4	Xtriage
Anisotropy	0.067	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 102.6	EDS
Estimated twinning fraction	0.036 for h,-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 33054 reflections (0.003%)	Xtriage
F_o, F_c correlation	0.91	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, 0.375 respectively for untwinned datasets, and 0.333, 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: ZN, CD

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	0.46	0/1802	0.67	0/2463
1	B	0.47	0/1756	0.65	0/2402
1	C	0.47	0/1777	0.70	0/2430
1	D	0.47	0/1753	0.68	0/2397
All	All	0.47	0/7088	0.67	0/9692

There are no bond length outliers.

There are no bond angle outliers.

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	18	0
1	C	1736	0	1775	21	0
1	D	1712	0	1741	20	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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	C	13	0	0	0	0
4	D	13	0	0	0	0
All	All	6986	0	7078	69	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 (69) 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:D:112:ILE:HD13	1:D:112:ILE:O	2.08	0.54
1:B:81:VAL:HG23	1:B:85:ARG:HD2	1.89	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:N	1:C:34:TRP:CD1	2.79	0.49
1:A:80:HIS:CE1	1:A:146:PHE:HE1	2.31	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:D:3:GLU:O	1:D:7:ILE:HG13	2.14	0.48
1:B:168:VAL:O	1:B:172:HIS:HD2	1.97	0.47
1:B:19:ALA:HB1	1:B:67:ILE:HG12	1.95	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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
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:A:182:SER:C	1:A:184:ASN:H	2.22	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:B:177:HIS:CG	1:C:33:ASN:HB3	2.53	0.43
1:A:32:LEU:HD21	1:A:104:LEU:HD21	2.01	0.43
1:D:121:LEU:HD21	1:D:130:ALA:CB	2.48	0.42
1:A:7:ILE:HG13	1:A:7:ILE:H	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: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:D:121:LEU:HD21	1:D:130:ALA:HB2	2.00	0.42
1:A:7:ILE:O	1:A:11:ARG:HG3	2.19	0.42
1:C:15:ALA:HB2	1:C:62:ILE:HD11	2.01	0.41
1:D:98:VAL:HG12	1:D:190:ALA:HA	2.03	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:B:182:SER:C	1:B:184:ASN:H	2.24	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 [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	A	237/242 (98%)	223 (94%)	11 (5%)	3 (1%)	15	40
1	B	231/242 (96%)	210 (91%)	18 (8%)	3 (1%)	15	40
1	C	234/242 (97%)	217 (93%)	12 (5%)	5 (2%)	9	25
1	D	230/242 (95%)	216 (94%)	8 (4%)	6 (3%)	7	19
All	All	932/968 (96%)	866 (93%)	49 (5%)	17 (2%)	11	30

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	35	PRO
1	C	33	ASN
1	C	35	PRO
1	D	155	GLU
1	B	196	GLY
1	C	155	GLU
1	C	181	CYS
1	D	79	CYS
1	D	80	HIS
1	D	196	GLY
1	A	181	CYS
1	D	181	CYS
1	B	80	HIS
1	B	67	ILE
1	C	67	ILE
1	A	67	ILE
1	D	67	ILE

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	A	182/184 (99%)	167 (92%)	15 (8%)	14	35
1	B	177/184 (96%)	166 (94%)	11 (6%)	23	51
1	C	179/184 (97%)	164 (92%)	15 (8%)	14	34
1	D	177/184 (96%)	158 (89%)	19 (11%)	8	21
All	All	715/736 (97%)	655 (92%)	60 (8%)	14	34

All (60) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	ILE
1	A	20	THR
1	A	34	TRP
1	A	103	LEU
1	A	139	LEU
1	A	143	LEU
1	A	184	ASN
1	A	187	ARG
1	A	195	THR
1	A	200	ASP
1	A	214	LEU
1	A	224	PHE
1	A	228	LYS
1	A	238	LYS
1	A	240	LEU
1	B	7	ILE
1	B	20	THR
1	B	75	CYS
1	B	103	LEU
1	B	115	ASP
1	B	137	LEU
1	B	139	LEU
1	B	187	ARG
1	B	199	ASP
1	B	200	ASP
1	B	214	LEU
1	C	7	ILE
1	C	20	THR

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Mol	Chain	Res	Type
1	C	32	LEU
1	C	34	TRP
1	C	62	ILE
1	C	103	LEU
1	C	139	LEU
1	C	143	LEU
1	C	155	GLU
1	C	173	LEU
1	C	187	ARG
1	C	200	ASP
1	C	214	LEU
1	C	240	LEU
1	C	241	GLU
1	D	7	ILE
1	D	20	THR
1	D	76	LEU
1	D	77	VAL
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	187	ARG
1	D	200	ASP
1	D	214	LEU
1	D	228	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	80	HIS
1	A	93	GLN
1	A	105	HIS
1	A	172	HIS
1	A	184	ASN
1	B	119	ASN

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Mol	Chain	Res	Type
1	B	172	HIS
1	B	177	HIS
1	C	61	HIS
1	C	93	GLN
1	C	105	HIS
1	C	172	HIS
1	C	177	HIS
1	D	119	ASN
1	D	172	HIS
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 carbohydrates 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

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%)	0.94	26 (10%) 7 4	38, 88, 142, 183	0
1	B	233/242 (96%)	0.97	33 (14%) 4 2	42, 90, 145, 235	1 (0%)
1	C	236/242 (97%)	0.80	18 (7%) 17 11	43, 81, 124, 193	0
1	D	232/242 (95%)	1.33	55 (23%) 1 1	38, 91, 133, 190	2 (0%)
All	All	940/968 (97%)	1.01	132 (14%) 4 2	38, 88, 137, 235	3 (0%)

All (132) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	154	GLY	10.5
1	D	84	LEU	8.9
1	B	79	CYS	6.9
1	D	82	SER	6.5
1	D	85	ARG	6.2
1	D	83	VAL	5.9
1	C	112	ILE	5.7
1	D	79	CYS	5.4
1	D	193	VAL	5.1
1	D	206	ILE	4.9
1	A	106	GLU	4.8
1	D	204	PHE	4.7
1	D	81	VAL	4.6
1	B	238	LYS	4.5
1	B	178	TYR	4.5
1	B	81	VAL	4.3
1	D	196	GLY	4.2
1	D	203	VAL	4.2
1	D	217	LEU	4.0
1	D	221	TYR	4.0
1	D	201	HIS	3.9

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Mol	Chain	Res	Type	RSRZ
1	B	175	GLY	3.8
1	A	227	ALA	3.8
1	A	234	LEU	3.7
1	B	110	ALA	3.7
1	D	4	LEU	3.7
1	B	107	ILE	3.6
1	D	75	CYS	3.6
1	B	8	ALA	3.6
1	B	180	GLY	3.6
1	A	115	ASP	3.5
1	B	25	PHE	3.5
1	C	155	GLU	3.5
1	D	112	ILE	3.5
1	D	76	LEU	3.4
1	D	66	HIS	3.4
1	D	103	LEU	3.3
1	B	234	LEU	3.3
1	D	151	GLU	3.3
1	D	131	VAL	3.3
1	C	135	LEU	3.3
1	B	176	ILE	3.2
1	B	106	GLU	3.2
1	B	24	VAL	3.2
1	A	124	SER	3.2
1	A	235	ALA	3.2
1	A	24	VAL	3.2
1	D	77	VAL	3.2
1	C	118	VAL	3.1
1	D	233	ARG	3.1
1	B	194	VAL	3.1
1	C	116	LEU	3.1
1	D	198	PHE	3.1
1	C	117	ALA	3.0
1	D	202	TRP	3.0
1	B	174	LEU	3.0
1	B	80	HIS	3.0
1	B	151	GLU	3.0
1	D	209	LEU	2.9
1	D	25	PHE	2.9
1	B	155	GLU	2.9
1	D	70	ALA	2.9
1	C	106	GLU	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	127	ALA	2.9
1	A	103	LEU	2.8
1	A	79	CYS	2.8
1	D	222	VAL	2.8
1	B	232	GLU	2.8
1	A	41	VAL	2.8
1	D	3	GLU	2.7
1	D	87	ALA	2.7
1	A	25	PHE	2.7
1	A	195	THR	2.7
1	B	233	ARG	2.7
1	A	201	HIS	2.7
1	B	181	CYS	2.6
1	D	19	ALA	2.6
1	C	179	THR	2.6
1	C	240	LEU	2.6
1	D	64	GLY	2.6
1	A	107	ILE	2.5
1	C	32	LEU	2.5
1	C	131	VAL	2.5
1	D	213	ILE	2.5
1	D	195	THR	2.5
1	B	179	THR	2.5
1	B	102	ALA	2.5
1	D	200	ASP	2.4
1	A	82	SER	2.4
1	D	224	PHE	2.4
1	D	32	LEU	2.4
1	D	191	PRO	2.4
1	D	192	ALA	2.4
1	C	195	THR	2.4
1	D	124	SER	2.4
1	A	101	ALA	2.3
1	A	137	LEU	2.3
1	D	65	ALA	2.3
1	A	7	ILE	2.3
1	C	29	GLY	2.3
1	D	78	GLY	2.3
1	C	104	LEU	2.3
1	B	101	ALA	2.3
1	A	102	ALA	2.3
1	A	204	PHE	2.3

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Mol	Chain	Res	Type	RSRZ
1	D	142	VAL	2.3
1	A	128	GLY	2.2
1	A	194	VAL	2.2
1	B	193	VAL	2.2
1	A	32	LEU	2.2
1	B	116	LEU	2.2
1	B	199	ASP	2.2
1	D	155	GLU	2.2
1	A	121	LEU	2.2
1	A	173	LEU	2.2
1	C	136	PHE	2.2
1	D	73	VAL	2.2
1	D	71	VAL	2.1
1	D	208	PRO	2.1
1	D	86	ALA	2.1
1	D	205	TRP	2.1
1	D	123	ASN	2.1
1	C	178	TYR	2.1
1	B	121	LEU	2.1
1	B	158	GLY	2.1
1	C	108	THR	2.1
1	A	4	LEU	2.1
1	D	38	LEU	2.1
1	B	230	LEU	2.0
1	C	176	ILE	2.0
1	B	82	SER	2.0
1	D	116	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 carbohydrates 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. 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	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	CD	A	301	1/1	0.99	0.26	2.66	48,48,48,48	0
2	CD	D	301	1/1	0.94	0.21	-0.74	87,87,87,87	1
3	ZN	A	302	1/1	0.93	0.29	-	77,77,77,77	1

6.5 Other polymers [i](#)

There are no such residues in this entry.