



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 12:14 AM UTC

PDB ID : 4LLO / pdb_00004llo
Title : Structure of the eag domain-CNBHD complex of the mouse EAG1 channel
Authors : Haitin, Y.; Carlson, A.E.; Zagotta, W.N.
Deposited on : 2013-07-09
Resolution : 2.00 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
Xtrriage (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

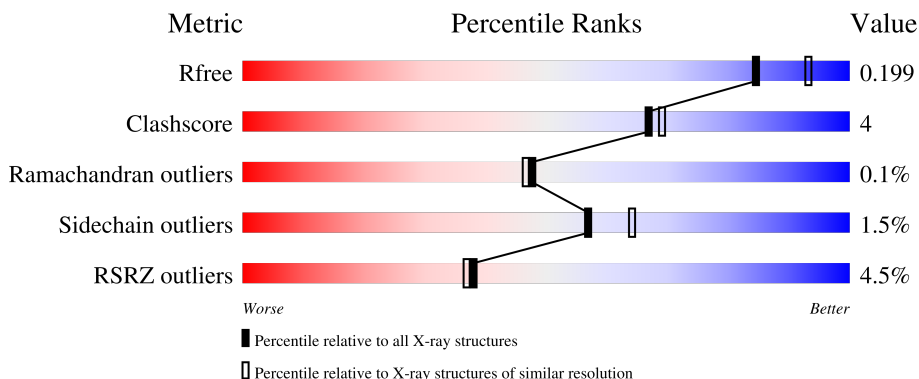
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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.



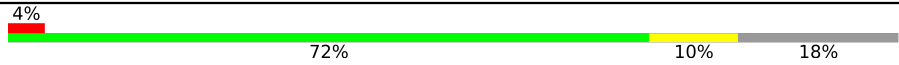

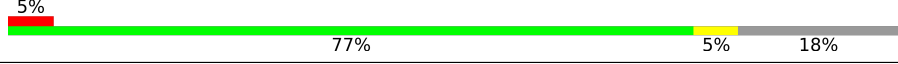
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	177	 90% 7%
1	C	177	 85% 9% 5%
1	E	177	 85% 11%
1	G	177	 90% 6% 5%
2	B	134	 84% 7% 10%

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Mol	Chain	Length	Quality of chain
2	D	134	 4% 72% 10% 18%
2	F	134	 8% 80% 10% 10%
2	H	134	 5% 77% 5% 18%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9889 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 Potassium voltage-gated channel subfamily H member 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	173	1328	845	233	240	10	0	0	0
1	C	168	1291	825	226	230	10	0	0	0
1	E	171	1328	844	235	239	10	0	0	0
1	G	169	1304	831	227	236	10	0	0	0

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	548	GLY	-	expression tag	UNP Q60603
A	549	ALA	-	expression tag	UNP Q60603
A	550	MET	-	expression tag	UNP Q60603
A	551	GLY	-	expression tag	UNP Q60603
C	548	GLY	-	expression tag	UNP Q60603
C	549	ALA	-	expression tag	UNP Q60603
C	550	MET	-	expression tag	UNP Q60603
C	551	GLY	-	expression tag	UNP Q60603
E	548	GLY	-	expression tag	UNP Q60603
E	549	ALA	-	expression tag	UNP Q60603
E	550	MET	-	expression tag	UNP Q60603
E	551	GLY	-	expression tag	UNP Q60603
G	548	GLY	-	expression tag	UNP Q60603
G	549	ALA	-	expression tag	UNP Q60603
G	550	MET	-	expression tag	UNP Q60603
G	551	GLY	-	expression tag	UNP Q60603

- Molecule 2 is a protein called Potassium voltage-gated channel subfamily H member 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	121	947	613	154	173	7	0	0	0
2	D	110	856	555	138	156	7	0	0	0
2	F	121	959	618	156	178	7	0	0	0
2	H	110	858	556	137	158	7	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	3	GLY	-	expression tag	UNP Q60603
B	4	ALA	-	expression tag	UNP Q60603
B	5	MET	-	expression tag	UNP Q60603
D	3	GLY	-	expression tag	UNP Q60603
D	4	ALA	-	expression tag	UNP Q60603
D	5	MET	-	expression tag	UNP Q60603
F	3	GLY	-	expression tag	UNP Q60603
F	4	ALA	-	expression tag	UNP Q60603
F	5	MET	-	expression tag	UNP Q60603
H	3	GLY	-	expression tag	UNP Q60603
H	4	ALA	-	expression tag	UNP Q60603
H	5	MET	-	expression tag	UNP Q60603

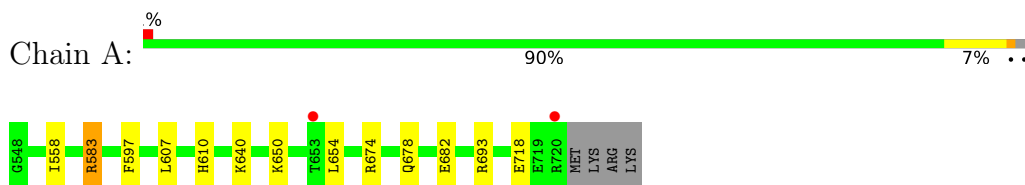
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	185	185	185	0	0
3	B	107	107	107	0	0
3	C	156	156	156	0	0
3	D	57	57	57	0	0
3	E	178	178	178	0	0
3	F	153	153	153	0	0
3	G	132	132	132	0	0
3	H	50	50	50	0	0

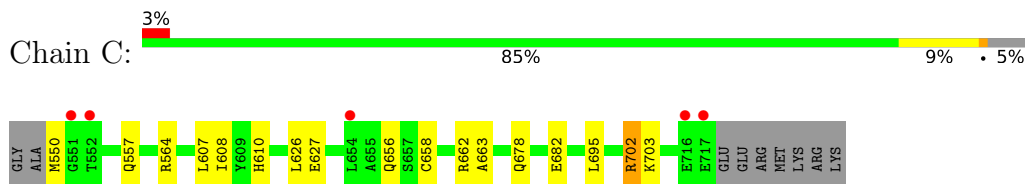
3 Residue-property plots [i](#)

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.

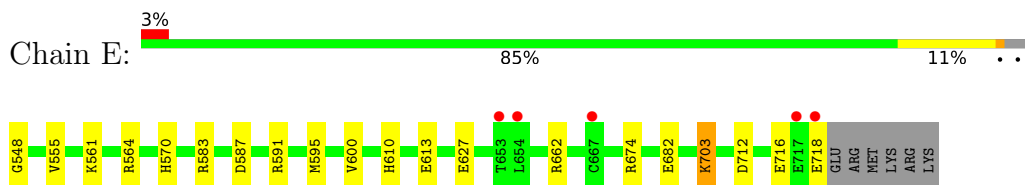
- Molecule 1: Potassium voltage-gated channel subfamily H member 1



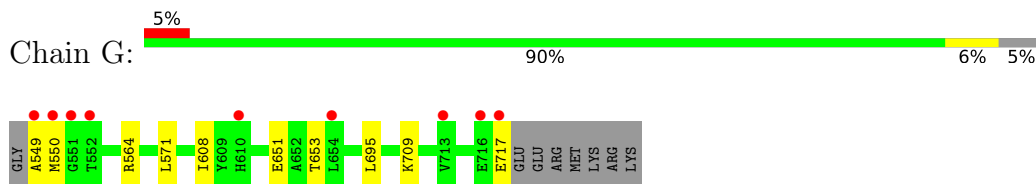
- Molecule 1: Potassium voltage-gated channel subfamily H member 1



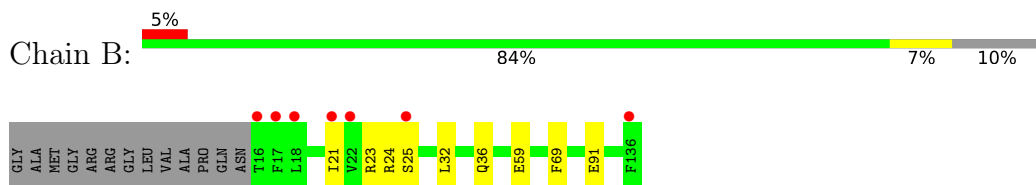
- Molecule 1: Potassium voltage-gated channel subfamily H member 1



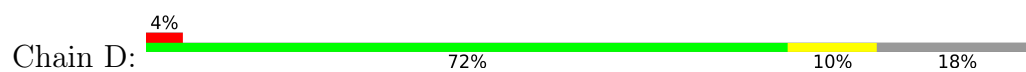
- Molecule 1: Potassium voltage-gated channel subfamily H member 1



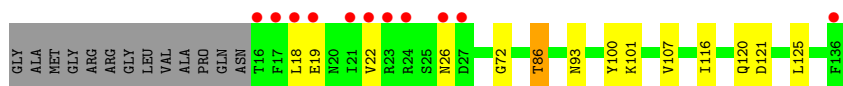
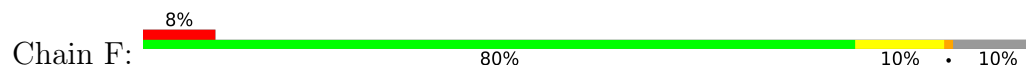
- Molecule 2: Potassium voltage-gated channel subfamily H member 1



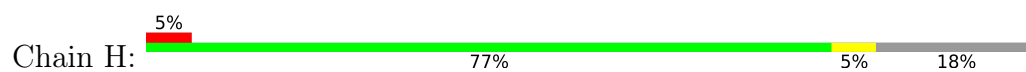
- Molecule 2: Potassium voltage-gated channel subfamily H member 1



- Molecule 2: Potassium voltage-gated channel subfamily H member 1



- Molecule 2: Potassium voltage-gated channel subfamily H member 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	162.38Å 162.38Å 100.44Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	42.71 – 2.00 42.71 – 2.00	Depositor EDS
% Data completeness (in resolution range)	100.0 (42.71-2.00) 99.9 (42.71-2.00)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.30 (at 2.00Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: dev_1269)	Depositor
R, R_{free}	0.167 , 0.197 0.170 , 0.199	Depositor DCC
R_{free} test set	5113 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	33.7	Xtrriage
Anisotropy	0.174	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 55.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.024 for h,-h-k,-l	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9889	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.25% 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](#)

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	0/1352	0.76	1/1828 (0.1%)
1	C	0.43	0/1315	0.75	1/1778 (0.1%)
1	E	0.47	0/1352	0.78	1/1825 (0.1%)
1	G	0.40	0/1328	0.71	0/1796
2	B	0.44	0/969	0.71	0/1314
2	D	0.37	0/877	0.71	0/1192
2	F	0.48	0/981	0.73	0/1328
2	H	0.36	0/879	0.72	0/1195
All	All	0.43	0/9053	0.74	3/12256 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	583	ARG	N-CA-C	8.88	122.07	111.33
1	A	583	ARG	N-CA-C	6.20	118.55	111.11
1	C	608	ILE	CB-CA-C	-5.26	105.14	112.04

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	1328	0	1298	9	0
1	C	1291	0	1269	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	1328	0	1317	14	0
1	G	1304	0	1283	5	0
2	B	947	0	892	6	0
2	D	856	0	795	8	0
2	F	959	0	906	7	0
2	H	858	0	801	4	0
3	A	185	0	0	6	0
3	B	107	0	0	4	0
3	C	156	0	0	6	0
3	D	57	0	0	1	0
3	E	178	0	0	6	0
3	F	153	0	0	2	0
3	G	132	0	0	3	0
3	H	50	0	0	0	0
All	All	9889	0	8561	64	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.

All (64) 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:583:ARG:O	3:A:974:HOH:O	1.83	0.94
2:B:91:GLU:OE1	3:B:302:HOH:O	1.87	0.90
2:D:134:THR:O	3:D:257:HOH:O	1.89	0.89
1:C:656:GLN:OE1	3:C:946:HOH:O	1.90	0.88
2:B:59:GLU:OE2	3:B:295:HOH:O	1.95	0.85
1:A:682:GLU:OE2	3:A:983:HOH:O	1.96	0.83
2:D:101:LYS:HE3	2:D:107:VAL:HG21	1.61	0.81
1:E:716:GLU:OE1	3:E:886:HOH:O	2.00	0.79
1:G:651:GLU:OE1	3:G:901:HOH:O	2.01	0.76
1:A:682:GLU:OE1	3:A:890:HOH:O	2.03	0.75
1:E:570:HIS:ND1	3:E:864:HOH:O	2.28	0.66
1:C:658:CYS:SG	3:C:815:HOH:O	2.52	0.66
1:C:550:MET:N	3:C:915:HOH:O	2.29	0.66
1:E:561:LYS:HA	1:E:595:MET:HE1	1.81	0.62
1:G:549:ALA:HB1	1:G:608:ILE:HG23	1.81	0.62
2:H:99:MET:HE3	2:H:109:PHE:HD2	1.63	0.62
1:C:564:ARG:NH2	3:C:848:HOH:O	2.16	0.60
2:B:36:GLN:OE1	3:B:250:HOH:O	2.16	0.60
2:F:101:LYS:HE3	2:F:107:VAL:HG21	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:70:MET:HE1	2:H:109:PHE:HE2	1.68	0.59
2:D:116:ILE:HB	2:D:125:LEU:HB2	1.85	0.58
1:G:717:GLU:N	3:G:891:HOH:O	2.40	0.55
1:C:627:GLU:OE2	1:C:662:ARG:NH2	2.35	0.55
1:C:702:ARG:HG3	1:C:703:LYS:HG2	1.87	0.55
1:C:626:LEU:HD23	1:C:663:ALA:HA	1.89	0.54
1:A:718:GLU:O	3:A:964:HOH:O	2.18	0.53
1:A:640:LYS:HE2	3:A:936:HOH:O	2.09	0.53
1:E:548:GLY:N	1:E:610:HIS:HD1	2.07	0.53
2:D:40:TRP:O	2:D:65:SER:OG	2.23	0.52
1:G:564:ARG:HD2	3:G:911:HOH:O	2.10	0.51
1:E:682:GLU:OE1	3:E:943:HOH:O	2.19	0.51
2:B:21:ILE:HG21	2:B:32:LEU:HD21	1.92	0.51
1:C:557:GLN:NE2	3:C:898:HOH:O	1.96	0.50
1:C:678:GLN:O	1:C:682:GLU:HG2	2.11	0.50
1:G:651:GLU:OE2	1:G:653:THR:OG1	2.20	0.48
2:H:57:ARG:O	2:H:61:MET:HG2	2.14	0.48
2:B:23:ARG:HA	2:B:24:ARG:HA	1.58	0.46
1:A:650:LYS:HZ2	1:A:678:GLN:HE22	1.64	0.46
1:E:564:ARG:NH2	3:E:973:HOH:O	2.20	0.46
2:F:125:LEU:HB3	3:F:292:HOH:O	2.16	0.46
1:A:693:ARG:HD3	3:A:962:HOH:O	2.15	0.45
2:D:70:MET:HE1	2:D:109:PHE:HE2	1.81	0.45
1:E:627:GLU:OE2	1:E:662:ARG:NH2	2.45	0.45
2:F:18:LEU:O	2:F:22:VAL:HG23	2.16	0.45
1:C:702:ARG:HD2	3:C:859:HOH:O	2.17	0.45
1:E:712:ASP:OD2	3:E:938:HOH:O	2.21	0.43
1:A:558:ILE:HD12	1:A:597:PHE:HB3	1.99	0.43
1:E:716:GLU:O	1:E:718:GLU:HG2	2.19	0.43
2:H:40:TRP:O	2:H:65:SER:OG	2.31	0.43
2:B:69:PHE:HD1	3:B:296:HOH:O	2.02	0.43
2:D:33:GLY:HA3	2:D:65:SER:OG	2.19	0.42
1:E:627:GLU:OE2	1:E:662:ARG:NE	2.47	0.42
2:F:22:VAL:HG21	2:F:116:ILE:HG21	2.02	0.42
1:E:587:ASP:HB3	1:E:591:ARG:NH1	2.35	0.41
1:C:607:LEU:HG	1:C:610:HIS:CD2	2.56	0.41
2:D:38:VAL:O	2:D:39:ASP:HB2	2.21	0.41
2:F:72:GLY:HA3	2:F:100:TYR:CE1	2.57	0.40
2:F:19:GLU:HG3	3:F:292:HOH:O	2.21	0.40
1:E:555:VAL:HG22	1:E:600:VAL:HG22	2.03	0.40
1:E:613:GLU:OE1	3:E:829:HOH:O	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:703:LYS:HE3	1:E:703:LYS:HB2	1.95	0.40
1:A:607:LEU:HG	1:A:610:HIS:CE1	2.57	0.40
2:D:72:GLY:HA3	2:D:100:TYR:CE2	2.56	0.40
2:F:86:THR:HG1	2:F:93:ASN:HD22	1.64	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	171/177 (97%)	170 (99%)	1 (1%)	0	100	100
1	C	166/177 (94%)	161 (97%)	5 (3%)	0	100	100
1	E	169/177 (96%)	168 (99%)	1 (1%)	0	100	100
1	G	167/177 (94%)	163 (98%)	4 (2%)	0	100	100
2	B	119/134 (89%)	118 (99%)	1 (1%)	0	100	100
2	D	108/134 (81%)	105 (97%)	3 (3%)	0	100	100
2	F	119/134 (89%)	116 (98%)	2 (2%)	1 (1%)	16	11
2	H	108/134 (81%)	106 (98%)	2 (2%)	0	100	100
All	All	1127/1244 (91%)	1107 (98%)	19 (2%)	1 (0%)	48	46

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	F	26	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	A	138/153 (90%)	136 (99%)	2 (1%)	59	66
1	C	135/153 (88%)	133 (98%)	2 (2%)	57	64
1	E	141/153 (92%)	139 (99%)	2 (1%)	59	66
1	G	138/153 (90%)	134 (97%)	4 (3%)	37	40
2	B	99/120 (82%)	98 (99%)	1 (1%)	68	75
2	D	89/120 (74%)	89 (100%)	0	100	100
2	F	102/120 (85%)	99 (97%)	3 (3%)	37	40
2	H	90/120 (75%)	90 (100%)	0	100	100
All	All	932/1092 (85%)	918 (98%)	14 (2%)	57	64

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	654	LEU
1	A	674	ARG
2	B	25	SER
1	C	695	LEU
1	C	702	ARG
1	E	674	ARG
1	E	703	LYS
2	F	86	THR
2	F	120	GLN
2	F	121	ASP
1	G	550	MET
1	G	571	LEU
1	G	695	LEU
1	G	709	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	678	GLN
1	A	694	ASN
1	C	678	GLN
1	C	694	ASN
2	D	62	GLN
1	E	694	ASN
1	G	694	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](#)

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

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	173/177 (97%)	-0.21	2 (1%) 76 76	18, 29, 57, 93	0
1	C	168/177 (94%)	-0.05	5 (2%) 52 51	19, 33, 75, 110	0
1	E	171/177 (96%)	-0.17	5 (2%) 53 52	21, 32, 53, 94	0
1	G	169/177 (95%)	0.14	9 (5%) 32 31	24, 39, 83, 115	0
2	B	121/134 (90%)	0.17	7 (5%) 29 27	24, 36, 77, 116	0
2	D	110/134 (82%)	0.44	6 (5%) 30 29	29, 52, 85, 104	0
2	F	121/134 (90%)	-0.05	11 (9%) 15 13	20, 30, 72, 86	0
2	H	110/134 (82%)	0.53	7 (6%) 25 24	33, 55, 94, 109	0
All	All	1143/1244 (91%)	0.06	52 (4%) 38 37	18, 36, 80, 116	0

All (52) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	17	PHE	5.6
2	B	18	LEU	5.2
1	G	549	ALA	4.8
2	F	17	PHE	4.5
2	F	18	LEU	4.2
2	F	16	THR	3.9
2	B	22	VAL	3.8
1	C	552	THR	3.7
2	D	26	ASN	3.6
1	G	717	GLU	3.6
2	D	134	THR	3.6
2	F	22	VAL	3.5
2	D	25	SER	3.4
1	A	653	THR	3.4
2	F	23	ARG	3.2
1	C	654	LEU	3.2

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Mol	Chain	Res	Type	RSRZ
2	B	136	PHE	3.2
1	G	654	LEU	3.2
2	B	16	THR	3.1
2	B	25	SER	3.0
1	C	551	GLY	3.0
1	G	713	VAL	2.9
2	H	26	ASN	2.9
1	E	717	GLU	2.8
2	H	119	GLU	2.6
1	G	551	GLY	2.6
2	D	27	ASP	2.6
2	D	28	THR	2.6
1	E	653	THR	2.5
2	H	134	THR	2.5
2	H	27	ASP	2.5
1	G	716	GLU	2.3
2	H	92	MET	2.3
2	D	119	GLU	2.3
1	G	552	THR	2.3
1	C	717	GLU	2.3
1	E	667	CYS	2.3
2	H	116	ILE	2.3
2	F	19	GLU	2.3
1	G	610	HIS	2.3
1	G	550	MET	2.2
1	E	718	GLU	2.2
2	F	136	PHE	2.2
1	C	716	GLU	2.2
2	F	26	ASN	2.1
2	B	21	ILE	2.1
2	F	27	ASP	2.1
2	H	135	ALA	2.1
2	F	21	ILE	2.1
1	E	654	LEU	2.0
2	F	24	ARG	2.0
1	A	720	ARG	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 [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.