



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 12, 2023 – 09:48 AM EDT

PDB ID : 4NPP
Title : The GLIC-His10 wild-type structure in equilibrium between the open and locally-closed (LC) forms
Authors : Sauguet, L.; Shahsavar, A.; Poitevin, F.; Huon, C.; Menny, A.; Nemezc, A.; Haouz, A.; Changeux, J.P.; Corringer, P.J.; Delarue, M.
Deposited on : 2013-11-22
Resolution : 3.35 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 : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.35.1
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35.1

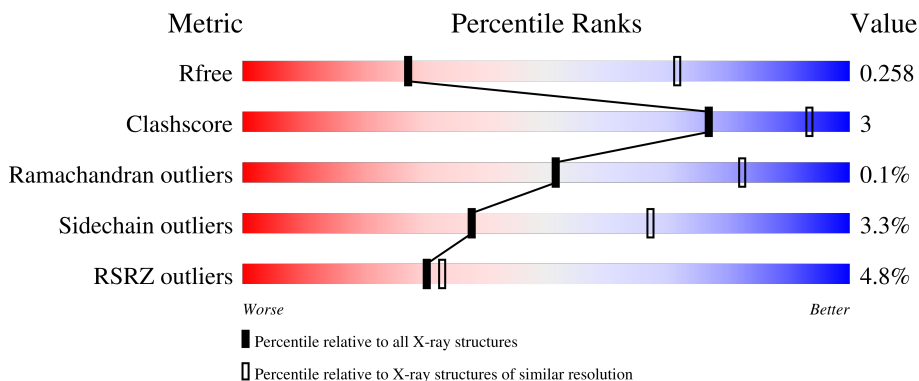
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.35 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}	130704	1558 (3.42-3.30)
Clashscore	141614	1627 (3.42-3.30)
Ramachandran outliers	138981	1599 (3.42-3.30)
Sidechain outliers	138945	1598 (3.42-3.30)
RSRZ outliers	127900	1507 (3.42-3.30)

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	329	<div style="display: flex; align-items: center;"> <div style="width: 5%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 84%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 10%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 5%; height: 10px; background-color: grey;"></div> </div>
1	B	329	<div style="display: flex; align-items: center;"> <div style="width: 5%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 84%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 11%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 5%; height: 10px; background-color: grey;"></div> </div>
1	C	329	<div style="display: flex; align-items: center;"> <div style="width: 4%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 85%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 9%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 5%; height: 10px; background-color: grey;"></div> </div>
1	D	329	<div style="display: flex; align-items: center;"> <div style="width: 6%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 84%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 10%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 5%; height: 10px; background-color: grey;"></div> </div>
1	E	329	<div style="display: flex; align-items: center;"> <div style="width: 3%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 85%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 9%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 5%; height: 10px; background-color: grey;"></div> </div>

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 13465 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 Proton-gated ion channel.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	311	2692	1775	430	482	5	0	21	0
1	B	311	2692	1775	430	482	5	0	21	0
1	C	311	2692	1775	430	482	5	0	21	0
1	D	311	2692	1775	430	482	5	0	21	0
1	E	311	2692	1775	430	482	5	0	21	0

There are 65 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	ALA	-	expression tag	UNP Q7NDN8
A	318	GLY	-	expression tag	UNP Q7NDN8
A	319	GLY	-	expression tag	UNP Q7NDN8
A	320	HIS	-	expression tag	UNP Q7NDN8
A	321	HIS	-	expression tag	UNP Q7NDN8
A	322	HIS	-	expression tag	UNP Q7NDN8
A	323	HIS	-	expression tag	UNP Q7NDN8
A	324	HIS	-	expression tag	UNP Q7NDN8
A	325	HIS	-	expression tag	UNP Q7NDN8
A	326	HIS	-	expression tag	UNP Q7NDN8
A	327	HIS	-	expression tag	UNP Q7NDN8
A	328	HIS	-	expression tag	UNP Q7NDN8
A	329	HIS	-	expression tag	UNP Q7NDN8
B	1	ALA	-	expression tag	UNP Q7NDN8
B	318	GLY	-	expression tag	UNP Q7NDN8
B	319	GLY	-	expression tag	UNP Q7NDN8
B	320	HIS	-	expression tag	UNP Q7NDN8
B	321	HIS	-	expression tag	UNP Q7NDN8
B	322	HIS	-	expression tag	UNP Q7NDN8

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Chain	Residue	Modelled	Actual	Comment	Reference
B	323	HIS	-	expression tag	UNP Q7NDN8
B	324	HIS	-	expression tag	UNP Q7NDN8
B	325	HIS	-	expression tag	UNP Q7NDN8
B	326	HIS	-	expression tag	UNP Q7NDN8
B	327	HIS	-	expression tag	UNP Q7NDN8
B	328	HIS	-	expression tag	UNP Q7NDN8
B	329	HIS	-	expression tag	UNP Q7NDN8
C	1	ALA	-	expression tag	UNP Q7NDN8
C	318	GLY	-	expression tag	UNP Q7NDN8
C	319	GLY	-	expression tag	UNP Q7NDN8
C	320	HIS	-	expression tag	UNP Q7NDN8
C	321	HIS	-	expression tag	UNP Q7NDN8
C	322	HIS	-	expression tag	UNP Q7NDN8
C	323	HIS	-	expression tag	UNP Q7NDN8
C	324	HIS	-	expression tag	UNP Q7NDN8
C	325	HIS	-	expression tag	UNP Q7NDN8
C	326	HIS	-	expression tag	UNP Q7NDN8
C	327	HIS	-	expression tag	UNP Q7NDN8
C	328	HIS	-	expression tag	UNP Q7NDN8
C	329	HIS	-	expression tag	UNP Q7NDN8
D	1	ALA	-	expression tag	UNP Q7NDN8
D	318	GLY	-	expression tag	UNP Q7NDN8
D	319	GLY	-	expression tag	UNP Q7NDN8
D	320	HIS	-	expression tag	UNP Q7NDN8
D	321	HIS	-	expression tag	UNP Q7NDN8
D	322	HIS	-	expression tag	UNP Q7NDN8
D	323	HIS	-	expression tag	UNP Q7NDN8
D	324	HIS	-	expression tag	UNP Q7NDN8
D	325	HIS	-	expression tag	UNP Q7NDN8
D	326	HIS	-	expression tag	UNP Q7NDN8
D	327	HIS	-	expression tag	UNP Q7NDN8
D	328	HIS	-	expression tag	UNP Q7NDN8
D	329	HIS	-	expression tag	UNP Q7NDN8
E	1	ALA	-	expression tag	UNP Q7NDN8
E	318	GLY	-	expression tag	UNP Q7NDN8
E	319	GLY	-	expression tag	UNP Q7NDN8
E	320	HIS	-	expression tag	UNP Q7NDN8
E	321	HIS	-	expression tag	UNP Q7NDN8
E	322	HIS	-	expression tag	UNP Q7NDN8
E	323	HIS	-	expression tag	UNP Q7NDN8
E	324	HIS	-	expression tag	UNP Q7NDN8
E	325	HIS	-	expression tag	UNP Q7NDN8

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Chain	Residue	Modelled	Actual	Comment	Reference
E	326	HIS	-	expression tag	UNP Q7NDN8
E	327	HIS	-	expression tag	UNP Q7NDN8
E	328	HIS	-	expression tag	UNP Q7NDN8
E	329	HIS	-	expression tag	UNP Q7NDN8

- Molecule 2 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Ni 1 1	0	0
2	B	1	Total Ni 1 1	0	0
2	C	1	Total Ni 1 1	0	0
2	D	1	Total Ni 1 1	0	0
2	E	1	Total Ni 1 1	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	113.55Å 127.62Å 185.81Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.16 – 3.35 19.16 – 3.35	Depositor EDS
% Data completeness (in resolution range)	99.8 (19.16-3.35) 99.8 (19.16-3.35)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.14 (at 3.36Å)	Xtrriage
Refinement program	BUSTER 2.11.4	Depositor
R, R_{free}	0.227 , 0.248 0.235 , 0.258	Depositor DCC
R_{free} test set	1969 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	108.2	Xtrriage
Anisotropy	0.454	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 65.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	13465	wwPDB-VP
Average B, all atoms (Å ²)	116.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.66% 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](#)

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

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	0/2765	0.65	0/3782
1	B	0.44	0/2765	0.63	0/3782
1	C	0.44	0/2765	0.64	0/3782
1	D	0.45	0/2765	0.65	0/3782
1	E	0.43	0/2765	0.63	0/3782
All	All	0.44	0/13825	0.64	0/18910

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	2692	0	2718	18	2
1	B	2692	0	2717	19	0
1	C	2692	0	2718	18	0
1	D	2692	0	2718	18	2
1	E	2692	0	2718	18	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	1	0	0	0	0
2	E	1	0	0	0	0
All	All	13465	0	13589	80	2

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 3.

All (80) 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:B:201:ILE:HG12	1:B:242[B]:VAL:HG11	1.65	0.79
1:C:63:VAL:HG21	1:D:136:ASP:CG	2.10	0.72
1:B:201:ILE:HG12	1:B:242[B]:VAL:CG1	2.20	0.70
1:D:7:PRO:HG3	1:D:135:VAL:HG21	1.80	0.62
1:E:204:PRO:HB2	1:E:238[B]:PHE:CZ	2.35	0.62
1:C:78:PHE:CE2	1:C:85:ARG:HD3	2.34	0.62
1:D:78:PHE:CE2	1:D:85:ARG:HD3	2.35	0.61
1:B:78:PHE:CE2	1:B:85:ARG:HD3	2.35	0.61
1:E:78:PHE:CE2	1:E:85:ARG:HD3	2.36	0.61
1:E:201:ILE:HG12	1:E:242[B]:VAL:CG1	2.31	0.61
1:E:242[B]:VAL:HG12	1:E:246[B]:LEU:HG	1.81	0.60
1:C:201:ILE:HG12	1:C:242[B]:VAL:CG1	2.33	0.59
1:A:78:PHE:CE2	1:A:85:ARG:HD3	2.37	0.58
1:C:204:PRO:HB2	1:C:238[B]:PHE:CZ	2.37	0.58
1:A:242[B]:VAL:HG12	1:A:246[B]:LEU:HG	1.86	0.58
1:B:7:PRO:HG3	1:B:135:VAL:HG21	1.86	0.57
1:C:78:PHE:HE2	1:C:85:ARG:HD3	1.68	0.57
1:A:7:PRO:HG3	1:A:135:VAL:HG21	1.86	0.57
1:D:204:PRO:HB2	1:D:238[B]:PHE:CZ	2.39	0.57
1:B:204:PRO:HB2	1:B:238[B]:PHE:CZ	2.40	0.56
1:B:78:PHE:HE2	1:B:85:ARG:HD3	1.69	0.56
1:D:78:PHE:HE2	1:D:85:ARG:HD3	1.68	0.55
1:E:78:PHE:HE2	1:E:85:ARG:HD3	1.71	0.55
1:A:78:PHE:HE2	1:A:85:ARG:HD3	1.71	0.55
1:E:7:PRO:HG3	1:E:135:VAL:HG21	1.88	0.55
1:C:201:ILE:HG12	1:C:242[B]:VAL:HG13	1.89	0.54
1:A:201:ILE:HG12	1:A:242[B]:VAL:CG1	2.37	0.54
1:E:201:ILE:HG12	1:E:242[B]:VAL:HG11	1.89	0.54
1:C:7:PRO:HG3	1:C:135:VAL:HG21	1.89	0.53
1:D:201:ILE:HG12	1:D:242[B]:VAL:CG1	2.40	0.52
1:A:79:VAL:HG21	1:A:183:LYS:HD2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:289:ALA:HB1	1:A:293:ARG:NH2	2.27	0.50
1:D:242[B]:VAL:HG12	1:D:246[B]:LEU:HG	1.92	0.49
1:C:11:ILE:HG13	1:C:14:GLU:OE2	2.11	0.49
1:D:11:ILE:HG13	1:D:14:GLU:OE2	2.12	0.49
1:C:63:VAL:HG21	1:D:136:ASP:CB	2.42	0.49
1:B:205:MET:CE	1:B:238[A]:PHE:HB3	2.42	0.49
1:C:289:ALA:HB1	1:C:293:ARG:NH2	2.29	0.48
1:E:11:ILE:HG13	1:E:14:GLU:OE2	2.14	0.48
1:B:289:ALA:HB1	1:B:293:ARG:NH2	2.29	0.48
1:C:79:VAL:HG21	1:C:183:LYS:HD2	1.93	0.48
1:A:242[B]:VAL:HG12	1:A:242[B]:VAL:O	2.14	0.48
1:D:289:ALA:HB1	1:D:293:ARG:NH2	2.28	0.48
1:C:117:ARG:HG3	1:C:251[A]:TYR:CD2	2.49	0.48
1:E:79:VAL:HG21	1:E:183:LYS:HD2	1.95	0.47
1:B:79:VAL:HG21	1:B:183:LYS:HD2	1.96	0.47
1:A:11:ILE:HG13	1:A:14:GLU:OE2	2.15	0.47
1:A:204:PRO:HB2	1:A:238[B]:PHE:CZ	2.50	0.47
1:A:144:VAL:HG11	1:A:167:ALA:HB3	1.97	0.47
1:B:11:ILE:HG13	1:B:14:GLU:OE2	2.15	0.46
1:D:144:VAL:HG11	1:D:167:ALA:HB3	1.96	0.46
1:A:136:ASP:CG	1:E:63:VAL:HG21	2.35	0.46
1:C:131:ILE:HD11	1:C:181:GLU:HG2	1.96	0.46
1:D:79:VAL:HG21	1:D:183:LYS:HD2	1.95	0.46
1:A:240[B]:ILE:HD11	1:E:237[B]:ALA:O	2.15	0.46
1:B:230:SER:HB3	1:C:233[B]:ILE:HD11	1.98	0.46
1:D:247[B]:PRO:HB2	1:D:249[B]:THR:HG23	1.98	0.46
1:E:247[B]:PRO:HB2	1:E:249[B]:THR:HG23	1.97	0.46
1:E:289:ALA:HB1	1:E:293:ARG:NH2	2.31	0.45
1:A:201:ILE:HG12	1:A:242[B]:VAL:HG11	1.97	0.45
1:B:117:ARG:HG3	1:B:251[A]:TYR:CD2	2.52	0.44
1:A:236[A]:ILE:HG12	1:E:238[A]:PHE:HE2	1.82	0.44
1:B:242[B]:VAL:HG12	1:B:246[B]:LEU:HG	1.98	0.44
1:A:239[B]:ASN:CB	1:E:241[B]:LEU:HD11	2.49	0.43
1:A:205:MET:HE2	1:A:238[A]:PHE:HB3	2.01	0.42
1:C:241[B]:LEU:HD11	1:D:239[B]:ASN:HB2	2.02	0.42
1:C:230:SER:HB3	1:D:233[B]:ILE:HD11	2.01	0.42
1:B:205:MET:HE2	1:B:238[A]:PHE:HB3	2.01	0.42
1:D:78:PHE:HE2	1:D:85:ARG:CD	2.33	0.41
1:E:241[B]:LEU:HD23	1:E:242[B]:VAL:HG23	2.01	0.41
1:B:130:LEU:HD23	1:B:130:LEU:HA	1.91	0.41
1:D:130:LEU:HD23	1:D:130:LEU:HA	1.92	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:90:VAL:CG1	1:C:133:ARG:HD3	2.51	0.41
1:A:234[B]:ALA:O	1:A:238[B]:PHE:HB2	2.21	0.40
1:C:238[A]:PHE:HE2	1:D:236[A]:ILE:HG12	1.85	0.40
1:E:254:TYR:CZ	1:E:258:ILE:HD11	2.56	0.40
1:B:8:PRO:HA	1:B:9:PRO:HD3	1.99	0.40
1:B:78:PHE:HE2	1:B:85:ARG:CD	2.34	0.40
1:B:254:TYR:CZ	1:B:258:ILE:HD11	2.56	0.40
1:E:205:MET:HE2	1:E:238[A]:PHE:HB3	2.03	0.40

All (2) 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	Interatomic distance (Å)	Clash overlap (Å)
1:A:145:ASP:OD2	1:D:145:ASP:OD2[3_555]	1.85	0.35
1:A:166:THR:CG2	1:D:97:ASP:OD2[3_555]	2.18	0.02

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	330/329 (100%)	317 (96%)	13 (4%)	0	100	100
1	B	330/329 (100%)	319 (97%)	9 (3%)	2 (1%)	25	59
1	C	330/329 (100%)	318 (96%)	12 (4%)	0	100	100
1	D	330/329 (100%)	323 (98%)	7 (2%)	0	100	100
1	E	330/329 (100%)	316 (96%)	14 (4%)	0	100	100
All	All	1650/1645 (100%)	1593 (96%)	55 (3%)	2 (0%)	51	82

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	244[A]	THR
1	B	244[B]	THR

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	299/294 (102%)	288 (96%)	11 (4%)	34	63
1	B	299/294 (102%)	290 (97%)	9 (3%)	41	69
1	C	299/294 (102%)	289 (97%)	10 (3%)	38	67
1	D	299/294 (102%)	289 (97%)	10 (3%)	38	67
1	E	299/294 (102%)	291 (97%)	8 (3%)	44	72
All	All	1495/1470 (102%)	1447 (97%)	48 (3%)	38	68

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	42	PHE
1	A	48	LYS
1	A	69	GLU
1	A	111	LEU
1	A	166	THR
1	A	170	LYS
1	A	245[A]	ASN
1	A	245[B]	ASN
1	A	248[A]	LYS
1	A	248[B]	LYS
1	A	259	ILE
1	B	42	PHE
1	B	63	VAL
1	B	69	GLU
1	B	111	LEU
1	B	136	ASP
1	B	166	THR
1	B	170	LYS

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Mol	Chain	Res	Type
1	B	181	GLU
1	B	259	ILE
1	C	33	LYS
1	C	42	PHE
1	C	63	VAL
1	C	69	GLU
1	C	111	LEU
1	C	166	THR
1	C	170	LYS
1	C	181	GLU
1	C	222	GLU
1	C	259	ILE
1	D	42	PHE
1	D	63	VAL
1	D	69	GLU
1	D	111	LEU
1	D	136	ASP
1	D	166	THR
1	D	170	LYS
1	D	181	GLU
1	D	222	GLU
1	D	259	ILE
1	E	42	PHE
1	E	63	VAL
1	E	69	GLU
1	E	111	LEU
1	E	166	THR
1	E	170	LYS
1	E	222	GLU
1	E	259	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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](#)

Of 5 ligands modelled in this entry, 5 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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	311/329 (94%)	-0.04	16 (5%) 28 30	66, 109, 154, 219	0
1	B	311/329 (94%)	0.03	17 (5%) 25 27	77, 119, 162, 222	0
1	C	311/329 (94%)	0.02	14 (4%) 33 36	75, 122, 165, 213	0
1	D	311/329 (94%)	-0.05	19 (6%) 21 23	72, 110, 150, 193	0
1	E	311/329 (94%)	-0.06	9 (2%) 51 54	71, 110, 153, 183	0
All	All	1555/1645 (94%)	-0.02	75 (4%) 30 33	66, 114, 158, 222	0

All (75) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	59	SER	4.8
1	C	58	ARG	4.7
1	A	244[A]	THR	4.2
1	A	178	ASP	4.1
1	A	68	PRO	4.1
1	D	283	SER	3.8
1	E	58	ARG	3.8
1	A	281	VAL	3.7
1	C	315	PHE	3.6
1	B	62	ARG	3.5
1	A	145	ASP	3.5
1	B	60	GLY	3.4
1	B	61	VAL	3.4
1	E	57	VAL	3.4
1	D	136	ASP	3.4
1	A	286	ALA	3.4
1	C	59	SER	3.4
1	A	220	SER	3.0
1	D	285	PRO	3.0
1	C	11	ILE	2.9

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Mol	Chain	Res	Type	RSRZ
1	D	58	ARG	2.9
1	C	57	VAL	2.9
1	D	67	GLU	2.8
1	C	136	ASP	2.8
1	C	178	ASP	2.8
1	A	194	TYR	2.8
1	B	11	ILE	2.7
1	E	12	ALA	2.7
1	D	62	ARG	2.7
1	D	286	ALA	2.7
1	A	283	SER	2.6
1	C	60	GLY	2.6
1	A	69	GLU	2.6
1	A	290	SER	2.6
1	C	175	ALA	2.5
1	E	278	TYR	2.5
1	B	136	ASP	2.5
1	B	276	GLN	2.5
1	E	312	PHE	2.5
1	B	86	ASP	2.5
1	A	58	ARG	2.4
1	E	117	ARG	2.4
1	D	33	LYS	2.4
1	B	54	PHE	2.4
1	E	11	ILE	2.4
1	A	222	GLU	2.4
1	C	12	ALA	2.4
1	B	315	PHE	2.4
1	B	146	LEU	2.4
1	B	147	GLU	2.4
1	A	11	ILE	2.4
1	D	12	ALA	2.4
1	D	68	PRO	2.4
1	C	283	SER	2.3
1	B	68	PRO	2.2
1	B	137	THR	2.2
1	B	281	VAL	2.2
1	C	82	GLU	2.2
1	D	194	TYR	2.2
1	E	59	SER	2.2
1	D	281	VAL	2.2
1	C	290	SER	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	178	ASP	2.1
1	D	277	HIS	2.1
1	D	175	ALA	2.1
1	A	315	PHE	2.1
1	D	60	GLY	2.1
1	B	285	PRO	2.1
1	B	278	TYR	2.1
1	D	13	ASP	2.1
1	A	13	ASP	2.1
1	D	11	ILE	2.1
1	E	60	GLY	2.1
1	D	69	GLU	2.0
1	C	61	VAL	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 monosaccharides 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(Å ²)	Q<0.9
2	NI	C	401	1/1	0.84	0.10	116,116,116,116	0
2	NI	B	401	1/1	0.86	0.25	141,141,141,141	0
2	NI	E	401	1/1	0.88	0.18	119,119,119,119	0
2	NI	D	401	1/1	0.91	0.14	110,110,110,110	0
2	NI	A	401	1/1	0.94	0.14	135,135,135,135	0

6.5 Other polymers [i](#)

There are no such residues in this entry.