



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:09 AM GMT

PDB ID : 3O8Y
Title : Stable-5-Lipoxygenase
Authors : Newcomer, M.E.; Gilbert, N.C.; Bartlett, S.G.; Waight, M.T.; Neau, D.B.;
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Deposited on : 2010-08-03
Resolution : 2.39 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

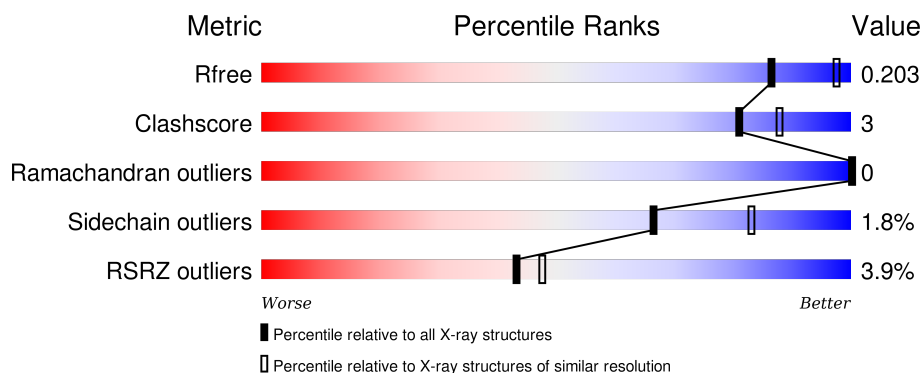
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

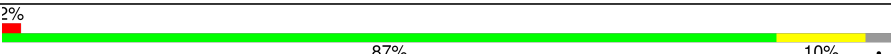
The reported resolution of this entry is 2.39 Å.

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	4019 (2.40-2.36)
Clashscore	102246	4595 (2.40-2.36)
Ramachandran outliers	100387	4520 (2.40-2.36)
Sidechain outliers	100360	4522 (2.40-2.36)
RSRZ outliers	91569	4034 (2.40-2.36)

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	691	 6% 89% 9% •
1	B	691	 2% 87% 10% •

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 22240 atoms, of which 10629 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 Arachidonate 5-lipoxygenase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	676	Total	C	H	N	O	S	0	2	0
			10830	3517	5334	935	1016	28			
1	B	670	Total	C	H	N	O	S	0	2	0
			10736	3486	5295	919	1008	28			

There are 68 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-14	MET	-	EXPRESSION TAG	UNP P09917
A	-13	GLY	-	EXPRESSION TAG	UNP P09917
A	-12	SER	-	EXPRESSION TAG	UNP P09917
A	-11	SER	-	EXPRESSION TAG	UNP P09917
A	-10	HIS	-	EXPRESSION TAG	UNP P09917
A	-9	HIS	-	EXPRESSION TAG	UNP P09917
A	-8	HIS	-	EXPRESSION TAG	UNP P09917
A	-7	HIS	-	EXPRESSION TAG	UNP P09917
A	-6	HIS	-	EXPRESSION TAG	UNP P09917
A	-6A	HIS	-	EXPRESSION TAG	UNP P09917
A	-6B	SER	-	EXPRESSION TAG	UNP P09917
A	-6C	SER	-	EXPRESSION TAG	UNP P09917
A	-6D	GLY	-	EXPRESSION TAG	UNP P09917
A	-6E	LEU	-	EXPRESSION TAG	UNP P09917
A	-6F	VAL	-	EXPRESSION TAG	UNP P09917
A	-6G	PRO	-	EXPRESSION TAG	UNP P09917
A	-6H	ARG	-	EXPRESSION TAG	UNP P09917
A	-6I	GLY	-	EXPRESSION TAG	UNP P09917
A	-6J	SER	-	EXPRESSION TAG	UNP P09917
A	-6K	HIS	-	EXPRESSION TAG	UNP P09917
A	16	GLU	TRP	engineered	UNP P09917
A	17	HIS	PHE	engineered	UNP P09917
A	?	-	PRO	DELETION	UNP P09917
A	?	-	PHE	DELETION	UNP P09917
A	?	-	TYR	DELETION	UNP P09917

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Chain	Residue	Modelled	Actual	Comment	Reference
A	43	GLY	ASN	SEE REMARK 999	UNP P09917
A	44	SER	ASP	SEE REMARK 999	UNP P09917
A	75	GLY	TRP	engineered	UNP P09917
A	76	SER	LEU	engineered	UNP P09917
A	240	ALA	CYS	engineered	UNP P09917
A	561	ALA	CYS	engineered	UNP P09917
A	653	GLU	LYS	engineered	UNP P09917
A	654	ASN	LYS	engineered	UNP P09917
A	655	LEU	LYS	engineered	UNP P09917
B	-17	MET	-	EXPRESSION TAG	UNP P09917
B	-16	GLY	-	EXPRESSION TAG	UNP P09917
B	-15	SER	-	EXPRESSION TAG	UNP P09917
B	-14	SER	-	EXPRESSION TAG	UNP P09917
B	-13	HIS	-	EXPRESSION TAG	UNP P09917
B	-12	HIS	-	EXPRESSION TAG	UNP P09917
B	-11	HIS	-	EXPRESSION TAG	UNP P09917
B	-10	HIS	-	EXPRESSION TAG	UNP P09917
B	-9	HIS	-	EXPRESSION TAG	UNP P09917
B	-8	HIS	-	EXPRESSION TAG	UNP P09917
B	-7	SER	-	EXPRESSION TAG	UNP P09917
B	-6	SER	-	EXPRESSION TAG	UNP P09917
B	-5	GLY	-	EXPRESSION TAG	UNP P09917
B	-4	LEU	-	EXPRESSION TAG	UNP P09917
B	-3	VAL	-	EXPRESSION TAG	UNP P09917
B	-2	PRO	-	EXPRESSION TAG	UNP P09917
B	-1	ARG	-	EXPRESSION TAG	UNP P09917
B	0	GLY	-	EXPRESSION TAG	UNP P09917
B	1	SER	-	EXPRESSION TAG	UNP P09917
B	2	HIS	-	EXPRESSION TAG	UNP P09917
B	16	GLU	TRP	engineered	UNP P09917
B	17	HIS	PHE	engineered	UNP P09917
B	?	-	PRO	DELETION	UNP P09917
B	?	-	PHE	DELETION	UNP P09917
B	?	-	TYR	DELETION	UNP P09917
B	43	GLY	ASN	SEE REMARK 999	UNP P09917
B	44	SER	ASP	SEE REMARK 999	UNP P09917
B	75	GLY	TRP	engineered	UNP P09917
B	76	SER	LEU	engineered	UNP P09917
B	240	ALA	CYS	engineered	UNP P09917
B	561	ALA	CYS	engineered	UNP P09917
B	653	GLU	LYS	engineered	UNP P09917
B	654	ASN	LYS	engineered	UNP P09917

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Chain	Residue	Modelled	Actual	Comment	Reference
B	655	LEU	LYS	engineered	UNP P09917

- Molecule 2 is FE (II) ION (three-letter code: FE2) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Fe	0	0
			1	1		
2	A	1	Total	Fe	0	0
			1	1		

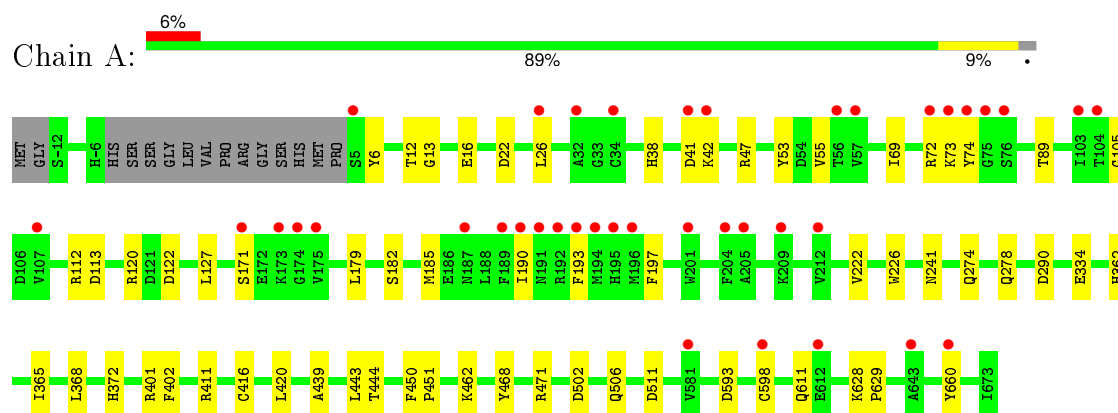
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	307	Total	O	0	0
			307	307		
3	B	365	Total	O	0	0
			365	365		

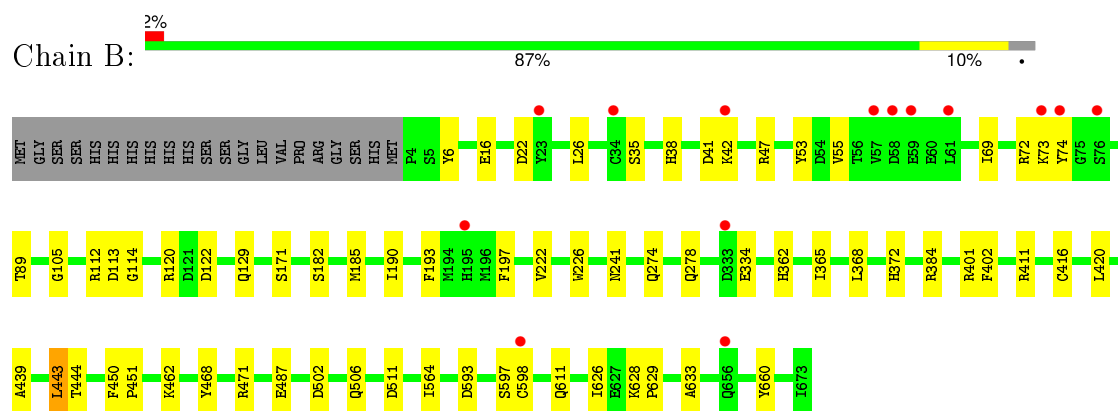
3 Residue-property plots [i](#)

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 ($\text{RSRZ} > 2$). 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: Arachidonate 5-lipoxygenase



• Molecule 1: Arachidonate 5-lipoxygenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	55.17Å 202.89Å 76.80Å 90.00° 109.56° 90.00°	Depositor
Resolution (Å)	40.77 – 2.39 51.99 – 2.39	Depositor EDS
% Data completeness (in resolution range)	94.2 (40.77-2.39) 94.0 (51.99-2.39)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.53 (at 2.39Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.2_432)	Depositor
R, R_{free}	0.182 , 0.210 0.176 , 0.203	Depositor DCC
R_{free} test set	1892 reflections (3.20%)	DCC
Wilson B-factor (Å ²)	20.1	Xtriage
Anisotropy	0.291	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.42 , 38.4	EDS
Estimated twinning fraction	0.031 for h,-k,-h-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 62694 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	22240	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.86% 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: FE2

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	0.23	0/5643	0.41	0/7655
1	B	0.23	0/5585	0.41	0/7578
All	All	0.23	0/11228	0.41	0/15233

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	5496	5334	5372	35	0
1	B	5441	5295	5333	37	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	307	0	0	2	0
3	B	365	0	0	3	0
All	All	11611	10629	10705	72	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 3.

All (72) 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:384:ARG:NH2	3:B:956:HOH:O	2.09	0.84
1:B:41:ASP:HB2	1:B:53:TYR:OH	1.93	0.69
1:A:41:ASP:HB2	1:A:53:TYR:OH	1.94	0.67
1:A:193:PHE:HB2	1:A:598[B]:CYS:SG	2.35	0.66
1:A:290:ASP:OD2	3:A:723:HOH:O	2.14	0.65
1:B:193:PHE:HB2	1:B:598[B]:CYS:SG	2.37	0.64
1:A:450:PHE:HB3	1:A:451:PRO:HD3	1.85	0.58
1:B:450:PHE:HB3	1:B:451:PRO:HD3	1.85	0.58
1:A:41:ASP:O	1:A:42:LYS:HB2	2.03	0.57
1:B:41:ASP:O	1:B:42:LYS:HB2	2.04	0.57
1:B:38:HIS:ND1	1:B:55:VAL:HG13	2.20	0.56
1:A:38:HIS:ND1	1:A:55:VAL:HG13	2.20	0.56
1:B:73:LYS:N	1:B:73:LYS:HD2	2.21	0.56
1:A:182:SER:HA	1:A:185:MET:HE2	1.86	0.55
1:B:182:SER:HA	1:B:185:MET:HE2	1.88	0.55
1:A:73:LYS:N	1:A:73:LYS:HD2	2.21	0.55
1:A:12:THR:O	3:A:786:HOH:O	2.19	0.54
1:A:73:LYS:NZ	1:A:105:GLY:HA3	2.25	0.52
1:B:502:ASP:O	1:B:506:GLN:HG2	2.10	0.52
1:B:73:LYS:NZ	1:B:105:GLY:HA3	2.25	0.52
1:A:365:ILE:HD12	1:A:439:ALA:CB	2.40	0.51
1:B:365:ILE:HD12	1:B:439:ALA:CB	2.41	0.51
1:B:35:SER:O	3:B:1024:HOH:O	2.18	0.50
1:B:222:VAL:O	1:B:226:TRP:HB3	2.12	0.50
1:A:222:VAL:O	1:A:226:TRP:HB3	2.11	0.50
1:A:502:ASP:O	1:A:506:GLN:HG2	2.11	0.50
1:B:197:PHE:HA	1:B:593:ASP:OD1	2.12	0.49
1:A:401:ARG:O	1:A:402:PHE:HB2	2.13	0.49
1:A:274:GLN:O	1:A:278:GLN:HG2	2.12	0.48
1:B:274:GLN:O	1:B:278:GLN:HG2	2.13	0.48
1:A:197:PHE:HA	1:A:593:ASP:OD1	2.14	0.48
1:B:22:ASP:HA	1:B:74:TYR:HB3	1.97	0.47
1:B:241:ASN:HB2	1:B:362:HIS:CD2	2.50	0.47
1:A:241:ASN:HB2	1:A:362:HIS:CD2	2.50	0.47
1:B:443:LEU:C	1:B:443:LEU:HD23	2.35	0.47
1:A:443:LEU:C	1:A:443:LEU:HD23	2.35	0.46
1:B:41:ASP:O	1:B:42:LYS:CB	2.62	0.46
1:A:443:LEU:C	1:A:443:LEU:CD2	2.84	0.46
1:B:443:LEU:C	1:B:443:LEU:CD2	2.84	0.46
1:A:26:LEU:HD12	1:A:69:ILE:HD11	1.98	0.46
1:A:6:TYR:CD1	1:A:89:THR:HA	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:26:LEU:HD12	1:B:69:ILE:HD11	1.97	0.45
1:A:22:ASP:HA	1:A:74:TYR:HB3	1.97	0.45
1:A:41:ASP:O	1:A:42:LYS:CB	2.62	0.45
1:A:193:PHE:CB	1:A:598[B]:CYS:SG	3.03	0.45
1:B:401:ARG:O	1:B:402:PHE:HB2	2.16	0.45
1:B:6:TYR:CD1	1:B:89:THR:HA	2.52	0.45
1:B:443:LEU:HD23	1:B:444:THR:N	2.32	0.45
1:A:443:LEU:HD23	1:A:444:THR:N	2.32	0.44
1:B:368:LEU:O	1:B:372:HIS:HB2	2.17	0.44
1:B:129:GLN:HG3	3:B:981:HOH:O	2.17	0.44
1:A:368:LEU:O	1:A:372:HIS:HB2	2.17	0.43
1:B:193:PHE:CB	1:B:598[B]:CYS:SG	3.05	0.43
1:B:462:LYS:HD3	1:B:471:ARG:NH2	2.34	0.42
1:B:190:ILE:HB	1:B:598[B]:CYS:SG	2.59	0.42
1:A:628:LYS:HB3	1:A:629:PRO:HD3	2.02	0.42
1:B:411:ARG:O	1:B:416:CYS:HB3	2.20	0.42
1:B:112:ARG:HH22	1:B:122:ASP:CG	2.23	0.42
1:B:564:ILE:CD1	1:B:597:SER:HB3	2.50	0.42
1:A:411:ARG:O	1:A:416:CYS:HB3	2.19	0.42
1:A:462:LYS:HD3	1:A:471:ARG:NH2	2.35	0.41
1:B:628:LYS:HB3	1:B:629:PRO:HD3	2.02	0.41
1:B:16:GLU:HA	1:B:47:ARG:HE	1.85	0.41
1:A:73:LYS:HZ1	1:A:105:GLY:HA3	1.86	0.41
1:A:22:ASP:HB3	1:A:72:ARG:O	2.20	0.41
1:B:22:ASP:HB3	1:B:72:ARG:O	2.20	0.41
1:A:112:ARG:HH22	1:A:122:ASP:CG	2.23	0.41
1:A:190:ILE:HB	1:A:598[B]:CYS:SG	2.60	0.41
1:A:12:THR:HG22	1:A:13:GLY:N	2.36	0.41
1:A:16:GLU:HA	1:A:47:ARG:HE	1.85	0.41
1:B:114:GLY:HA3	1:B:626:ILE:HD13	2.04	0.40
1:B:487:GLU:OE1	1:B:633:ALA:HA	2.21	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	674/691 (98%)	649 (96%)	25 (4%)	0	100	100
1	B	670/691 (97%)	646 (96%)	24 (4%)	0	100	100
All	All	1344/1382 (97%)	1295 (96%)	49 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	598/608 (98%)	587 (98%)	11 (2%)	66	83
1	B	592/608 (97%)	582 (98%)	10 (2%)	68	84
All	All	1190/1216 (98%)	1169 (98%)	21 (2%)	66	83

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	113	ASP
1	A	120	ARG
1	A	127	LEU
1	A	171	SER
1	A	179	LEU
1	A	334	GLU
1	A	420	LEU
1	A	468	TYR
1	A	511	ASP
1	A	611	GLN
1	A	660	TYR
1	B	113	ASP
1	B	120	ARG
1	B	171	SER
1	B	334	GLU

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Mol	Chain	Res	Type
1	B	420	LEU
1	B	443	LEU
1	B	468	TYR
1	B	511	ASP
1	B	611	GLN
1	B	660	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	191	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 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.

No monomer is involved in short contacts.

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	676/691 (97%)	0.51	39 (5%)	26 31	13, 25, 62, 96	0
1	B	670/691 (96%)	0.39	14 (2%)	67 70	12, 24, 62, 95	0
All	All	1346/1382 (97%)	0.45	53 (3%)	43 47	12, 25, 62, 96	0

All (53) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	42	LYS	5.8
1	A	190	ILE	5.2
1	A	74	TYR	4.3
1	A	196	MET	3.8
1	A	189	PHE	3.8
1	A	75	GLY	3.7
1	B	59	GLU	3.5
1	A	195	HIS	3.4
1	A	612	GLU	3.4
1	A	174	GLY	3.4
1	A	73	LYS	3.3
1	A	57	VAL	3.3
1	A	5	SER	3.3
1	A	104	THR	3.2
1	A	103	ILE	3.2
1	A	34[A]	CYS	3.1
1	A	212	VAL	3.1
1	B	57	VAL	3.1
1	B	195	HIS	3.0
1	A	192	ARG	3.0
1	B	58	ASP	2.9
1	A	191	ASN	2.9
1	A	581	VAL	2.8
1	B	598[A]	CYS	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	41	ASP	2.8
1	B	76	SER	2.7
1	B	23	TYR	2.6
1	B	74	TYR	2.6
1	A	32	ALA	2.6
1	A	201	TRP	2.5
1	A	175	VAL	2.5
1	A	173	LYS	2.5
1	A	209	LYS	2.5
1	A	193	PHE	2.4
1	A	76	SER	2.4
1	A	205	ALA	2.4
1	A	598[A]	CYS	2.4
1	A	171	SER	2.4
1	B	42	LYS	2.4
1	B	61	LEU	2.3
1	B	34[A]	CYS	2.3
1	B	73	LYS	2.3
1	A	187	ASN	2.3
1	B	333	ASP	2.2
1	A	107	VAL	2.2
1	A	660	TYR	2.2
1	A	204	PHE	2.2
1	B	656	GLN	2.2
1	A	56	THR	2.1
1	A	194	MET	2.1
1	A	72	ARG	2.1
1	A	26	LEU	2.1
1	A	643	ALA	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 [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	FE2	A	1	1/1	0.99	0.16	1.14	17,17,17,17	0
2	FE2	B	674	1/1	0.99	0.16	0.23	17,17,17,17	0

6.5 Other polymers [i](#)

There are no such residues in this entry.