



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2024 – 01:36 AM EST

PDB ID : 4W8I
Title : Crystal structure of LpSPL/Lpp2128, Legionella pneumophila sphingosine-1 phosphate lyase
Authors : Stogios, P.J.; Daniels, C.; Skarina, T.; Cuff, M.; Di Leo, R.; Savchenko, A.; Joachimiak, A.; Midwest Center for Structural Genomics (MCSG)
Deposited on : 2014-08-24
Resolution : 2.85 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
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

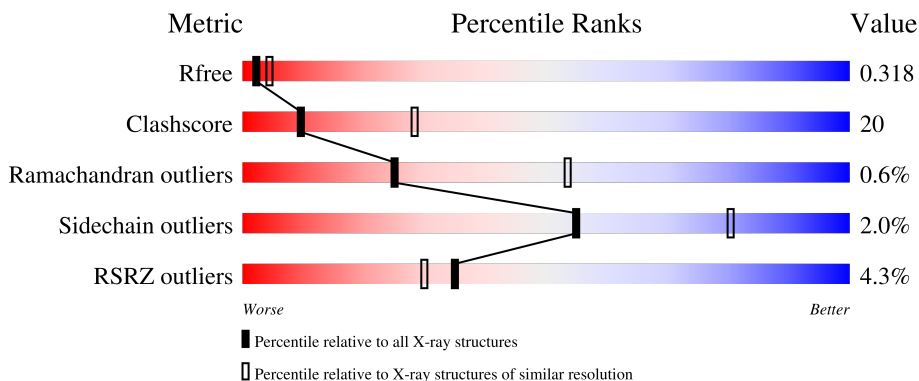
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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	3168 (2.90-2.82)
Clashscore	141614	3438 (2.90-2.82)
Ramachandran outliers	138981	3348 (2.90-2.82)
Sidechain outliers	138945	3351 (2.90-2.82)
RSRZ outliers	127900	3103 (2.90-2.82)

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	551	 4% 44% 20% 34%
1	B	551	 4% 42% 20% 36%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5515 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 Probable sphingosine-1-phosphate lyase.

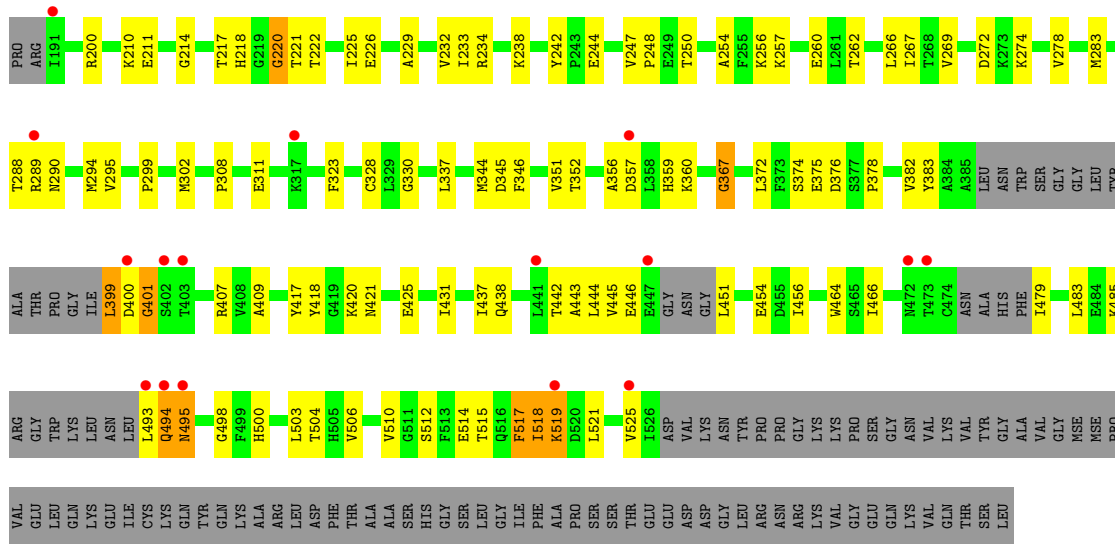
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	363	2784	1780	463	528	7	6	0	0	0
1	B	354	2715	1729	449	523	8	6	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	55	GLY	-	expression tag	UNP Q5X3A8
B	55	GLY	-	expression tag	UNP Q5X3A8

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	12	Total	O	0	0
			12	12		
2	B	4	Total	O	0	0
			4	4		



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	57.78Å 118.25Å 57.79Å 90.00° 114.38° 90.00°	Depositor
Resolution (Å)	19.71 – 2.85 19.71 – 2.46	Depositor EDS
% Data completeness (in resolution range)	89.8 (19.71-2.85) 84.5 (19.71-2.46)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.44 (at 2.47Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, R_{free}	0.262 , 0.316 0.265 , 0.318	Depositor DCC
R_{free} test set	1149 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	36.0	Xtrriage
Anisotropy	0.630	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 32.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.047 for l,-k,h	Xtrriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	5515	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.44% 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	0.36	0/2833	0.63	2/3831 (0.1%)
1	B	0.39	0/2760	0.64	2/3727 (0.1%)
All	All	0.38	0/5593	0.63	4/7558 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	2
All	All	0	4

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	495	ASN	C-N-CD	5.62	140.19	128.40
1	A	115	SER	C-N-CD	5.59	140.15	128.40
1	A	450	GLY	N-CA-C	-5.42	99.54	113.10
1	B	400	ASP	CB-CG-OD2	5.17	122.95	118.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	399	LEU	Peptide
1	A	449	ASN	Peptide
1	B	220	GLY	Peptide
1	B	454	GLU	Mainchain

5.2 Too-close contacts

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	2784	0	2773	100	0
1	B	2715	0	2684	126	0
2	A	12	0	0	1	0
2	B	4	0	0	0	0
All	All	5515	0	5457	214	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 20.

All (214) 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:359:HIS:CD2	1:B:360:LYS:HG3	1.56	1.41
1:B:383:TYR:CE1	1:B:399:LEU:HD13	1.73	1.22
1:B:383:TYR:HE1	1:B:399:LEU:HD13	1.11	0.97
1:B:359:HIS:CD2	1:B:360:LYS:CG	2.51	0.90
1:B:383:TYR:CE1	1:B:399:LEU:CD1	2.54	0.89
1:B:359:HIS:NE2	1:B:360:LYS:HG3	1.88	0.86
1:B:359:HIS:HD2	1:B:360:LYS:HG3	1.40	0.86
1:B:383:TYR:CD1	1:B:399:LEU:HD13	2.11	0.84
1:B:493:LEU:HB3	1:B:498:GLY:O	1.75	0.84
1:B:221:THR:O	1:B:225:ILE:HD13	1.79	0.83
1:B:357:ASP:HB3	1:B:359:HIS:CE1	2.15	0.82
1:B:466:ILE:HD13	1:B:500:HIS:CE1	2.16	0.81
1:A:295:VAL:HG22	1:A:324:HIS:HB3	1.63	0.80
1:B:383:TYR:HE1	1:B:399:LEU:CD1	1.92	0.80
1:B:256:LYS:HG2	1:B:266:LEU:HD23	1.66	0.78
1:A:495:ASN:HB3	1:A:496:PRO:HD3	1.66	0.77
1:B:256:LYS:HG2	1:B:266:LEU:CD2	2.16	0.75
1:B:302:MSE:HB2	1:B:493:LEU:HD11	1.67	0.75
1:A:495:ASN:HB3	1:A:496:PRO:CD	2.17	0.75
1:A:367:GLY:O	1:A:407:ARG:NH2	2.20	0.74
1:A:483:LEU:HD11	1:A:490:LEU:HD22	1.69	0.74
1:A:494:GLN:HA	1:A:494:GLN:OE1	1.87	0.74
1:B:220:GLY:O	1:B:222:THR:N	2.19	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:443:ALA:O	1:A:444:LEU:HG	1.88	0.74
1:B:232:VAL:HG21	1:B:262:THR:HB	1.70	0.73
1:A:524:ALA:O	1:A:528:VAL:HG23	1.89	0.73
1:B:162:ILE:HD12	1:B:162:ILE:O	1.90	0.70
1:B:200:ARG:HD2	1:B:210:LYS:HE2	1.75	0.68
1:A:446:GLU:HG3	1:A:447:GLU:H	1.57	0.68
1:A:194:MSE:HE3	1:A:412:TYR:CB	2.22	0.68
1:B:375:GLU:OE1	1:B:375:GLU:N	2.26	0.68
1:B:220:GLY:N	1:B:357:ASP:OD1	2.27	0.68
1:A:194:MSE:HE1	1:A:409:ALA:HA	1.76	0.67
1:B:344:MSE:HE1	1:B:464:TRP:HZ2	1.58	0.66
1:B:383:TYR:CD1	1:B:399:LEU:CD1	2.76	0.66
1:A:194:MSE:SE	1:B:123:PHE:CE1	2.99	0.65
1:A:328:CYS:HA	1:A:356:ALA:HA	1.79	0.65
1:A:163:HIS:HB2	1:A:168:THR:HG23	1.79	0.65
1:A:448:GLY:O	1:A:450:GLY:HA2	1.97	0.65
1:A:495:ASN:CB	1:A:496:PRO:CD	2.74	0.65
1:A:225:ILE:HG22	1:A:258:ALA:HB2	1.79	0.64
1:A:220:GLY:N	1:A:357:ASP:OD1	2.29	0.64
1:A:200:ARG:HD2	1:B:107:GLU:HA	1.78	0.64
1:B:242:TYR:O	1:B:290:ASN:ND2	2.30	0.64
1:A:194:MSE:HE3	1:A:412:TYR:CG	2.33	0.63
1:B:225:ILE:HD12	1:B:225:ILE:N	2.13	0.63
1:B:256:LYS:O	1:B:260:GLU:HG3	1.98	0.63
1:A:221:THR:HG22	1:A:254:ALA:HB2	1.80	0.63
1:A:383:TYR:CE1	1:A:399:LEU:HG	2.33	0.62
1:A:504:THR:H	1:A:507:HIS:CD2	2.18	0.62
1:B:221:THR:O	1:B:225:ILE:CD1	2.46	0.62
1:B:367:GLY:O	1:B:407:ARG:NH2	2.33	0.62
1:A:173:GLU:OE2	1:B:172:LYS:NZ	2.33	0.61
1:A:192:ASN:OD1	1:A:193:ALA:N	2.28	0.61
1:B:221:THR:HG22	1:B:254:ALA:HB2	1.82	0.61
1:A:444:LEU:HD12	1:A:518:ILE:HG21	1.82	0.61
1:A:180:LEU:HD13	1:B:163:HIS:ND1	2.17	0.60
1:B:504:THR:HG22	1:B:506:VAL:HG12	1.82	0.60
1:B:211:GLU:N	1:B:211:GLU:OE1	2.35	0.59
1:A:197:GLU:OE2	1:A:200:ARG:NH2	2.36	0.59
1:A:421:ASN:ND2	1:B:111:GLU:O	2.31	0.59
1:A:444:LEU:C	1:A:446:GLU:H	2.06	0.59
1:B:299:PRO:HD2	1:B:330:GLY:HA3	1.84	0.59
1:A:433:LEU:HD11	1:A:513:PHE:HB3	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:284:SER:OG	1:A:319:LYS:NZ	2.36	0.58
1:B:466:ILE:HD13	1:B:500:HIS:ND1	2.18	0.58
1:A:398:ILE:O	1:B:257:LYS:NZ	2.35	0.57
1:B:493:LEU:HB3	1:B:498:GLY:C	2.24	0.57
1:A:504:THR:H	1:A:507:HIS:HD2	1.52	0.57
1:A:300:SER:OG	1:A:303:ASN:OD1	2.23	0.57
1:A:424:GLN:O	1:A:428:LYS:HG3	2.05	0.57
1:B:308:PRO:HB2	1:B:311:GLU:OE1	2.04	0.56
1:A:521:LEU:O	1:A:525:VAL:HG23	2.06	0.56
1:B:504:THR:HG22	1:B:506:VAL:H	1.69	0.56
1:B:328:CYS:O	1:B:357:ASP:HB2	2.06	0.56
1:A:444:LEU:HD12	1:A:518:ILE:CG2	2.36	0.55
1:B:302:MSE:HB2	1:B:493:LEU:CD1	2.35	0.55
1:A:386:LEU:HD12	1:A:399:LEU:CD2	2.37	0.55
1:B:344:MSE:HE1	1:B:464:TRP:CZ2	2.40	0.55
1:B:451:LEU:HD21	1:B:525:VAL:HG21	1.89	0.54
1:A:446:GLU:HG3	1:A:447:GLU:N	2.22	0.54
1:B:272:ASP:OD1	1:B:274:LYS:NZ	2.35	0.54
1:B:357:ASP:HB3	1:B:359:HIS:ND1	2.21	0.54
1:B:493:LEU:CB	1:B:498:GLY:O	2.53	0.54
1:A:241:ASP:OD1	1:A:242:TYR:N	2.41	0.53
1:B:225:ILE:N	1:B:225:ILE:CD1	2.71	0.53
1:B:437:ILE:HD12	1:B:503:LEU:HD11	1.90	0.53
1:A:280:PRO:HG3	1:A:312:LEU:HD12	1.90	0.53
1:A:428:LYS:O	1:A:432:ARG:HG3	2.08	0.53
1:B:116:PRO:HB2	1:B:132:PHE:HB3	1.91	0.53
1:A:220:GLY:O	1:A:223:SER:N	2.43	0.52
1:A:449:ASN:N	1:A:450:GLY:HA3	2.25	0.52
1:B:165:LYS:HE3	1:B:169:GLU:OE1	2.10	0.52
1:B:250:THR:HA	1:B:302:MSE:SE	2.59	0.52
1:A:194:MSE:HE2	1:A:408:VAL:HG12	1.91	0.52
1:A:443:ALA:O	1:A:444:LEU:CG	2.55	0.52
1:A:210:LYS:NZ	1:A:211:GLU:OE2	2.43	0.52
1:B:512:SER:O	1:B:512:SER:OG	2.24	0.52
1:A:449:ASN:N	1:A:450:GLY:CA	2.73	0.52
1:A:162:ILE:HG22	1:A:163:HIS:O	2.10	0.51
1:B:323:PHE:CD2	1:B:351:VAL:HG22	2.45	0.51
1:B:283:MSE:SE	1:B:294:MSE:HE3	2.61	0.51
1:A:443:ALA:O	1:A:444:LEU:CD2	2.59	0.51
1:A:386:LEU:HD12	1:A:399:LEU:HD21	1.94	0.50
1:A:452:THR:OG1	1:A:453:SER:N	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:229:ALA:O	1:B:233:ILE:HG12	2.12	0.50
1:B:421:ASN:O	1:B:425:GLU:HG3	2.12	0.50
1:B:234:ARG:O	1:B:238:LYS:N	2.38	0.50
1:B:278:VAL:HG21	1:B:283:MSE:HE3	1.94	0.50
1:B:517:PHE:C	1:B:517:PHE:CD2	2.85	0.50
1:A:440:GLU:HB3	1:A:518:ILE:HD12	1.93	0.49
1:B:218:HIS:HB2	1:B:222:THR:HG21	1.94	0.49
1:B:256:LYS:CG	1:B:266:LEU:CD2	2.90	0.49
1:B:166:GLU:OE2	1:B:417:TYR:OH	2.24	0.49
1:B:218:HIS:ND1	1:B:218:HIS:N	2.59	0.49
1:B:256:LYS:HA	1:B:266:LEU:HD22	1.95	0.49
1:B:352:THR:O	1:B:374:SER:N	2.41	0.48
1:B:248:PRO:HA	1:B:269:VAL:O	2.13	0.48
1:B:233:ILE:HG21	1:B:382:VAL:HG13	1.95	0.48
1:B:359:HIS:CG	1:B:360:LYS:N	2.82	0.48
1:B:226:GLU:OE1	1:B:383:TYR:OH	2.26	0.47
1:B:479:ILE:O	1:B:483:LEU:HB2	2.14	0.47
1:A:231:TYR:O	1:A:234:ARG:NH1	2.46	0.47
1:B:506:VAL:O	1:B:510:VAL:HG23	2.13	0.47
1:B:514:GLU:HG2	1:B:515:THR:N	2.29	0.47
1:B:214:GLY:HA3	1:B:372:LEU:HD23	1.96	0.47
1:A:194:MSE:O	1:A:197:GLU:HB2	2.15	0.47
1:A:427:ALA:O	1:A:431:ILE:HG12	2.14	0.47
1:A:475:ASN:HB3	1:A:478:PHE:HD2	1.79	0.47
1:B:217:THR:HG21	1:B:226:GLU:HG3	1.97	0.47
1:A:253:ALA:O	1:A:257:LYS:HG2	2.15	0.47
1:A:322:PRO:HG3	1:A:378:PRO:HG2	1.97	0.47
1:A:440:GLU:O	1:A:444:LEU:HG	2.15	0.47
1:A:443:ALA:C	1:A:444:LEU:HG	2.36	0.46
1:B:169:GLU:HG3	1:B:170:LEU:N	2.30	0.46
1:B:220:GLY:O	1:B:221:THR:C	2.52	0.46
1:A:443:ALA:O	1:A:444:LEU:HD23	2.16	0.46
1:B:485:LYS:HD2	1:B:485:LYS:N	2.31	0.46
1:A:202:CYS:O	1:A:206:PHE:HD2	1.99	0.46
1:A:454:GLU:HG3	1:A:472:ASN:HB2	1.96	0.46
1:A:492:LEU:HD12	1:A:492:LEU:H	1.80	0.46
1:B:218:HIS:N	1:B:218:HIS:HD1	2.14	0.45
1:A:456:ILE:HD13	1:A:521:LEU:HD21	1.98	0.45
1:B:247:VAL:HG12	1:B:295:VAL:HB	1.97	0.45
1:B:466:ILE:CD1	1:B:500:HIS:CE1	2.96	0.45
1:A:231:TYR:O	1:A:234:ARG:HG3	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:448:GLY:HA3	1:A:449:ASN:OD1	2.16	0.45
1:A:437:ILE:HA	1:A:514:GLU:HB2	1.99	0.45
1:A:216:LEU:HA	1:A:216:LEU:HD12	1.81	0.45
1:A:420:LYS:HD2	1:B:111:GLU:HA	1.98	0.45
1:B:443:ALA:O	1:B:444:LEU:C	2.52	0.45
1:A:210:LYS:O	2:A:701:HOH:O	2.21	0.45
1:A:274:LYS:HA	1:A:459:TYR:CE1	2.52	0.45
1:B:127:VAL:N	1:B:128:GLU:HG3	2.32	0.45
1:B:504:THR:CG2	1:B:506:VAL:HG12	2.47	0.44
1:A:444:LEU:CD1	1:A:518:ILE:CG2	2.95	0.44
1:B:443:ALA:O	1:B:445:VAL:N	2.51	0.44
1:A:218:HIS:HD2	1:A:222:THR:HG21	1.82	0.44
1:B:494:GLN:HB3	1:B:495:ASN:H	1.59	0.44
1:A:172:LYS:NZ	1:B:173:GLU:HG3	2.33	0.44
1:A:215:LEU:O	1:A:370:VAL:HA	2.18	0.43
1:A:295:VAL:HG13	1:A:324:HIS:O	2.18	0.43
1:A:474:CYS:SG	1:A:529:LYS:HG2	2.59	0.43
1:B:127:VAL:H	1:B:128:GLU:HG3	1.83	0.43
1:A:194:MSE:HE3	1:A:412:TYR:HB3	1.99	0.43
1:B:328:CYS:HA	1:B:356:ALA:HA	1.99	0.43
1:B:515:THR:OG1	1:B:519:LYS:HD3	2.19	0.43
1:B:517:PHE:O	1:B:521:LEU:N	2.52	0.43
1:A:324:HIS:ND1	1:A:353:SER:OG	2.44	0.43
1:B:443:ALA:O	1:B:446:GLU:N	2.52	0.43
1:A:218:HIS:CD2	1:B:218:HIS:HD2	2.37	0.43
1:B:493:LEU:HD12	1:B:494:GLN:H	1.83	0.43
1:B:233:ILE:HB	1:B:382:VAL:HG21	2.00	0.43
1:B:323:PHE:CE2	1:B:351:VAL:HG22	2.54	0.43
1:B:517:PHE:CE2	1:B:518:ILE:HD12	2.54	0.43
1:B:220:GLY:HA2	1:B:357:ASP:OD2	2.19	0.42
1:A:445:VAL:HA	1:A:451:LEU:O	2.18	0.42
1:B:345:ASP:HB2	1:B:346:PHE:H	1.69	0.42
1:A:257:LYS:HE3	1:A:257:LYS:HB3	1.79	0.42
1:B:244:GLU:HB3	1:B:267:ILE:HG12	2.00	0.42
1:A:232:VAL:HG13	1:A:243:PRO:HG2	2.01	0.42
1:A:244:GLU:OE1	1:A:288:THR:OG1	2.34	0.42
1:A:301:PHE:CZ	1:A:500:HIS:CE1	3.07	0.42
1:B:238:LYS:HE2	1:B:289:ARG:HH12	1.84	0.42
1:B:374:SER:HB3	1:B:376:ASP:OD1	2.20	0.42
1:A:437:ILE:O	1:A:518:ILE:HD11	2.18	0.42
1:B:288:THR:HG23	1:B:290:ASN:H	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:456:ILE:HD12	1:B:521:LEU:HD21	2.00	0.42
1:B:200:ARG:HB2	1:B:210:LYS:NZ	2.35	0.42
1:B:337:LEU:HD13	1:B:431:ILE:HD11	2.02	0.42
1:B:163:HIS:NE2	1:B:418:TYR:OH	2.53	0.41
1:A:307:ASP:O	1:A:309:ILE:N	2.53	0.41
1:A:399:LEU:HA	1:B:257:LYS:CE	2.51	0.41
1:B:218:HIS:NE2	1:B:401:GLY:HA2	2.35	0.41
1:B:233:ILE:HG22	1:B:382:VAL:HG22	2.02	0.41
1:B:165:LYS:O	1:B:169:GLU:HG2	2.21	0.41
1:B:274:LYS:N	1:B:274:LYS:HD3	2.36	0.41
1:B:438:GLN:O	1:B:442:THR:HG23	2.20	0.41
1:B:483:LEU:HD11	1:B:521:LEU:HA	2.01	0.41
1:A:265:ILE:HD12	1:A:265:ILE:N	2.35	0.41
1:B:323:PHE:O	1:B:323:PHE:CG	2.74	0.41
1:A:173:GLU:CD	1:B:128:GLU:HG2	2.41	0.41
1:A:215:LEU:CD2	1:A:398:ILE:HD13	2.51	0.41
1:B:234:ARG:HD2	1:B:378:PRO:HB2	2.02	0.41
1:A:116:PRO:O	1:A:117:GLN:C	2.56	0.41
1:A:302:MSE:HB3	1:A:302:MSE:HE2	1.76	0.41
1:B:357:ASP:HB3	1:B:359:HIS:HE1	1.80	0.41
1:B:420:LYS:HB3	1:B:420:LYS:HE3	1.42	0.40
1:B:174:VAL:CG2	1:B:409:ALA:HB1	2.51	0.40
1:B:357:ASP:CB	1:B:359:HIS:CE1	2.93	0.40
1:A:221:THR:O	1:A:225:ILE:HG12	2.21	0.40
1:A:399:LEU:HA	1:B:257:LYS:HE3	2.03	0.40
1:A:272:ASP:HB3	1:A:275:THR:HB	2.04	0.40
1:A:448:GLY:C	1:A:450:GLY:CA	2.90	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	351/551 (64%)	323 (92%)	27 (8%)	1 (0%)	41	68
1	B	338/551 (61%)	295 (87%)	40 (12%)	3 (1%)	17	43
All	All	689/1102 (62%)	618 (90%)	67 (10%)	4 (1%)	25	53

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	495	ASN
1	B	494	GLN
1	B	401	GLY
1	B	367	GLY

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	299/448 (67%)	292 (98%)	7 (2%)	50	78
1	B	294/448 (66%)	289 (98%)	5 (2%)	60	83
All	All	593/896 (66%)	581 (98%)	12 (2%)	55	80

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	112	GLU
1	A	115	SER
1	A	118	ASP
1	A	252	HIS
1	A	357	ASP
1	A	368	THR
1	A	494	GLN
1	B	173	GLU
1	B	399	LEU
1	B	517	PHE
1	B	518	ILE
1	B	519	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	218	HIS
1	A	281	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 monosaccharides 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	357/551 (64%)	-0.16	8 (2%) 62 59	30, 52, 110, 149	0
1	B	348/551 (63%)	0.07	22 (6%) 20 15	35, 60, 135, 172	0
All	All	705/1102 (63%)	-0.05	30 (4%) 35 30	30, 57, 127, 172	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	403	THR	5.4
1	B	472	ASN	5.1
1	B	495	ASN	4.7
1	B	473	THR	4.2
1	B	447	GLU	4.2
1	B	402	SER	4.1
1	B	400	ASP	3.9
1	B	132	PHE	3.8
1	B	131	HIS	3.8
1	A	125	VAL	3.4
1	B	129	LYS	3.4
1	B	289	ARG	3.4
1	A	117	GLN	3.3
1	B	107	GLU	3.2
1	A	495	ASN	3.0
1	A	482	GLU	3.0
1	B	169	GLU	2.8
1	B	493	LEU	2.8
1	B	317	LYS	2.6
1	A	111	GLU	2.5
1	A	449	ASN	2.4
1	B	160	TYR	2.3
1	B	441	LEU	2.3
1	B	525	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	494	GLN	2.3
1	B	519	LYS	2.1
1	A	242	TYR	2.1
1	B	191	ILE	2.1
1	B	357	ASP	2.0
1	A	445	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.