Full wwPDB X-ray Structure Validation Report ⓘ

Jun 18, 2024 – 03:14 AM EDT

PDB ID	:	5XSD
Title	:	XylFII-LytSN complex mutant - D103A
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Deposited on	:	2017-06-13
Resolution	:	2.50 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:

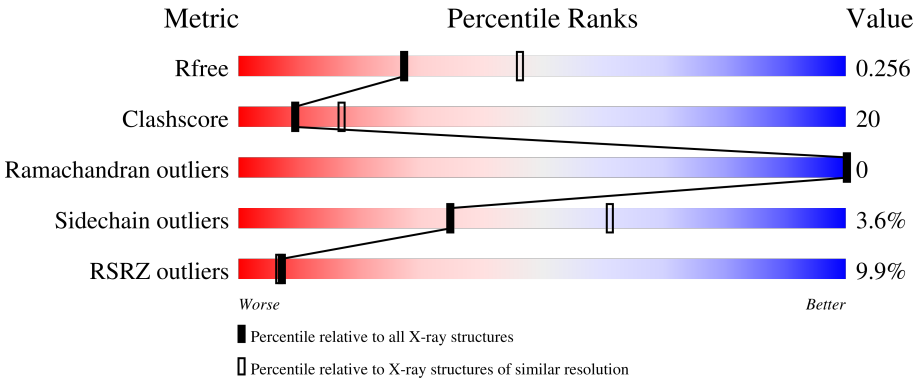
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 2.50 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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 <=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	306	10% 57% 21% 18%
1	B	306	4% 72% 16% 10%
2	L	147	13% 57% 24% 18%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 5138 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 Periplasmic binding protein/LacI transcriptional regulator.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	250	Total	C	N	O	S	0	0	0
			1918	1200	335	375	8			
1	B	276	Total	C	N	O	S	0	0	0
			2104	1314	363	418	9			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	MET	-	expression tag	UNP A6LW07
A	-2	ALA	-	expression tag	UNP A6LW07
A	-1	ARG	-	expression tag	UNP A6LW07
A	0	SER	-	expression tag	UNP A6LW07
A	103	ALA	ASP	engineered mutation	UNP A6LW07
B	-3	MET	-	expression tag	UNP A6LW07
B	-2	ALA	-	expression tag	UNP A6LW07
B	-1	ARG	-	expression tag	UNP A6LW07
B	0	SER	-	expression tag	UNP A6LW07
B	103	ALA	ASP	engineered mutation	UNP A6LW07

- Molecule 2 is a protein called Signal transduction histidine kinase, LytS.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	121	Total	C	N	O	S	0	0	0
			976	613	157	202	4			

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	-12	MET	-	expression tag	UNP A6LW08
L	-11	GLY	-	expression tag	UNP A6LW08
L	-10	SER	-	expression tag	UNP A6LW08
L	-9	SER	-	expression tag	UNP A6LW08

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Chain	Residue	Modelled	Actual	Comment	Reference
L	-8	HIS	-	expression tag	UNP A6LW08
L	-7	HIS	-	expression tag	UNP A6LW08
L	-6	HIS	-	expression tag	UNP A6LW08
L	-5	HIS	-	expression tag	UNP A6LW08
L	-4	HIS	-	expression tag	UNP A6LW08
L	-3	HIS	-	expression tag	UNP A6LW08
L	-2	GLN	-	expression tag	UNP A6LW08
L	-1	GLY	-	expression tag	UNP A6LW08
L	0	SER	-	expression tag	UNP A6LW08

- Molecule 3 is water.

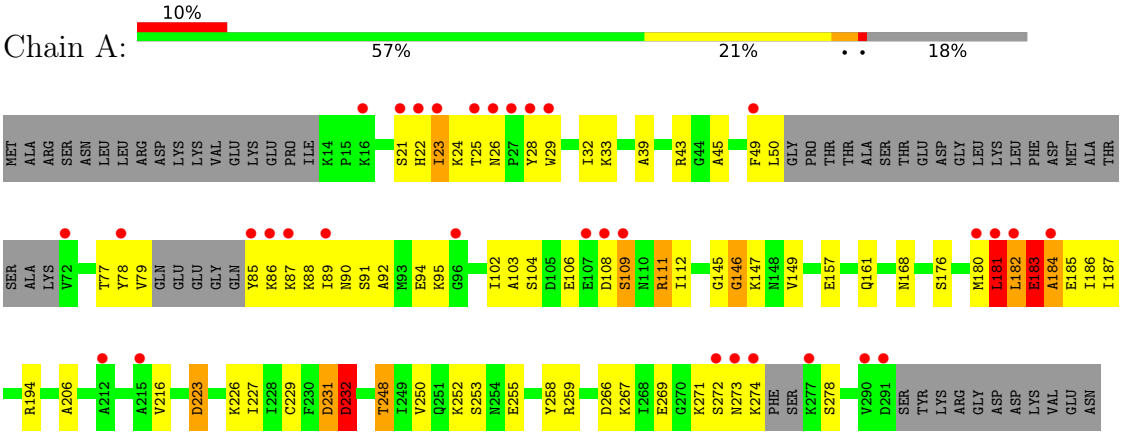
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	58	Total O 58 58	0	0
3	B	68	Total O 68 68	0	0
3	L	14	Total O 14 14	0	0

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.

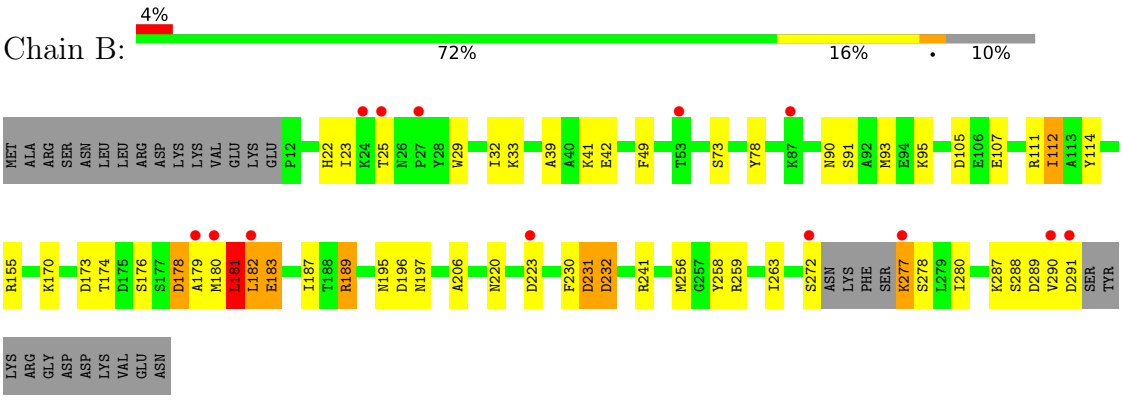
• Molecule 1: Periplasmic binding protein/LacI transcriptional regulator

Chain A:



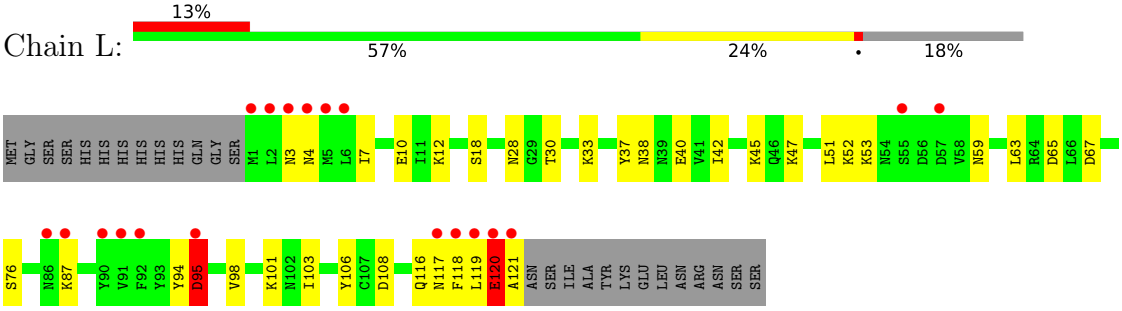
• Molecule 1: Periplasmic binding protein/LacI transcriptional regulator

Chain B:



• Molecule 2: Signal transduction histidine kinase, LytS

Chain L:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α, β, γ	144.96Å 144.96Å 103.07Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.64 – 2.50 29.64 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.7 (29.64-2.50) 99.7 (29.64-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.51 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.229 , 0.253 0.236 , 0.256	Depositor DCC
R_{free} test set	1892 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å^2)	46.4	Xtriage
Anisotropy	0.180	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 47.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	5138	wwPDB-VP
Average B, all atoms (Å^2)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.34% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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	0.57	0/1931	0.92	11/2594 (0.4%)
1	B	0.53	0/2122	0.95	9/2856 (0.3%)
2	L	0.38	0/991	0.93	5/1339 (0.4%)
All	All	0.52	0/5044	0.93	25/6789 (0.4%)

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
2	L	0	1
All	All	0	3

There are no bond length outliers.

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	L	120	GLU	N-CA-C	18.37	160.61	111.00
1	B	182	LEU	CB-CA-C	-16.32	79.19	110.20
1	B	231	ASP	N-CA-C	15.79	153.65	111.00
2	L	120	GLU	CB-CA-C	-14.66	81.07	110.40
1	B	182	LEU	N-CA-C	12.80	145.55	111.00
1	B	181	LEU	C-N-CA	12.16	152.10	121.70
1	B	232	ASP	N-CA-C	10.92	140.49	111.00
1	B	231	ASP	CB-CA-C	-10.73	88.93	110.40
1	A	184	ALA	CB-CA-C	-10.11	94.93	110.10
1	A	231	ASP	N-CA-C	9.86	137.61	111.00
2	L	95	ASP	CB-CA-C	-9.04	92.32	110.40
1	A	181	LEU	CB-CA-C	-7.69	95.59	110.20
1	A	182	LEU	CB-CG-CD2	7.69	124.07	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	181	LEU	N-CA-C	7.43	131.06	111.00
2	L	95	ASP	N-CA-C	7.15	130.30	111.00
1	A	232	ASP	N-CA-C	6.73	129.17	111.00
1	A	23	ILE	N-CA-C	-6.17	94.35	111.00
1	A	146	GLY	N-CA-C	-6.12	97.79	113.10
1	B	178	ASP	N-CA-C	-6.11	94.49	111.00
1	A	23	ILE	CB-CA-C	6.01	123.62	111.60
1	B	181	LEU	CA-C-N	-5.67	104.73	117.20
2	L	87	LYS	N-CA-C	5.27	125.23	111.00
1	B	189	ARG	NE-CZ-NH1	-5.09	117.76	120.30
1	A	184	ALA	N-CA-C	5.02	124.55	111.00
1	A	181	LEU	CA-C-N	5.01	128.23	117.20

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	181	LEU	Peptide
1	A	183	GLU	Peptide
2	L	120	GLU	Peptide

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	1918	0	1987	101	4
1	B	2104	0	2165	67	1
2	L	976	0	939	32	1
3	A	58	0	0	23	1
3	B	68	0	0	40	0
3	L	14	0	0	17	0
All	All	5138	0	5091	200	6

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 (200) 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)
2:L:119:LEU:HG	3:L:202:HOH:O	1.33	1.28
1:A:226:LYS:HE2	3:A:411:HOH:O	1.42	1.18
1:B:22:HIS:HA	3:B:409:HOH:O	1.43	1.18
1:A:182:LEU:HD13	1:A:187:ILE:CB	1.73	1.16
1:B:259:ARG:NE	3:B:401:HOH:O	1.81	1.13
1:A:147:LYS:NZ	3:A:402:HOH:O	1.83	1.10
1:B:288:SER:N	3:B:404:HOH:O	1.85	1.09
1:A:182:LEU:HD13	1:A:187:ILE:HB	1.04	1.04
1:B:259:ARG:CD	3:B:401:HOH:O	2.06	1.03
1:B:287:LYS:HB3	3:B:404:HOH:O	1.59	1.02
1:A:111:ARG:HG2	1:A:111:ARG:HH11	1.19	1.01
1:A:28:TYR:OH	1:A:232:ASP:OD1	1.79	0.98
1:A:94:GLU:OE2	3:A:401:HOH:O	1.81	0.98
1:B:195:ASN:ND2	3:B:406:HOH:O	1.90	0.97
1:B:259:ARG:HD2	3:B:401:HOH:O	1.65	0.97
1:A:182:LEU:CD1	1:A:187:ILE:HB	1.95	0.96
1:A:157:GLU:OE1	3:A:403:HOH:O	1.84	0.96
2:L:95:ASP:OD1	3:L:201:HOH:O	1.81	0.96
1:B:22:HIS:ND1	3:B:409:HOH:O	1.98	0.95
1:B:272:SER:O	3:B:402:HOH:O	1.82	0.94
1:B:189:ARG:NH2	3:B:407:HOH:O	1.92	0.93
1:A:182:LEU:HD11	1:A:187:ILE:HG21	1.51	0.92
1:B:189:ARG:NE	3:B:407:HOH:O	1.92	0.92
1:B:173:ASP:OD2	3:B:405:HOH:O	1.87	0.92
1:A:43:ARG:NH2	1:A:266:ASP:OD1	2.02	0.92
1:B:22:HIS:CG	3:B:409:HOH:O	2.20	0.92
1:B:277:LYS:NZ	3:B:401:HOH:O	1.95	0.92
1:A:45:ALA:O	3:A:404:HOH:O	1.86	0.91
1:B:22:HIS:CA	3:B:409:HOH:O	2.10	0.90
1:A:272:SER:HA	1:A:273:ASN:HB2	1.50	0.90
1:A:23:ILE:HB	3:A:416:HOH:O	1.70	0.89
1:B:78:TYR:CE2	3:B:409:HOH:O	2.24	0.87
2:L:116:GLN:O	3:L:202:HOH:O	1.91	0.87
1:A:86:LYS:HG3	1:A:108:ASP:CG	1.95	0.87
1:B:174:THR:OG1	3:B:408:HOH:O	1.92	0.86
1:A:91:SER:N	3:A:408:HOH:O	2.04	0.85
1:B:195:ASN:OD1	3:B:406:HOH:O	1.93	0.85
2:L:94:TYR:CD2	3:L:214:HOH:O	2.29	0.85
1:A:182:LEU:CD1	1:A:187:ILE:CB	2.53	0.85
2:L:119:LEU:CB	3:L:202:HOH:O	2.18	0.85
1:B:22:HIS:CB	3:B:409:HOH:O	2.24	0.83
2:L:98:VAL:N	3:L:205:HOH:O	2.11	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:168:ASN:O	3:A:406:HOH:O	1.96	0.82
1:A:182:LEU:CD1	1:A:187:ILE:CG2	2.57	0.82
1:B:195:ASN:CG	3:B:406:HOH:O	2.16	0.82
1:A:86:LYS:HG3	1:A:108:ASP:OD2	1.80	0.81
1:A:106:GLU:HG3	1:A:108:ASP:OD1	1.81	0.81
1:A:111:ARG:HG2	1:A:111:ARG:NH1	1.95	0.80
2:L:119:LEU:O	3:L:203:HOH:O	1.99	0.80
2:L:119:LEU:N	3:L:202:HOH:O	2.15	0.80
1:A:253:SER:N	3:A:410:HOH:O	2.07	0.80
1:A:183:GLU:HG3	1:A:184:ALA:HB3	1.64	0.79
1:B:105:ASP:OD2	1:B:111:ARG:NH1	2.14	0.79
1:A:182:LEU:CD1	1:A:187:ILE:HG21	2.13	0.78
1:B:287:LYS:CA	3:B:404:HOH:O	2.29	0.78
1:A:161:GLN:NE2	3:A:409:HOH:O	2.06	0.77
1:B:189:ARG:CZ	3:B:407:HOH:O	2.19	0.77
1:A:269:GLU:OE2	3:A:407:HOH:O	2.03	0.76
1:B:197:ASN:N	3:B:412:HOH:O	2.09	0.75
1:A:255:GLU:N	1:A:255:GLU:OE1	2.19	0.75
1:B:90:ASN:O	3:B:410:HOH:O	2.04	0.74
1:B:181:LEU:HB3	3:B:413:HOH:O	1.88	0.73
2:L:119:LEU:CG	3:L:202:HOH:O	2.00	0.72
1:B:42:GLU:OE2	3:B:411:HOH:O	2.08	0.71
1:A:176:SER:HB2	1:A:182:LEU:HD22	1.72	0.70
1:A:88:LYS:O	3:A:408:HOH:O	2.08	0.70
1:B:78:TYR:CD2	3:B:409:HOH:O	2.44	0.70
1:B:22:HIS:HD2	1:B:23:ILE:HG12	1.57	0.70
1:B:287:LYS:CB	3:B:404:HOH:O	2.24	0.70
2:L:65:ASP:OD1	3:L:204:HOH:O	2.10	0.68
1:A:259:ARG:HH11	1:A:278:SER:HB2	1.59	0.67
2:L:59:ASN:HB3	2:L:117:ASN:ND2	2.09	0.67
1:A:271:LYS:NZ	3:A:412:HOH:O	2.17	0.66
1:B:114:TYR:O	1:B:278:SER:OG	2.12	0.66
2:L:30:THR:OG1	2:L:33:LYS:HG3	1.95	0.66
1:B:178:ASP:O	1:B:179:ALA:HB3	1.96	0.66
1:A:89:ILE:HG21	1:A:109:SER:HB2	1.77	0.65
1:A:24:LYS:O	1:A:24:LYS:HG2	1.97	0.65
1:A:23:ILE:HG22	1:A:25:THR:HG23	1.79	0.64
1:B:155:ARG:HG2	1:B:230:PHE:CZ	2.33	0.63
1:B:173:ASP:CG	3:B:405:HOH:O	2.35	0.63
1:B:23:ILE:HG22	1:B:25:THR:H	1.64	0.63
1:A:79:VAL:HG13	1:A:85:TYR:CD2	2.34	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:183:GLU:HG3	1:A:185:GLU:H	1.63	0.62
1:A:92:ALA:N	3:A:408:HOH:O	2.09	0.62
1:A:259:ARG:NH1	1:A:278:SER:HB2	2.15	0.60
1:A:79:VAL:HB	1:A:104:SER:HB2	1.84	0.60
1:A:272:SER:CA	1:A:273:ASN:HB2	2.25	0.59
1:B:174:THR:CB	3:B:408:HOH:O	2.46	0.59
1:A:272:SER:HB3	1:A:274:LYS:HG2	1.85	0.58
2:L:94:TYR:HD2	3:L:214:HOH:O	1.73	0.58
1:B:197:ASN:CA	3:B:412:HOH:O	2.50	0.58
1:A:106:GLU:HG3	1:A:106:GLU:O	2.03	0.58
1:B:107:GLU:HG3	1:B:111:ARG:HH12	1.68	0.58
1:B:176:SER:HB2	1:B:182:LEU:HD23	1.86	0.58
1:A:91:SER:HA	1:A:94:GLU:HB2	1.86	0.57
1:B:22:HIS:CD2	1:B:23:ILE:HG12	2.39	0.57
2:L:120:GLU:CA	3:L:203:HOH:O	2.51	0.57
1:B:181:LEU:O	3:B:413:HOH:O	2.17	0.57
2:L:94:TYR:CE2	3:L:214:HOH:O	2.52	0.57
1:B:290:VAL:N	3:B:419:HOH:O	2.37	0.57
1:A:180:MET:O	1:A:181:LEU:HB2	2.05	0.56
1:A:223:ASP:OD1	3:A:411:HOH:O	2.17	0.56
1:A:229:CYS:SG	1:A:248:THR:HG23	2.45	0.56
2:L:3:ASN:OD1	2:L:3:ASN:N	2.36	0.56
1:A:272:SER:HA	1:A:273:ASN:CB	2.31	0.56
1:B:107:GLU:HG3	1:B:111:ARG:NH1	2.20	0.56
1:A:21:SER:HB2	1:A:49:PHE:HE1	1.69	0.56
1:A:272:SER:CB	1:A:274:LYS:HG2	2.35	0.56
1:B:178:ASP:O	1:B:179:ALA:CB	2.54	0.56
1:B:29:TRP:CE3	1:B:32:ILE:HD12	2.40	0.56
1:A:102:ILE:O	1:A:103:ALA:HB3	2.07	0.55
1:B:287:LYS:C	3:B:404:HOH:O	2.24	0.55
1:B:111:ARG:HG2	1:B:111:ARG:O	2.07	0.54
1:A:182:LEU:O	1:A:182:LEU:HD12	2.06	0.54
1:B:93:MET:HE1	1:B:112:ILE:HD13	1.89	0.54
2:L:121:ALA:N	3:L:203:HOH:O	2.40	0.54
1:A:86:LYS:CG	1:A:108:ASP:OD2	2.53	0.54
1:A:232:ASP:HB3	1:A:250:VAL:HG11	1.88	0.54
1:A:253:SER:CB	3:A:410:HOH:O	2.54	0.54
1:B:241:ARG:HG3	1:B:290:VAL:HG11	1.90	0.54
1:A:106:GLU:O	1:A:109:SER:OG	2.26	0.53
1:B:73:SER:OG	3:B:414:HOH:O	2.19	0.53
1:B:91:SER:O	1:B:95:LYS:HG3	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:87:LYS:HG2	1:A:90:ASN:HB2	1.91	0.53
1:A:77:THR:O	1:A:102:ILE:HG22	2.10	0.52
2:L:59:ASN:HB3	2:L:117:ASN:HD22	1.75	0.52
2:L:12:LYS:NZ	2:L:108:ASP:HB3	2.25	0.51
1:A:22:HIS:HB2	1:A:29:TRP:CE2	2.46	0.51
1:A:272:SER:OG	1:A:274:LYS:HG2	2.11	0.51
1:B:33:LYS:HD2	1:B:49:PHE:CD2	2.47	0.50
1:A:206:ALA:HB2	1:A:231:ASP:HB2	1.94	0.50
1:A:176:SER:CB	1:A:182:LEU:HD22	2.41	0.49
1:A:194:ARG:NH1	3:A:417:HOH:O	2.45	0.49
1:A:28:TYR:CZ	1:A:232:ASP:OD1	2.63	0.49
2:L:38:ASN:O	2:L:42:ILE:HG13	2.12	0.49
1:A:183:GLU:CG	1:A:184:ALA:HB3	2.40	0.49
2:L:4:ASN:HB3	2:L:118:PHE:CE2	2.48	0.49
1:A:86:LYS:N	1:A:106:GLU:OE1	2.47	0.48
1:B:220:ASN:ND2	3:B:403:HOH:O	1.85	0.48
1:A:21:SER:HB2	1:A:49:PHE:CE1	2.48	0.48
1:A:23:ILE:CG2	1:A:25:THR:HG23	2.44	0.48
1:A:146:GLY:HA3	1:A:149:VAL:HG23	1.96	0.47
1:B:259:ARG:NH2	1:B:278:SER:HA	2.29	0.47
1:A:29:TRP:CE3	1:A:32:ILE:HD12	2.49	0.47
1:A:106:GLU:CG	1:A:108:ASP:OD1	2.56	0.47
2:L:10:GLU:OE1	2:L:47:LYS:NZ	2.34	0.47
1:A:23:ILE:CA	3:A:416:HOH:O	2.63	0.46
1:A:252:LYS:HE2	1:A:255:GLU:OE2	2.16	0.46
1:A:22:HIS:HA	1:A:78:TYR:CD2	2.50	0.46
1:A:26:ASN:HB3	1:A:29:TRP:HD1	1.79	0.46
1:A:22:HIS:HD2	3:A:416:HOH:O	1.97	0.46
1:A:267:LYS:HE2	1:A:274:LYS:HE2	1.98	0.46
1:B:263:ILE:HG12	1:B:277:LYS:HE3	1.98	0.46
2:L:30:THR:OG1	2:L:30:THR:O	2.32	0.46
1:A:252:LYS:HB3	1:A:255:GLU:CD	2.37	0.45
1:A:183:GLU:O	1:A:186:ILE:N	2.44	0.45
1:A:23:ILE:N	3:A:416:HOH:O	2.49	0.45
2:L:118:PHE:C	3:L:202:HOH:O	2.48	0.45
1:A:182:LEU:O	1:A:182:LEU:HG	2.17	0.45
1:B:39:ALA:HB2	1:B:258:TYR:CD1	2.52	0.45
1:B:206:ALA:HB2	1:B:231:ASP:HB2	1.99	0.45
1:B:170:LYS:NZ	3:B:422:HOH:O	2.48	0.44
2:L:95:ASP:C	3:L:205:HOH:O	2.56	0.44
1:B:174:THR:HB	3:B:408:HOH:O	2.15	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:102:ILE:O	1:A:102:ILE:HG23	2.16	0.44
1:B:291:ASP:N	3:B:419:HOH:O	2.50	0.44
2:L:52:LYS:HG2	2:L:63:LEU:HD13	1.99	0.44
1:B:197:ASN:CB	3:B:412:HOH:O	2.64	0.44
1:B:277:LYS:HA	1:B:278:SER:HA	1.80	0.44
1:A:22:HIS:CD2	3:A:416:HOH:O	2.71	0.44
2:L:18:SER:HB2	2:L:40:GLU:HB2	2.00	0.43
1:B:256:MET:HG2	1:B:280:ILE:HG13	1.99	0.43
1:A:91:SER:CA	3:A:408:HOH:O	2.59	0.43
1:A:232:ASP:HB3	1:A:250:VAL:CG1	2.48	0.43
1:A:253:SER:HB2	3:A:410:HOH:O	2.18	0.43
2:L:121:ALA:O	3:L:203:HOH:O	2.20	0.43
1:A:91:SER:HA	1:A:94:GLU:CB	2.49	0.43
1:A:182:LEU:O	1:A:182:LEU:CG	2.67	0.43
2:L:45:LYS:NZ	2:L:67:ASP:OD1	2.43	0.43
1:A:91:SER:O	1:A:95:LYS:HG3	2.19	0.42
1:A:216:VAL:HG21	1:A:227:ILE:HD11	2.01	0.42
1:B:182:LEU:O	1:B:183:GLU:C	2.58	0.42
1:A:111:ARG:NH1	1:A:111:ARG:CG	2.72	0.42
1:B:179:ALA:O	1:B:180:MET:C	2.58	0.42
1:A:79:VAL:HG13	1:A:85:TYR:CE2	2.54	0.42
1:A:89:ILE:HD12	1:A:106:GLU:HG2	2.02	0.42
1:A:49:PHE:C	1:A:50:LEU:HD23	2.40	0.42
1:A:272:SER:HB3	1:A:274:LYS:H	1.85	0.42
1:B:41:LYS:HB2	1:B:41:LYS:HE3	1.86	0.41
1:A:39:ALA:HB2	1:A:258:TYR:CD1	2.56	0.41
1:A:29:TRP:CZ3	1:A:32:ILE:HD12	2.55	0.41
1:A:182:LEU:HD13	1:A:187:ILE:CG1	2.44	0.41
1:A:87:LYS:HA	1:A:90:ASN:HB2	2.03	0.41
1:A:112:ILE:HD13	1:A:112:ILE:HA	1.94	0.41
2:L:7:ILE:HG21	2:L:51:LEU:HD21	2.03	0.41
1:A:183:GLU:CG	1:A:183:GLU:O	2.69	0.40
1:B:182:LEU:HD22	1:B:187:ILE:HG12	2.03	0.40
2:L:103:ILE:HA	2:L:106:TYR:CD2	2.56	0.40
2:L:53:LYS:HB3	2:L:53:LYS:HE2	1.80	0.40

All (6) 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:GLY:CA	1:A:181:LEU:CD2[7_555]	1.58	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:181:LEU:O	1:A:181:LEU:O[7_555]	1.59	0.61
1:B:180:MET:CG	1:B:183:GLU:OE2[8_554]	2.00	0.20
1:A:145:GLY:C	1:A:181:LEU:CD2[7_555]	2.02	0.18
2:L:28:ASN:OD1	3:A:401:HOH:O[8_554]	2.11	0.09
1:A:145:GLY:O	1:A:181:LEU:CD2[7_555]	2.17	0.03

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	242/306 (79%)	223 (92%)	19 (8%)	0	100	100
1	B	272/306 (89%)	256 (94%)	16 (6%)	0	100	100
2	L	119/147 (81%)	114 (96%)	5 (4%)	0	100	100
All	All	633/759 (83%)	593 (94%)	40 (6%)	0	100	100

There are no Ramachandran outliers to report.

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	213/261 (82%)	205 (96%)	8 (4%)	33	58
1	B	233/261 (89%)	225 (97%)	8 (3%)	37	63
2	L	110/133 (83%)	106 (96%)	4 (4%)	35	61
All	All	556/655 (85%)	536 (96%)	20 (4%)	35	61

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33	LYS
1	A	109	SER
1	A	111	ARG
1	A	181	LEU
1	A	183	GLU
1	A	223	ASP
1	A	232	ASP
1	A	248	THR
1	B	112	ILE
1	B	181	LEU
1	B	183	GLU
1	B	196	ASP
1	B	223	ASP
1	B	232	ASP
1	B	277	LYS
1	B	289	ASP
2	L	37	TYR
2	L	76	SER
2	L	95	ASP
2	L	101	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	110	ASN
1	A	273	ASN
2	L	117	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, 95^{th} 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	250/306 (81%)	0.76	32 (12%) 3 3	32, 50, 90, 98	0
1	B	276/306 (90%)	0.29	13 (4%) 31 33	31, 47, 68, 75	0
2	L	121/147 (82%)	0.84	19 (15%) 2 1	52, 76, 94, 108	0
All	All	647/759 (85%)	0.57	64 (9%) 7 7	31, 52, 90, 108	0

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	25	THR	8.0
2	L	1	MET	7.3
1	A	181	LEU	7.0
2	L	2	LEU	6.7
1	A	85	TYR	6.4
2	L	121	ALA	5.9
1	A	184	ALA	5.6
1	A	273	ASN	5.6
1	A	182	LEU	5.4
1	A	72	VAL	5.4
1	A	108	ASP	5.0
1	A	23	ILE	4.8
1	B	182	LEU	4.5
1	A	28	TYR	4.3
2	L	3	ASN	4.2
2	L	87	LYS	4.1
1	A	277	LYS	4.0
1	A	96	GLY	4.0
2	L	91	VAL	4.0
2	L	6	LEU	4.0
1	B	25	THR	3.9
1	A	22	HIS	3.9
1	B	272	SER	3.9

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Mol	Chain	Res	Type	RSRZ
1	A	274	LYS	3.9
2	L	120	GLU	3.7
1	A	290	VAL	3.6
1	A	86	LYS	3.3
2	L	92	PHE	3.3
2	L	90	TYR	3.3
2	L	57	ASP	3.2
1	B	179	ALA	3.2
1	B	290	VAL	3.2
2	L	5	MET	3.1
1	B	277	LYS	3.1
1	A	180	MET	3.0
1	A	291	ASP	3.0
1	A	78	TYR	3.0
1	A	49	PHE	2.9
1	A	89	ILE	2.9
2	L	86	ASN	2.9
1	B	223	ASP	2.9
1	A	27	PRO	2.9
1	A	26	ASN	2.8
1	B	180	MET	2.8
2	L	55	SER	2.7
1	B	291	ASP	2.7
2	L	118	PHE	2.7
1	A	107	GLU	2.6
2	L	117	ASN	2.5
1	A	87	LYS	2.5
1	A	16	LYS	2.5
2	L	95	ASP	2.4
1	B	27	PRO	2.4
2	L	4	ASN	2.4
2	L	119	LEU	2.3
1	A	272	SER	2.3
1	B	53	THR	2.2
1	B	87	LYS	2.2
1	A	29	TRP	2.2
1	A	109	SER	2.2
1	B	24	LYS	2.1
1	A	215	ALA	2.0
1	A	212	ALA	2.0
1	A	21	SER	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.