Full wwPDB X-ray Structure Validation Report (i)

Feb 4, 2024 – 11:02 PM EST

PDB ID	:	1S4M
Title	:	Crystal structure of flavin binding to FAD synthetase from Thermotoga maritina
Authors	:	Wang, W.; Kim, R.; Yokota, H.; Kim, S.-H.; Berkeley Structural Genomics Center (BSGC)
Deposited on	:	2004-01-16
Resolution	:	2.10 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 (i) 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 (i)) were used in the production of this report:

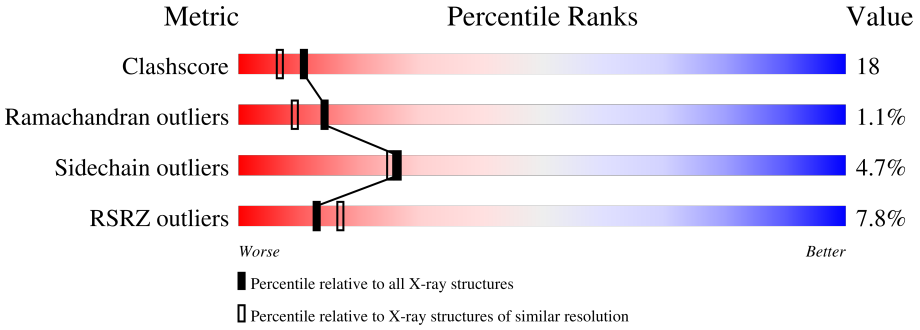
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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))
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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	293	9% 69% 22% • • 5%
1	B	293	5% 62% 26% 5% 7%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 4715 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.

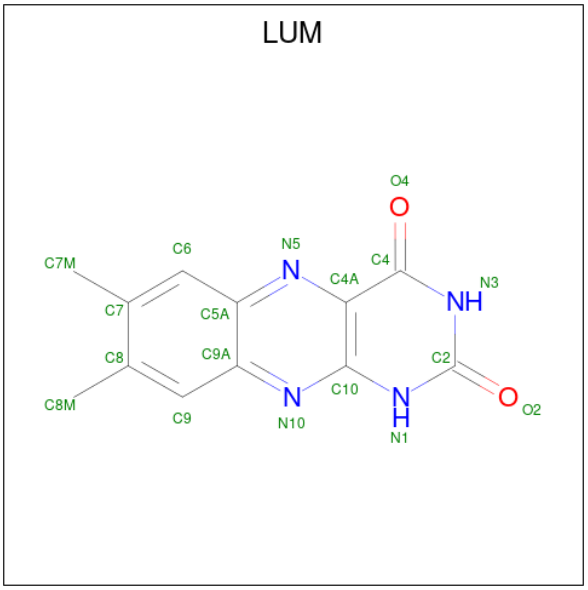
- Molecule 1 is a protein called riboflavin kinase/FMN adenylyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	277	2244	1443	387	407	7	0	0	0
1	B	272	2206	1424	376	399	7	0	0	0

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
2	A	1	1	1	0	0

- Molecule 3 is LUMICHROME (three-letter code: LUM) (formula: $C_{12}H_{10}N_4O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	18	12	4	2	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	B	1	18	12	4	2	0	0

- Molecule 4 is water.

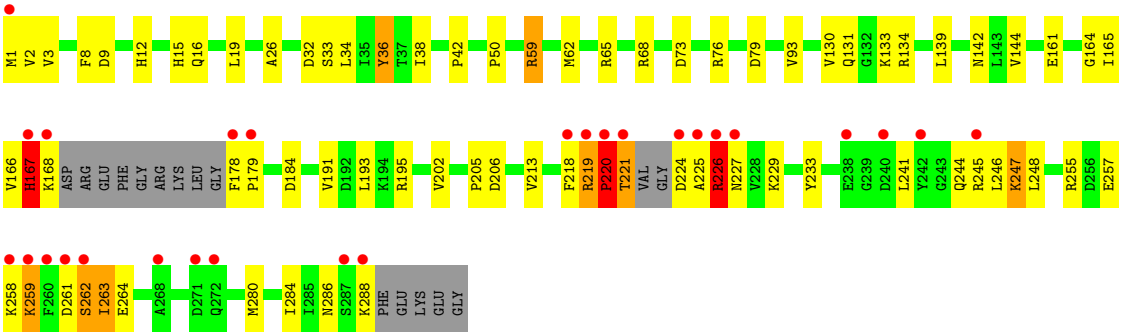
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	116	116	116	0	0
			Total	O		
4	B	112	112	112	0	0

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.

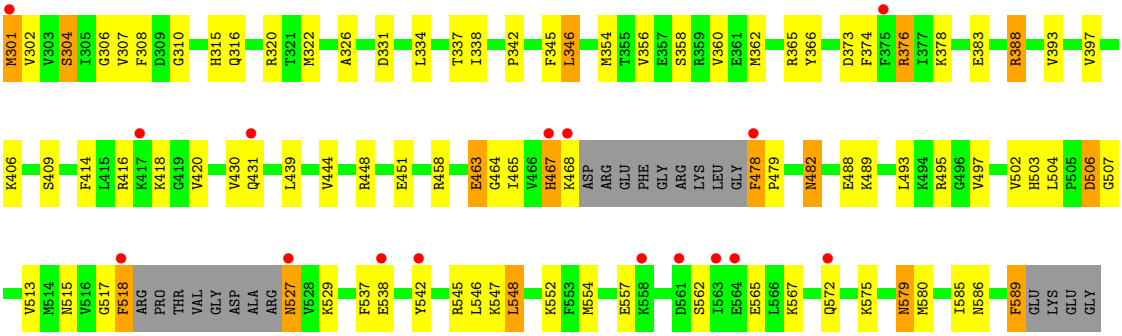
• Molecule 1: riboflavin kinase/FMN adenylyltransferase

Chain A:



• Molecule 1: riboflavin kinase/FMN adenylyltransferase

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	66.09Å 82.16Å 66.75Å 90.00° 116.57° 90.00°	Depositor
Resolution (Å)	20.00 – 2.10 19.97 – 2.00	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-2.10) 88.5 (19.97-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$< I/\sigma(I) >$ [1]	1.19 (at 2.01Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.212 , 0.259 0.207 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	32.9	Xtriage
Anisotropy	0.217	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 50.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.027 for l,-k,h	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	4715	wwPDB-VP
Average B, all atoms (Å^2)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.37% 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 (i)

5.1 Standard geometry (i)

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

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	0.63	0/2284	0.84	3/3067 (0.1%)
1	B	0.64	0/2246	0.79	1/3015 (0.0%)
All	All	0.64	0/4530	0.81	4/6082 (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	1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	59	ARG	NE-CZ-NH2	-7.00	116.80	120.30
1	A	224	ASP	CA-C-N	-6.20	103.56	117.20
1	B	548	LEU	CA-CB-CG	5.68	128.35	115.30
1	A	219	ARG	N-CA-C	-5.31	96.67	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	36	TYR	Sidechain

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	2244	0	2286	73	0
1	B	2206	0	2243	98	0
2	A	1	0	0	0	0
3	A	18	0	10	1	0
3	B	18	0	10	1	0
4	A	116	0	0	2	1
4	B	112	0	0	10	1
All	All	4715	0	4549	165	1

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 18.

All (165) 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:388:ARG:HH11	1:B:388:ARG:HG3	1.06	1.10
1:A:219:ARG:HG3	1:A:229:LYS:HE2	1.49	0.93
1:B:388:ARG:HG3	1:B:388:ARG:NH1	1.81	0.89
1:A:195:ARG:HH11	1:A:218:PHE:H	0.94	0.88
1:A:2:VAL:HG11	1:A:26:ALA:HB2	1.56	0.88
1:B:482:ASN:HD21	1:B:529:LYS:HG3	1.39	0.86
1:A:195:ARG:NH1	1:A:218:PHE:H	1.76	0.83
1:A:195:ARG:HH11	1:A:218:PHE:N	1.77	0.82
1:A:225:ALA:C	1:A:227:ASN:H	1.83	0.81
1:A:219:ARG:HG3	1:A:229:LYS:CE	2.15	0.76
1:A:245:ARG:C	1:A:246:LEU:HD12	2.06	0.75
1:B:301:MET:HE1	1:B:334:LEU:HD23	1.69	0.73
1:A:130:VAL:HG12	1:A:131:GLN:HG2	1.71	0.73
1:B:482:ASN:OD1	1:B:529:LYS:HE3	1.89	0.72
1:A:142:ASN:HD22	1:B:507:GLY:HA3	1.52	0.72
1:B:465:ILE:HD11	1:B:545:ARG:NH1	2.08	0.68
1:A:178:PHE:N	1:A:179:PRO:HD3	2.09	0.68
1:B:463:GLU:OE1	1:B:545:ARG:NH2	2.26	0.68
1:B:414:PHE:CZ	1:B:418:LYS:HE3	2.28	0.68
1:A:225:ALA:O	1:A:227:ASN:N	2.26	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:259:LYS:O	1:A:259:LYS:HD2	1.93	0.67
1:A:286:ASN:C	1:A:288:LYS:H	1.98	0.67
1:A:205:PRO:O	1:A:206:ASP:HB2	1.96	0.66
1:B:495:ARG:HG2	1:B:517:GLY:HA2	1.78	0.65
1:B:467:HIS:CG	1:B:542:TYR:HE1	2.16	0.63
1:B:572:GLN:HA	1:B:575:LYS:HE3	1.79	0.63
1:B:310:GLY:HA2	1:B:354:MET:HE1	1.81	0.62
1:A:225:ALA:C	1:A:227:ASN:N	2.52	0.62
1:A:133:LYS:HD3	1:A:139:LEU:HD11	1.82	0.62
1:A:245:ARG:O	1:A:246:LEU:HD12	2.00	0.62
1:B:572:GLN:HG3	1:B:575:LYS:NZ	2.14	0.62
1:A:1:MET:O	1:A:93:VAL:HG13	1.99	0.62
1:A:255:ARG:HD2	1:A:258:LYS:HE3	1.80	0.62
1:B:586:ASN:HA	1:B:589:PHE:CE1	2.35	0.61
1:A:2:VAL:HG12	1:A:32:ASP:O	2.00	0.61
1:B:538:GLU:OE2	1:B:538:GLU:HA	2.00	0.61
1:A:133:LYS:NZ	1:B:506:ASP:HA	2.16	0.61
1:A:73:ASP:HB3	1:A:76:ARG:HB2	1.81	0.61
1:B:439:LEU:HD23	1:B:439:LEU:C	2.22	0.59
1:A:2:VAL:CG1	1:A:26:ALA:HB2	2.32	0.58
1:B:302:VAL:CG1	1:B:326:ALA:HB2	2.33	0.58
1:B:376:ARG:HH11	1:B:376:ARG:HG2	1.67	0.58
1:B:506:ASP:OD2	1:B:506:ASP:N	2.37	0.58
1:B:304:SER:OG	1:B:322:MET:SD	2.61	0.58
1:B:444:VAL:HG13	1:B:493:LEU:HD23	1.86	0.58
1:B:439:LEU:HD23	1:B:439:LEU:O	2.04	0.57
1:B:331:ASP:HB3	4:B:818:HOH:O	2.05	0.57
1:A:221:THR:CG2	1:A:221:THR:O	2.52	0.57
1:B:467:HIS:HB3	1:B:542:TYR:CE1	2.39	0.57
1:B:502:VAL:HG22	1:B:548:LEU:HD22	1.87	0.57
1:B:562:SER:HB3	1:B:565:GLU:HG3	1.87	0.57
1:B:517:GLY:O	1:B:518:PHE:CB	2.54	0.56
1:A:142:ASN:ND2	1:B:507:GLY:HA3	2.20	0.56
1:B:388:ARG:NH1	1:B:388:ARG:CG	2.60	0.55
1:B:373:ASP:OD1	1:B:376:ARG:HD3	2.06	0.55
1:B:376:ARG:HG2	1:B:376:ARG:NH1	2.21	0.55
1:B:310:GLY:HA2	1:B:354:MET:CE	2.36	0.55
1:A:1:MET:CE	1:A:32:ASP:HB2	2.37	0.54
1:A:2:VAL:HG11	1:A:26:ALA:CB	2.34	0.54
1:A:195:ARG:HD2	1:A:218:PHE:CG	2.43	0.54
1:B:416:ARG:HA	1:B:420:VAL:O	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:219:ARG:CG	1:A:229:LYS:HE2	2.32	0.53
1:A:79:ASP:HB2	4:A:647:HOH:O	2.08	0.53
1:B:502:VAL:HG13	1:B:548:LEU:CD2	2.39	0.53
1:B:513:VAL:HG13	1:B:554:MET:CE	2.39	0.53
1:B:302:VAL:HG11	1:B:326:ALA:HB2	1.91	0.52
1:A:1:MET:HE2	1:A:32:ASP:HB2	1.91	0.52
1:A:221:THR:O	1:A:221:THR:HG23	2.09	0.52
1:A:8:PHE:HA	1:A:15:HIS:CE1	2.44	0.52
1:A:220:PRO:O	1:A:221:THR:C	2.47	0.51
1:A:161:GLU:CD	1:A:247:LYS:NZ	2.64	0.51
1:B:497:VAL:HG22	1:B:515:ASN:HD22	1.76	0.51
1:B:345:PHE:O	1:B:346:LEU:HD13	2.11	0.51
1:B:579:ASN:CG	4:B:815:HOH:O	2.49	0.51
1:A:261:ASP:O	1:A:262:SER:CB	2.59	0.51
1:A:262:SER:O	1:A:264:GLU:N	2.44	0.51
1:A:42:PRO:HB3	1:B:585:ILE:HD13	1.91	0.50
1:A:133:LYS:HZ3	1:B:506:ASP:HA	1.75	0.50
1:B:354:MET:HE1	1:B:458:ARG:HH22	1.76	0.50
1:B:497:VAL:HG12	1:B:554:MET:CE	2.42	0.50
1:A:202:VAL:HG22	1:A:248:LEU:HD22	1.94	0.50
1:B:383:GLU:HG3	1:B:414:PHE:HZ	1.77	0.49
1:B:316:GLN:HG2	1:B:366:TYR:OH	2.12	0.49
1:A:34:LEU:HD13	1:A:68:ARG:NH2	2.28	0.49
1:A:261:ASP:O	1:A:262:SER:HB3	2.13	0.49
1:B:478:PHE:CG	4:B:821:HOH:O	2.66	0.49
1:B:586:ASN:HA	1:B:589:PHE:HE1	1.77	0.49
1:B:517:GLY:O	1:B:518:PHE:HB3	2.13	0.49
1:B:478:PHE:CD2	1:B:479:PRO:HD2	2.48	0.49
1:A:38:ILE:O	1:A:59:ARG:NH2	2.46	0.48
1:A:62:MET:HA	1:A:65:ARG:NH1	2.28	0.48
1:B:467:HIS:CB	1:B:542:TYR:CE1	2.96	0.48
1:B:513:VAL:HG12	3:B:594:LUM:H7M2	1.94	0.48
1:B:320:ARG:HD3	4:B:737:HOH:O	2.12	0.48
1:A:218:PHE:C	1:A:220:PRO:HD3	2.33	0.48
1:A:205:PRO:O	1:A:206:ASP:CB	2.62	0.48
1:B:362:MET:HA	1:B:365:ARG:NH1	2.28	0.48
1:B:552:LYS:HD2	1:B:580:MET:HE2	1.96	0.48
1:A:3:VAL:HG11	1:A:36:TYR:CD2	2.50	0.47
1:B:306:GLY:O	1:B:337:THR:HA	2.14	0.47
1:B:467:HIS:CG	1:B:542:TYR:CE1	3.01	0.47
1:A:202:VAL:HG13	1:A:248:LEU:CD2	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:59:ARG:HD3	4:A:606:HOH:O	2.14	0.47
1:B:463:GLU:HG2	1:B:464:GLY:N	2.30	0.47
1:B:497:VAL:HG12	1:B:554:MET:HE3	1.95	0.47
1:B:579:ASN:ND2	4:B:753:HOH:O	2.41	0.47
1:A:213:VAL:CG1	1:A:233:TYR:HB3	2.45	0.47
1:A:286:ASN:C	1:A:288:LYS:N	2.67	0.47
1:B:342:PRO:O	1:B:346:LEU:HD22	2.15	0.47
1:B:378:LYS:O	1:B:406:LYS:HA	2.13	0.47
1:A:12:HIS:O	1:A:16:GLN:HG3	2.14	0.46
1:B:373:ASP:OD2	1:B:373:ASP:C	2.54	0.46
1:B:465:ILE:CD1	1:B:545:ARG:NH1	2.78	0.46
1:B:301:MET:SD	1:B:334:LEU:HB2	2.55	0.46
1:B:513:VAL:HG13	1:B:554:MET:HE3	1.97	0.46
1:A:165:ILE:HD12	1:A:165:ILE:N	2.30	0.46
1:A:213:VAL:HG22	3:A:294:LUM:H7M2	1.98	0.46
1:B:552:LYS:HD2	1:B:580:MET:CE	2.46	0.46
1:A:134:ARG:HG2	1:A:134:ARG:HH11	1.80	0.45
1:A:164:GLY:HA3	1:A:184:ASP:O	2.17	0.45
1:A:263:ILE:H	1:A:263:ILE:HG13	1.34	0.45
1:B:362:MET:HA	1:B:365:ARG:HH11	1.81	0.45
1:B:545:ARG:HG2	1:B:545:ARG:HH11	1.81	0.45
1:B:374:PHE:CE2	1:B:378:LYS:HD3	2.50	0.45
1:A:241:LEU:O	1:A:244:GLN:HB2	2.16	0.45
1:B:354:MET:HE1	1:B:458:ARG:NH2	2.32	0.45
1:B:527:ASN:N	1:B:527:ASN:HD22	2.14	0.45
1:A:15:HIS:O	1:A:19:LEU:HG	2.18	0.44
1:A:280:MET:O	1:A:284:ILE:HG13	2.17	0.44
1:A:50:PRO:O	1:A:191:VAL:HA	2.18	0.44
1:B:307:VAL:O	1:B:308:PHE:HB2	2.17	0.44
1:B:409:SER:O	4:B:798:HOH:O	2.21	0.44
1:B:572:GLN:HG3	1:B:575:LYS:HZ2	1.81	0.44
1:A:9:ASP:HA	1:A:59:ARG:HD2	1.99	0.44
1:B:572:GLN:HG3	1:B:575:LYS:HZ1	1.82	0.44
1:B:465:ILE:HD11	1:B:545:ARG:HH11	1.81	0.44
1:B:356:VAL:O	1:B:360:VAL:HG23	2.18	0.43
1:B:301:MET:HA	4:B:818:HOH:O	2.18	0.43
1:B:482:ASN:HD21	1:B:529:LYS:CG	2.20	0.43
1:B:478:PHE:CD1	4:B:821:HOH:O	2.57	0.43
1:A:226:ARG:O	1:A:226:ARG:HG3	2.18	0.42
1:B:504:LEU:HD23	1:B:546:LEU:HD22	2.00	0.42
1:B:545:ARG:NH1	1:B:545:ARG:HG2	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:195:ARG:CZ	1:A:257:GLU:HG2	2.49	0.42
1:B:557:GLU:OE2	1:B:557:GLU:HA	2.20	0.42
1:A:166:VAL:HG23	1:A:244:GLN:O	2.20	0.42
1:B:482:ASN:HD22	1:B:482:ASN:HA	1.61	0.42
1:A:246:LEU:HD12	1:A:246:LEU:N	2.32	0.42
1:A:247:LYS:HE3	1:A:247:LYS:HB3	1.74	0.42
1:B:489:LYS:NZ	4:B:728:HOH:O	2.53	0.42
1:A:144:VAL:HG13	1:A:193:LEU:HD23	2.01	0.41
1:A:134:ARG:HH11	1:A:134:ARG:CG	2.33	0.41
1:B:439:LEU:C	1:B:439:LEU:CD2	2.88	0.41
1:B:301:MET:O	1:B:393:VAL:HG13	2.21	0.41
1:B:430:VAL:HG12	1:B:431:GLN:HG3	2.02	0.41
1:B:467:HIS:CD2	1:B:468:LYS:N	2.88	0.41
1:A:167:HIS:HB3	1:A:168:LYS:H	1.56	0.41
1:B:308:PHE:HA	1:B:315:HIS:CD2	2.55	0.41
1:B:503:HIS:HB3	1:B:547:LYS:HB2	2.02	0.41
1:A:241:LEU:HD13	1:A:246:LEU:HD21	2.02	0.41
1:B:304:SER:HA	1:B:397:VAL:O	2.21	0.41
1:B:338:ILE:HG21	4:B:732:HOH:O	2.20	0.41
1:B:504:LEU:CD1	1:B:537:PHE:CE1	3.04	0.41
1:A:142:ASN:ND2	1:B:507:GLY:CA	2.85	0.40
1:B:448:ARG:HB3	1:B:451:GLU:OE1	2.21	0.40

All (1) 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)
4:A:816:HOH:O	4:B:822:HOH:O[2_656]	2.19	0.01

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	271/293 (92%)	257 (95%)	9 (3%)	5 (2%)	8 4
1	B	266/293 (91%)	259 (97%)	6 (2%)	1 (0%)	34 32
All	All	537/586 (92%)	516 (96%)	15 (3%)	6 (1%)	14 9

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	220	PRO
1	A	263	ILE
1	A	226	ARG
1	A	262	SER
1	A	167	HIS
1	B	467	HIS

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	245/257 (95%)	238 (97%)	7 (3%)	42 46
1	B	241/257 (94%)	225 (93%)	16 (7%)	16 14
All	All	486/514 (95%)	463 (95%)	23 (5%)	26 25

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33	SER
1	A	167	HIS
1	A	220	PRO
1	A	221	THR
1	A	226	ARG
1	A	247	LYS
1	A	259	LYS
1	B	301	MET
1	B	304	SER
1	B	346	LEU

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Mol	Chain	Res	Type
1	B	358	SER
1	B	376	ARG
1	B	388	ARG
1	B	463	GLU
1	B	478	PHE
1	B	482	ASN
1	B	488	GLU
1	B	506	ASP
1	B	518	PHE
1	B	527	ASN
1	B	567	LYS
1	B	579	ASN
1	B	589	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	16	GLN
1	A	142	ASN
1	A	244	GLN
1	A	279	ASN
1	B	407	ASN
1	B	467	HIS
1	B	482	ASN
1	B	515	ASN
1	B	527	ASN
1	B	579	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)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	LUM	B	594	-	19,20,20	2.81	7 (36%)	24,30,30	4.52	10 (41%)
3	LUM	A	294	-	19,20,20	2.59	7 (36%)	24,30,30	4.53	10 (41%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	LUM	B	594	-	-	-	0/3/3/3
3	LUM	A	294	-	-	-	0/3/3/3

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	594	LUM	C4A-C4	6.62	1.52	1.41
3	B	594	LUM	C9A-N10	6.47	1.46	1.35
3	A	294	LUM	C4A-C4	6.01	1.51	1.41
3	A	294	LUM	C9A-N10	5.51	1.44	1.35
3	B	594	LUM	C4-N3	4.43	1.40	1.33
3	A	294	LUM	C5A-N5	3.81	1.41	1.35
3	A	294	LUM	C4-N3	3.70	1.39	1.33
3	B	594	LUM	C5A-N5	3.34	1.40	1.35
3	A	294	LUM	C8M-C8	3.02	1.57	1.51
3	B	594	LUM	C8M-C8	2.98	1.57	1.51
3	A	294	LUM	C8-C7	2.65	1.47	1.40
3	A	294	LUM	C6-C5A	2.33	1.45	1.41
3	B	594	LUM	C8-C7	2.30	1.46	1.40
3	B	594	LUM	C4A-C10	2.24	1.45	1.40

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	294	LUM	C2-N3-C4	16.82	129.34	115.14
3	B	594	LUM	C2-N3-C4	16.52	129.09	115.14
3	B	594	LUM	C4A-C4-N3	-7.93	112.59	123.43
3	A	294	LUM	C4A-C4-N3	-7.82	112.73	123.43
3	B	594	LUM	C8-C9-C9A	-6.57	111.92	121.22
3	A	294	LUM	C8-C9-C9A	-6.15	112.52	121.22
3	B	594	LUM	C5A-C9A-N10	-5.38	116.95	121.42
3	A	294	LUM	C5A-C9A-N10	-5.23	117.08	121.42
3	A	294	LUM	C7-C6-C5A	-4.37	115.04	121.22
3	B	594	LUM	C6-C5A-N5	-3.86	114.80	119.05
3	B	594	LUM	C7-C6-C5A	-3.74	115.92	121.22
3	A	294	LUM	C9-C8-C7	3.61	126.00	119.91
3	B	594	LUM	C9-C8-C7	3.60	125.98	119.91
3	A	294	LUM	C9-C9A-C5A	3.38	123.18	119.51
3	A	294	LUM	C6-C5A-N5	-3.09	115.64	119.05
3	B	594	LUM	C6-C5A-C9A	3.00	122.76	119.51
3	A	294	LUM	C6-C5A-C9A	2.93	122.68	119.51
3	B	594	LUM	C9-C9A-C5A	2.82	122.56	119.51
3	A	294	LUM	C10-C4A-C4	-2.30	118.43	119.95
3	B	594	LUM	C10-C4A-C4	-2.16	118.52	119.95

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	594	LUM	1	0
3	A	294	LUM	1	0

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	277/293 (94%)	0.55	27 (9%)	7	10	24, 39, 79, 94	0
1	B	272/293 (92%)	0.37	16 (5%)	22	27	26, 39, 65, 83	0
All	All	549/586 (93%)	0.46	43 (7%)	13	17	24, 39, 73, 94	0

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	221	THR	10.3
1	A	178	PHE	9.5
1	A	224	ASP	9.3
1	B	478	PHE	9.3
1	A	220	PRO	7.1
1	A	225	ALA	7.1
1	A	1	MET	6.5
1	B	468	LYS	6.1
1	A	259	LYS	6.1
1	B	301	MET	5.8
1	A	242	TYR	5.4
1	A	168	LYS	5.3
1	B	561	ASP	5.2
1	A	226	ARG	4.9
1	B	527	ASN	4.7
1	A	179	PRO	4.1
1	A	262	SER	3.9
1	B	542	TYR	3.9
1	A	219	ARG	3.6
1	A	260	PHE	3.3
1	A	240	ASP	3.3
1	A	167	HIS	3.1
1	A	261	ASP	3.1
1	A	271	ASP	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	218	PHE	3.1
1	A	288	LYS	3.1
1	B	563	ILE	3.1
1	B	467	HIS	2.8
1	A	238	GLU	2.8
1	B	572	GLN	2.6
1	B	375	PHE	2.5
1	A	227	ASN	2.5
1	B	431	GLN	2.4
1	B	518	PHE	2.4
1	A	258	LYS	2.3
1	A	245	ARG	2.3
1	B	417	LYS	2.3
1	B	538	GLU	2.2
1	A	272	GLN	2.1
1	B	558	LYS	2.1
1	B	564	GLU	2.0
1	A	287	SER	2.0
1	A	268	ALA	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
3	LUM	A	294	18/18	0.91	0.14	42,44,46,46	0
3	LUM	B	594	18/18	0.92	0.13	36,39,44,47	0
2	MG	A	295	1/1	0.98	0.03	36,36,36,36	0

6.5 Other polymers (i)

There are no such residues in this entry.