Full wwPDB X-ray Structure Validation Report (i)

Jun 17, 2024 – 04:04 AM EDT

PDB ID	:	5MKK
Title	:	Crystal structure of the heterodimeric ABC transporter TmrAB, a homolog of the antigen translocation complex TAP
Authors	:	Noell, A.; Thomas, C.; Tomasiak, T.M.; Olieric, V.; Wang, M.; Diederichs, K.; Stroud, R.M.; Pos, K.M.; Tampe, R.
Deposited on	:	2016-12-05
Resolution	:	2.70 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:

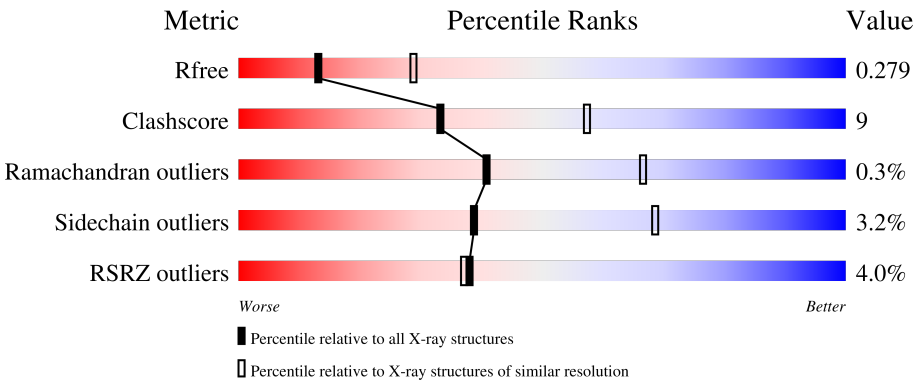
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.70 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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	611	3% 73% 22%
2	B	577	5% 78% 21%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 9311 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 Multidrug resistance ABC transporter ATP-binding and permease protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	593	4739	3085	824	822	8	0	0	0

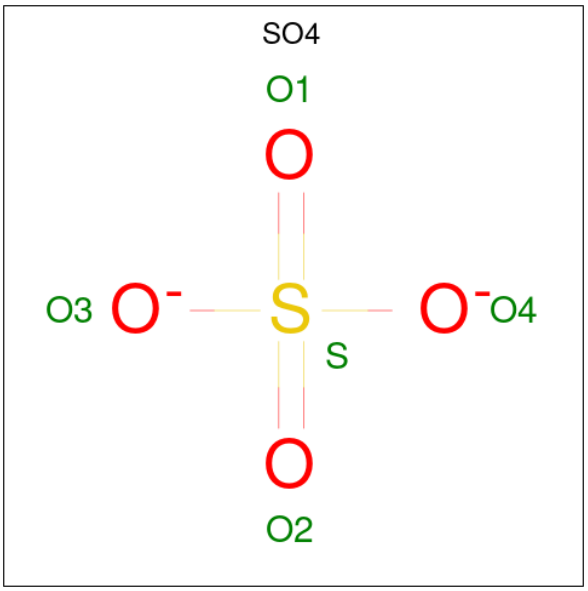
There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	601	LYS	-	expression tag	UNP Q72J05
A	602	LEU	-	expression tag	UNP Q72J05
A	603	GLY	-	expression tag	UNP Q72J05
A	604	GLY	-	expression tag	UNP Q72J05
A	605	GLY	-	expression tag	UNP Q72J05
A	606	GLY	-	expression tag	UNP Q72J05
A	607	GLU	-	expression tag	UNP Q72J05
A	608	ASN	-	expression tag	UNP Q72J05
A	609	LEU	-	expression tag	UNP Q72J05
A	610	TYR	-	expression tag	UNP Q72J05
A	611	PHE	-	expression tag	UNP Q72J05
A	612	GLN	-	expression tag	UNP Q72J05

- Molecule 2 is a protein called Multidrug resistance ABC transporter ATP-binding and permease protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	577	4552	2939	815	786	12	0	0	0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0

- Molecule 4 is water.

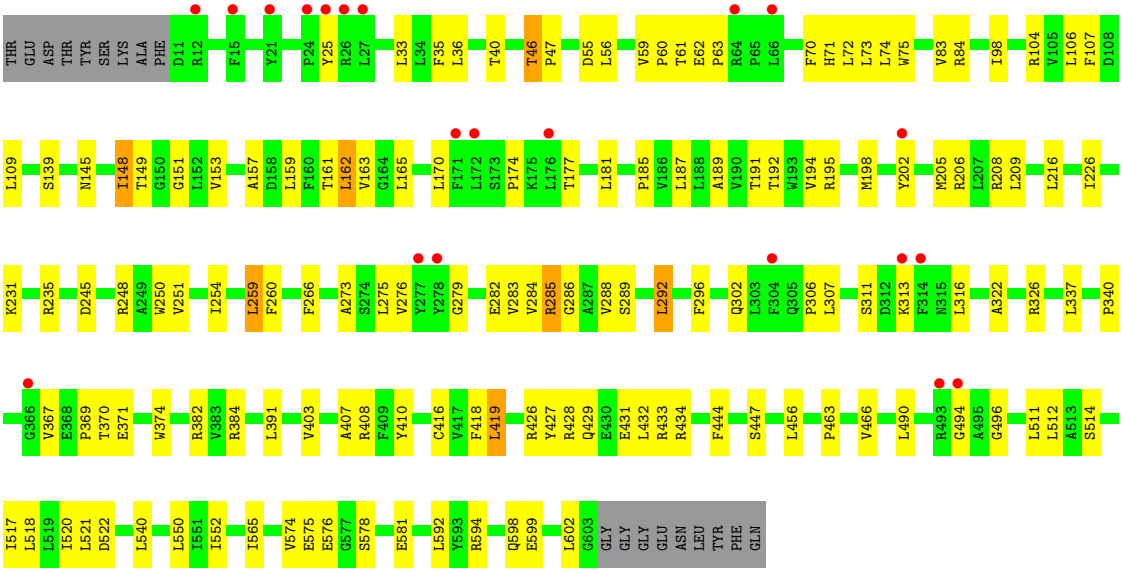
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	4	Total O 4 4	0	0
4	B	6	Total O 6 6	0	0

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.

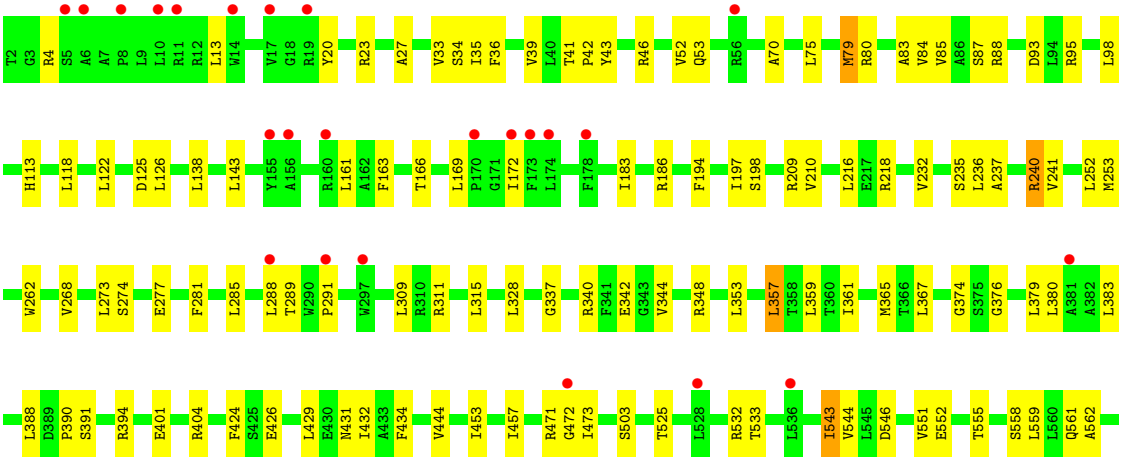
• Molecule 1: Multidrug resistance ABC transporter ATP-binding and permease protein

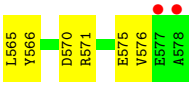
Chain A:



• Molecule 2: Multidrug resistance ABC transporter ATP-binding and permease protein

Chain B:




L565
Y566
D570
R571
E575
V576
E577
A578

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α, β, γ	93.37Å 93.37Å 1043.95Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.90 – 2.70 48.90 – 2.50	Depositor EDS
% Data completeness (in resolution range)	100.0 (48.90-2.70) 99.7 (48.90-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	0.94 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.226 , 0.272 0.232 , 0.279	Depositor DCC
R_{free} test set	4814 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	87.2	Xtriage
Anisotropy	0.152	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 59.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.44$, $< L^2 > = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.89	EDS
Total number of atoms	9311	wwPDB-VP
Average B, all atoms (Å^2)	106.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.32% 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: SO4

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	0.40	0/4843	0.57	2/6568 (0.0%)
2	B	0.39	0/4641	0.57	1/6282 (0.0%)
All	All	0.40	0/9484	0.57	3/12850 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	357	LEU	CA-CB-CG	6.44	130.11	115.30
1	A	259	LEU	CA-CB-CG	5.96	129.02	115.30
1	A	518	LEU	CA-CB-CG	5.35	127.60	115.30

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	4739	0	4868	87	0
2	B	4552	0	4716	91	0
3	A	5	0	0	0	0
3	B	5	0	0	1	0
4	A	4	0	0	0	0
4	B	6	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	9311	0	9584	162	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 9.

All (162) 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:B:46:ARG:HD2	2:B:277:GLU:HG2	1.60	0.83
1:A:514:SER:HB3	1:A:517:ILE:HG23	1.62	0.81
2:B:340:ARG:NH1	2:B:342:GLU:OE1	2.14	0.79
2:B:533:THR:HG21	2:B:570:ASP:HB2	1.62	0.79
1:A:208:ARG:HD3	1:A:245:ASP:HB3	1.65	0.79
2:B:143:LEU:HB3	2:B:291:PRO:HB3	1.66	0.77
1:A:371:GLU:HA	1:A:374:TRP:CD1	2.23	0.73
1:A:195:ARG:HH22	1:A:311:SER:HA	1.54	0.72
1:A:574:VAL:HG12	1:A:575:GLU:HG3	1.73	0.71
1:A:594:ARG:HG3	2:B:571:ARG:HH12	1.56	0.70
2:B:344:VAL:HG13	2:B:390:PRO:HB3	1.76	0.68
2:B:13:LEU:HB2	2:B:309:LEU:HD21	1.77	0.66
2:B:186:ARG:HE	2:B:237:ALA:HB1	1.61	0.66
1:A:578:SER:HB3	1:A:581:GLU:HG3	1.79	0.65
2:B:41:THR:HG23	2:B:42:PRO:HD3	1.79	0.65
1:A:98:ILE:HD13	1:A:153:VAL:HG11	1.77	0.65
1:A:599:GLU:HG3	2:B:565:LEU:HD11	1.78	0.65
1:A:151:GLY:HA2	1:A:313:LYS:HD2	1.80	0.64
1:A:282:GLU:OE2	1:A:285:ARG:NH2	2.31	0.64
1:A:187:LEU:O	1:A:191:THR:HG23	1.98	0.62
2:B:374:GLY:N	3:B:601:SO4:O4	2.31	0.62
1:A:410:TYR:OH	2:B:209:ARG:NH2	2.34	0.61
1:A:106:LEU:HD13	1:A:145:ASN:HB2	1.83	0.60
1:A:148:ILE:HG13	1:A:149:THR:HG23	1.82	0.60
1:A:40:THR:HG22	1:A:161:THR:HG22	1.83	0.60
1:A:521:LEU:HD13	1:A:540:LEU:HD13	1.84	0.60
1:A:434:ARG:HH22	2:B:218:ARG:HH22	1.49	0.60
2:B:533:THR:HG23	2:B:566:TYR:CZ	2.36	0.59
1:A:70:PHE:O	1:A:74:LEU:HB3	2.04	0.58
2:B:84:VAL:O	2:B:87:SER:OG	2.22	0.58
1:A:170:LEU:HG	1:A:177:THR:HG21	1.86	0.58
2:B:285:LEU:O	2:B:289:THR:HG23	2.03	0.58
2:B:359:LEU:HD22	2:B:543:ILE:HD12	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:391:LEU:HD11	1:A:550:LEU:HD23	1.86	0.57
2:B:348:ARG:HH21	2:B:388:LEU:HD22	1.70	0.57
1:A:25:TYR:CZ	1:A:104:ARG:HB3	2.41	0.56
2:B:365:MET:HE2	2:B:367:LEU:HB2	1.88	0.56
1:A:273:ALA:HA	1:A:276:VAL:HG12	1.88	0.55
1:A:283:VAL:HG11	2:B:52:VAL:HG13	1.87	0.55
1:A:447:SER:HA	1:A:490:LEU:O	2.07	0.55
2:B:172:ILE:HD13	2:B:253:MET:SD	2.45	0.55
2:B:471:ARG:O	2:B:473:ILE:N	2.34	0.55
2:B:183:ILE:HG22	2:B:241:VAL:HG12	1.88	0.55
2:B:43:TYR:HE1	2:B:46:ARG:HH11	1.55	0.55
1:A:407:ALA:O	1:A:433:ARG:HD3	2.06	0.54
2:B:503:SER:O	2:B:532:ARG:NH2	2.41	0.54
2:B:169:LEU:HD21	2:B:288:LEU:HD21	1.89	0.54
1:A:55:ASP:O	1:A:56:LEU:HD23	2.07	0.54
1:A:107:PHE:HB2	2:B:232:VAL:HG21	1.88	0.54
1:A:194:VAL:HG21	1:A:260:PHE:HD1	1.73	0.53
1:A:463:PRO:HA	1:A:466:VAL:HG13	1.90	0.53
2:B:83:ALA:HB3	2:B:138:LEU:HD11	1.91	0.53
2:B:337:GLY:O	2:B:525:THR:OG1	2.21	0.53
1:A:181:LEU:O	1:A:185:PRO:HD3	2.09	0.52
2:B:328:LEU:HD21	2:B:404:ARG:NH2	2.24	0.52
1:A:511:LEU:HD23	1:A:517:ILE:HD11	1.91	0.52
2:B:95:ARG:HB2	2:B:126:LEU:HD21	1.91	0.52
2:B:118:LEU:O	2:B:122:LEU:HB2	2.09	0.52
2:B:394:ARG:NH1	2:B:401:GLU:HG2	2.25	0.52
2:B:394:ARG:HH11	2:B:401:GLU:HG2	1.75	0.52
2:B:544:VAL:HB	2:B:552:GLU:HB3	1.91	0.52
2:B:376:GLY:HA2	2:B:379:LEU:HD23	1.92	0.51
1:A:428:ARG:NH1	1:A:431:GLU:OE1	2.39	0.51
1:A:494:GLY:O	1:A:496:GLY:N	2.37	0.51
2:B:348:ARG:HB2	2:B:353:LEU:HD11	1.92	0.51
1:A:284:VAL:C	1:A:286:GLY:H	2.15	0.50
1:A:382:ARG:HH22	1:A:384:ARG:HG2	1.76	0.50
1:A:56:LEU:HD13	1:A:72:LEU:HD13	1.93	0.50
1:A:408:ARG:O	1:A:433:ARG:NH1	2.45	0.50
1:A:36:LEU:HD21	1:A:157:ALA:HA	1.94	0.50
1:A:444:PHE:HB3	2:B:210:VAL:HG21	1.94	0.50
2:B:27:ALA:HB1	2:B:83:ALA:HB2	1.93	0.49
2:B:365:MET:HE3	2:B:367:LEU:HD13	1.94	0.49
1:A:61:THR:HG22	1:A:62:GLU:N	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:522:ASP:OD2	1:A:552:ILE:HD12	2.13	0.49
2:B:533:THR:HG21	2:B:570:ASP:CB	2.38	0.49
2:B:544:VAL:HG21	2:B:566:TYR:HB2	1.95	0.48
2:B:163:PHE:HA	2:B:166:THR:HG22	1.93	0.48
1:A:419:LEU:HD22	1:A:432:LEU:HD11	1.94	0.48
2:B:161:LEU:HD23	2:B:281:PHE:CE2	2.48	0.48
1:A:162:LEU:HD11	1:A:307:LEU:HD12	1.94	0.48
1:A:174:PRO:HA	1:A:177:THR:HG22	1.95	0.48
1:A:226:ILE:HD13	1:A:235:ARG:HG3	1.95	0.48
1:A:61:THR:C	1:A:63:PRO:HD3	2.34	0.47
1:A:245:ASP:OD1	1:A:248:ARG:NH1	2.46	0.47
2:B:571:ARG:O	2:B:575:GLU:HB2	2.13	0.47
1:A:466:VAL:HB	1:A:512:LEU:HD11	1.97	0.47
1:A:250:TRP:HB3	2:B:88:ARG:HG3	1.97	0.47
2:B:559:LEU:HB3	2:B:566:TYR:CD2	2.48	0.47
2:B:559:LEU:HD23	2:B:559:LEU:HA	1.80	0.47
1:A:514:SER:O	1:A:517:ILE:HG12	2.15	0.47
2:B:429:LEU:HD12	2:B:444:VAL:HG11	1.97	0.47
1:A:340:PRO:HG3	1:A:426:ARG:HA	1.97	0.46
1:A:46:THR:HG22	1:A:47:PRO:HD3	1.96	0.46
1:A:266:PHE:HE1	2:B:70:ALA:HB2	1.81	0.46
2:B:33:VAL:HG12	2:B:75:LEU:HD13	1.98	0.46
2:B:253:MET:HG3	2:B:289:THR:CG2	2.45	0.46
2:B:39:VAL:O	2:B:42:PRO:HD2	2.15	0.46
2:B:253:MET:HG3	2:B:289:THR:HG22	1.97	0.46
1:A:198:MET:HE3	1:A:202:TYR:HE2	1.81	0.46
1:A:288:VAL:HB	1:A:292:LEU:HD22	1.98	0.46
1:A:594:ARG:HG3	2:B:571:ARG:NH1	2.28	0.46
2:B:431:ASN:O	2:B:434:PHE:HB2	2.15	0.46
1:A:61:THR:O	1:A:63:PRO:HD3	2.16	0.45
1:A:74:LEU:HD13	2:B:262:TRP:CZ2	2.51	0.45
1:A:159:LEU:O	1:A:163:VAL:HG13	2.16	0.45
2:B:41:THR:CG2	2:B:42:PRO:HD3	2.47	0.45
2:B:98:LEU:HD13	2:B:122:LEU:HD11	1.98	0.45
2:B:125:ASP:OD1	2:B:311:ARG:NH2	2.47	0.45
1:A:205:MET:HE2	1:A:209:LEU:HD22	1.98	0.45
1:A:157:ALA:O	1:A:161:THR:HG23	2.17	0.45
1:A:74:LEU:HG	1:A:75:TRP:HD1	1.82	0.44
1:A:216:LEU:HD21	2:B:122:LEU:HD23	1.98	0.44
2:B:113:HIS:HB3	2:B:118:LEU:HD22	2.00	0.44
2:B:453:ILE:HG13	2:B:457:ILE:HG13	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:367:VAL:O	1:A:369:PRO:HD3	2.18	0.44
2:B:546:ASP:HB2	2:B:551:VAL:HG11	1.99	0.44
1:A:456:LEU:HD22	2:B:216:LEU:HD11	1.99	0.44
2:B:20:TYR:OH	2:B:93:ASP:OD2	2.22	0.44
2:B:432:ILE:HG21	2:B:444:VAL:HG13	2.00	0.44
1:A:189:ALA:O	1:A:192:THR:HG22	2.17	0.44
2:B:424:PHE:O	2:B:426:GLU:N	2.47	0.43
2:B:561:GLN:O	2:B:562:ALA:HB3	2.18	0.43
1:A:565:ILE:O	1:A:576:GLU:HA	2.18	0.43
2:B:79:MET:HG3	2:B:80:ARG:N	2.33	0.43
2:B:236:LEU:O	2:B:240:ARG:HD3	2.18	0.43
1:A:403:VAL:HG13	1:A:520:ILE:HG21	2.00	0.43
2:B:555:THR:HG23	2:B:558:SER:H	1.84	0.43
2:B:23:ARG:NH1	2:B:85:VAL:HG12	2.33	0.42
2:B:172:ILE:HG12	2:B:252:LEU:HB3	2.00	0.42
2:B:194:PHE:O	2:B:197:ILE:HG22	2.20	0.42
1:A:231:LYS:HG2	2:B:434:PHE:CZ	2.54	0.42
1:A:61:THR:HG22	1:A:62:GLU:H	1.85	0.42
1:A:251:VAL:HG22	2:B:85:VAL:HG22	2.02	0.42
1:A:322:ALA:HB1	1:A:326:ARG:HH12	1.84	0.42
1:A:165:LEU:HD23	1:A:165:LEU:HA	1.85	0.41
2:B:88:ARG:HD3	2:B:88:ARG:HA	1.86	0.41
1:A:370:THR:O	1:A:371:GLU:HB2	2.20	0.41
2:B:344:VAL:HG11	2:B:383:LEU:HD13	2.02	0.41
1:A:275:LEU:O	1:A:279:GLY:HA3	2.20	0.41
1:A:602:LEU:O	2:B:551:VAL:HG21	2.21	0.41
1:A:427:TYR:CD2	1:A:432:LEU:HD13	2.56	0.41
2:B:23:ARG:HH11	2:B:85:VAL:HG12	1.86	0.41
1:A:73:LEU:HD12	1:A:73:LEU:HA	1.88	0.41
1:A:429:GLN:OE1	1:A:433:ARG:NH2	2.52	0.41
2:B:35:ILE:HD13	2:B:35:ILE:HA	1.76	0.41
1:A:254:ILE:HD13	1:A:254:ILE:HA	1.84	0.41
1:A:148:ILE:HG13	1:A:149:THR:N	2.35	0.41
1:A:151:GLY:HA3	1:A:316:LEU:HD23	2.02	0.41
2:B:33:VAL:O	2:B:36:PHE:HB3	2.21	0.41
2:B:274:SER:OG	2:B:277:GLU:HG3	2.21	0.41
2:B:361:ILE:HG12	2:B:367:LEU:HD22	2.03	0.41
2:B:533:THR:HG23	2:B:566:TYR:OH	2.20	0.41
2:B:348:ARG:HD3	2:B:348:ARG:HA	1.79	0.40
1:A:162:LEU:HD12	1:A:306:PRO:HB2	2.03	0.40
2:B:98:LEU:HD22	2:B:315:LEU:HD23	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:165:LEU:HD21	1:A:302:GLN:OE1	2.21	0.40
1:A:416:CYS:HB2	1:A:418:PHE:CE1	2.56	0.40
2:B:20:TYR:HB3	2:B:23:ARG:HH21	1.85	0.40
2:B:268:VAL:HA	2:B:273:LEU:O	2.22	0.40
2:B:383:LEU:HD22	2:B:390:PRO:HD3	2.03	0.40
1:A:382:ARG:NH2	1:A:384:ARG:HG2	2.36	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	591/611 (97%)	559 (95%)	30 (5%)	2 (0%)	41	66
2	B	575/577 (100%)	534 (93%)	39 (7%)	2 (0%)	41	66
All	All	1166/1188 (98%)	1093 (94%)	69 (6%)	4 (0%)	41	66

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	285	ARG
2	B	576	VAL
2	B	472	GLY
1	A	60	PRO

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	495/510 (97%)	475 (96%)	20 (4%)	31	60
2	B	463/463 (100%)	452 (98%)	11 (2%)	49	77
All	All	958/973 (98%)	927 (97%)	31 (3%)	39	68

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33	LEU
1	A	35	PHE
1	A	46	THR
1	A	59	VAL
1	A	71	HIS
1	A	83	VAL
1	A	84	ARG
1	A	109	LEU
1	A	139	SER
1	A	148	ILE
1	A	162	LEU
1	A	206	ARG
1	A	259	LEU
1	A	289	SER
1	A	292	LEU
1	A	296	PHE
1	A	337	LEU
1	A	419	LEU
1	A	592	LEU
1	A	598	GLN
2	B	4	ARG
2	B	34	SER
2	B	53	GLN
2	B	79	MET
2	B	198	SER
2	B	235	SER
2	B	240	ARG
2	B	357	LEU
2	B	380	LEU
2	B	391	SER
2	B	543	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)

2 ligands are modelled in this entry.

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	SO4	A	701	-	4,4,4	0.30	0	6,6,6	0.39	0
3	SO4	B	601	-	4,4,4	0.23	0	6,6,6	0.17	0

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	601	SO4	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	593/611 (97%)	0.09	21 (3%)	44	44	63, 103, 161, 227	0
2	B	577/577 (100%)	-0.07	26 (4%)	33	31	63, 102, 149, 210	0
All	All	1170/1188 (98%)	0.01	47 (4%)	38	37	63, 102, 154, 227	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	578	ALA	8.6
2	B	173	PHE	5.5
2	B	577	GLU	4.9
2	B	472	GLY	4.8
1	A	172	LEU	4.3
1	A	304	PHE	4.2
2	B	174	LEU	3.8
2	B	536	LEU	3.6
1	A	171	PHE	3.6
1	A	15	PHE	3.5
2	B	19	ARG	3.3
2	B	5	SER	3.1
1	A	278	TYR	3.1
1	A	64	ARG	3.1
2	B	288	LEU	3.1
1	A	25	TYR	3.0
1	A	66	LEU	3.0
2	B	14	TRP	2.9
2	B	381	ALA	2.9
2	B	6	ALA	2.9
2	B	10	LEU	2.8
1	A	26	ARG	2.8
2	B	170	PRO	2.8
2	B	17	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
2	B	155	TYR	2.8
2	B	11	ARG	2.7
2	B	528	LEU	2.6
2	B	172	ILE	2.6
2	B	56	ARG	2.6
1	A	176	LEU	2.5
2	B	178	PHE	2.5
2	B	160	ARG	2.4
1	A	12	ARG	2.4
1	A	366	GLY	2.4
2	B	297	TRP	2.4
2	B	291	PRO	2.4
1	A	24	PRO	2.3
1	A	313	LYS	2.3
1	A	277	TYR	2.3
1	A	27	LEU	2.2
2	B	8	PRO	2.2
2	B	156	ALA	2.2
1	A	494	GLY	2.1
1	A	202	TYR	2.1
1	A	21	TYR	2.1
1	A	314	PHE	2.1
1	A	493	ARG	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.

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	SO4	A	701	5/5	0.97	0.21	72,78,85,89	0
3	SO4	B	601	5/5	0.99	0.09	96,100,109,114	0

6.5 Other polymers (i)

There are no such residues in this entry.