



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 03:11 am GMT

PDB ID : 4RKC
Title : Psychrophilic aromatic amino acids aminotransferase from Psychrobacter sp. B6
Authors : Bujacz, A.; Rutkiewicz-Krotewicz, M.; Bujacz, G.; Nowakowska-Sapota, K.; Turkiewicz, M.
Deposited on : 2014-10-12
Resolution : 2.19 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

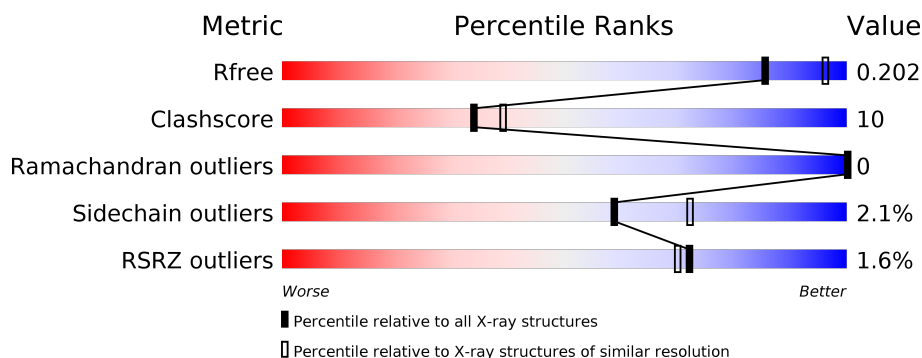
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.19 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}	100719	4002 (2.20-2.20)
Clashscore	112137	4730 (2.20-2.20)
Ramachandran outliers	110173	4656 (2.20-2.20)
Sidechain outliers	110143	4657 (2.20-2.20)
RSRZ outliers	101464	4033 (2.20-2.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	398	<div> <div>2%</div> <div> <div></div> <div>83%</div> <div>16%</div> <div>.</div> </div> </div>
1	B	398	<div> <div>%</div> <div> <div></div> <div>84%</div> <div>16%</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	NO3	A	403	-	-	-	X
3	NO3	A	406	-	-	-	X
3	NO3	B	402	-	-	-	X
3	NO3	B	403	-	-	-	X
3	NO3	B	404	-	-	-	X
4	PMP	A	409	-	-	X	X
4	PMP	B	405	-	-	X	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 7088 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.

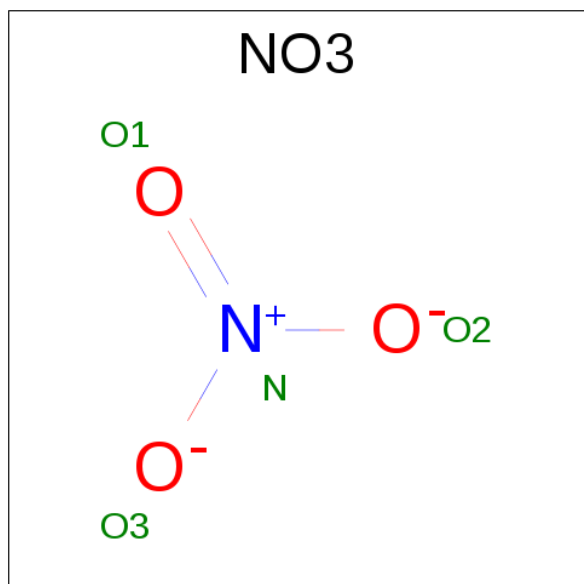
- Molecule 1 is a protein called Aromatic amino acid aminotransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	398	Total	C	N	O	S	0	2	0
			3113	1980	517	594	22			
1	B	398	Total	C	N	O	S	0	5	0
			3130	1990	518	600	22			

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

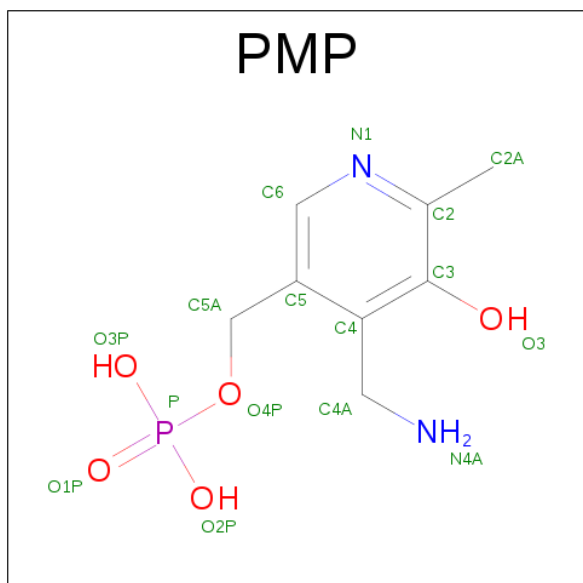
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Mg	0	0
			1	1		
2	A	1	Total	Mg	0	0
			1	1		

- Molecule 3 is NITRATE ION (three-letter code: NO3) (formula: NO₃).



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

- Molecule 4 is 4'-DEOXY-4'-AMINOPYRIDOXAL-5'-PHOSPHATE (three-letter code: PMP) (formula: C₈H₁₃N₂O₅P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C N O P 16 8 2 5 1	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	N	O	P	0	0
			16	8	2	5	1		

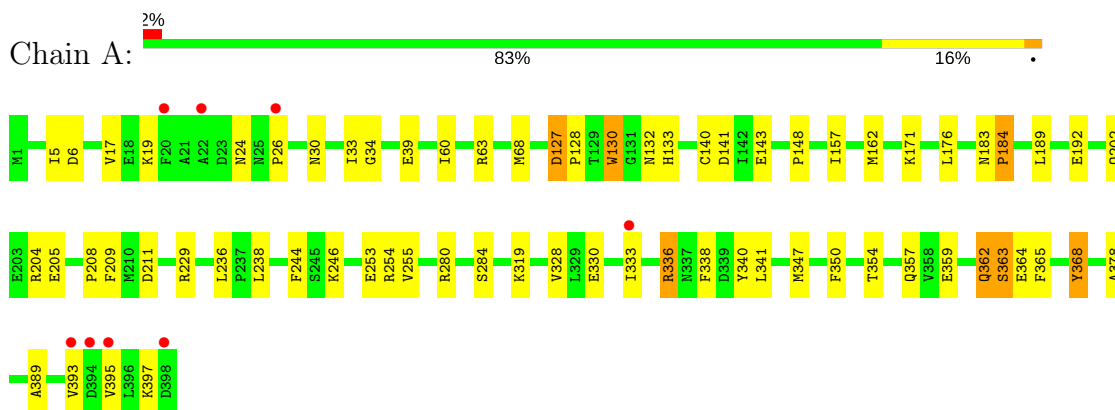
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	374	Total	O	0	0
			374	374		
5	B	397	Total	O	0	0
			397	397		

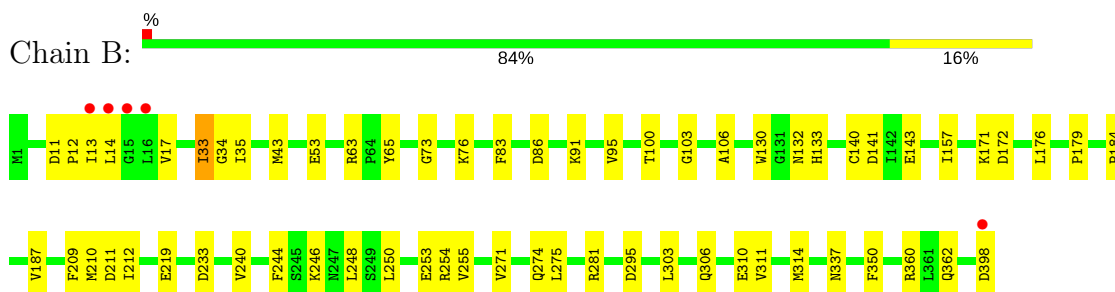
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: Aromatic amino acid aminotransferase



- Molecule 1: Aromatic amino acid aminotransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	74.69Å 62.11Å 85.89Å 90.00° 102.91° 90.00°	Depositor
Resolution (Å)	43.00 – 2.19 47.25 – 2.19	Depositor EDS
% Data completeness (in resolution range)	99.6 (43.00-2.19) 99.7 (47.25-2.19)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.24 (at 2.18Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.142 , 0.203 0.142 , 0.202	Depositor DCC
R_{free} test set	1989 reflections (5.28%)	DCC
Wilson B-factor (Å ²)	20.2	Xtriage
Anisotropy	0.070	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 39.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7088	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.16% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, PMP, NO3

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	1.00	1/3188 (0.0%)	1.02	5/4319 (0.1%)
1	B	1.03	0/3211	0.98	2/4350 (0.0%)
All	All	1.02	1/6399 (0.0%)	1.00	7/8669 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	130	TRP	CZ3-CH2	5.25	1.48	1.40

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	229	ARG	NE-CZ-NH2	-5.85	117.38	120.30
1	A	127	ASP	CB-CG-OD2	-5.71	113.16	118.30
1	B	303	LEU	CB-CG-CD1	-5.63	101.44	111.00
1	B	254	ARG	NE-CZ-NH2	-5.57	117.51	120.30
1	A	6	ASP	CB-CG-OD2	5.26	123.04	118.30
1	A	280	ARG	NE-CZ-NH1	5.14	122.87	120.30
1	A	204	ARG	NE-CZ-NH1	-5.06	117.77	120.30

There are no chirality outliers.

There are no planarity outliers.

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	3113	0	3055	60	0
1	B	3130	0	3069	60	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	28	0	0	0	0
3	B	12	0	0	2	0
4	A	16	0	10	8	0
4	B	16	0	11	9	0
5	A	374	0	0	9	0
5	B	397	0	0	14	0
All	All	7088	0	6145	120	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 10.

All (120) 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:246:LYS:NZ	4:B:405:PMP:HNA2	1.51	1.07
4:B:405:PMP:H6	5:B:870:HOH:O	1.52	1.07
1:B:14:LEU:HA	1:B:17:VAL:HG12	1.39	1.04
1:B:130:TRP:HE3	1:B:133:HIS:CD2	1.82	0.97
1:B:360:ARG:HH12	1:B:398:ASP:HB2	1.31	0.95
1:B:13:ILE:CD1	1:B:14:LEU:HD12	2.04	0.86
1:B:130:TRP:CE3	1:B:133:HIS:CD2	2.64	0.84
1:B:246:LYS:HZ3	4:B:405:PMP:HNA2	1.26	0.84
1:B:360:ARG:NH1	1:B:398:ASP:HB2	1.97	0.78
1:B:13:ILE:HD11	1:B:14:LEU:HD12	1.64	0.77
1:B:143:GLU:HB2	5:B:794:HOH:O	1.84	0.76
1:A:130:TRP:HE3	1:A:133:HIS:CD2	2.03	0.76
1:B:86:ASP:HB3	1:B:91[A]:LYS:HE2	1.68	0.73
1:B:246:LYS:CE	4:B:405:PMP:HNA2	2.01	0.72
1:A:246:LYS:NZ	4:A:409:PMP:H4A2	2.07	0.69
1:B:13:ILE:HD12	1:B:14:LEU:HD12	1.73	0.69
1:A:157:ILE:CD1	1:A:189:LEU:HD23	2.23	0.69
1:B:246:LYS:NZ	4:B:405:PMP:N4A	2.34	0.68
1:B:281:ARG:NH1	5:B:855:HOH:O	2.29	0.66
1:B:211:ASP:OD2	4:B:405:PMP:N1	2.28	0.65
1:A:211:ASP:OD2	4:A:409:PMP:N1	2.30	0.65
1:A:130:TRP:CE3	1:A:133:HIS:CD2	2.86	0.64
1:B:103:GLY:HA3	5:B:870:HOH:O	1.97	0.64
1:B:233:ASP:HB3	5:B:745:HOH:O	1.97	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:157:ILE:HD13	1:A:189:LEU:HD23	1.80	0.62
1:B:76:LYS:HE2	5:B:793:HOH:O	1.99	0.61
1:A:244:PHE:HB2	1:A:255:VAL:HG23	1.84	0.60
1:A:33:ILE:HD12	1:A:34:GLY:H	1.65	0.60
1:A:363:SER:HA	5:A:836:HOH:O	2.01	0.59
1:B:219:GLU:HG2	5:B:740:HOH:O	2.03	0.59
1:B:35:ILE:CG2	1:B:43:MET:HE2	2.32	0.58
1:B:130:TRP:HA	5:B:765:HOH:O	2.04	0.58
1:B:130:TRP:CE3	1:B:133:HIS:HD2	2.16	0.57
1:B:11:ASP:HB3	1:B:14:LEU:HD13	1.86	0.56
1:A:354:THR:OG1	1:A:357:GLN:HG3	2.05	0.55
1:A:253:GLU:HG2	1:B:63:ARG:HG2	1.88	0.55
1:A:319:LYS:NZ	5:A:733:HOH:O	2.40	0.55
1:B:360:ARG:HH12	1:B:398:ASP:CB	2.13	0.54
1:A:157:ILE:HD13	1:A:189:LEU:CD2	2.36	0.54
1:B:14:LEU:HA	1:B:17:VAL:CG1	2.25	0.54
1:A:202:GLN:HB2	1:A:236:LEU:HD21	1.90	0.53
1:B:171:LYS:O	1:B:172:ASP:HB2	2.08	0.53
1:B:33:ILE:HG13	1:B:34:GLY:H	1.74	0.52
1:B:210:MET:O	1:B:240:VAL:HA	2.10	0.52
1:B:157:ILE:HD11	1:B:187:VAL:HG12	1.92	0.52
1:A:246:LYS:NZ	4:A:409:PMP:C4A	2.73	0.51
4:B:405:PMP:C6	5:B:870:HOH:O	2.29	0.51
1:A:148:PRO:O	1:A:162:MET:HB2	2.11	0.51
1:A:363:SER:N	5:A:836:HOH:O	2.43	0.51
1:A:19[B]:LYS:NZ	5:A:677:HOH:O	2.44	0.50
1:A:357:GLN:HB3	1:A:395:VAL:CG1	2.41	0.50
1:A:208:PRO:HG2	1:A:238:LEU:HA	1.93	0.50
1:A:192:GLU:HG3	5:A:651:HOH:O	2.11	0.50
1:B:360:ARG:HD3	5:B:776:HOH:O	2.11	0.50
1:B:246:LYS:HZ1	4:B:405:PMP:HNA2	1.51	0.50
1:A:340:TYR:CE1	1:A:341:LEU:HG	2.47	0.49
1:A:130:TRP:CZ2	1:A:132:ASN:HB3	2.48	0.49
1:A:33:ILE:CD1	1:A:34:GLY:H	2.25	0.49
1:A:19[B]:LYS:NZ	1:A:362:GLN:HE21	2.11	0.49
1:B:14:LEU:HG	1:B:17:VAL:CG1	2.44	0.48
1:A:363:SER:CA	5:A:836:HOH:O	2.60	0.48
1:A:24:ASN:O	1:A:26:PRO:HD3	2.13	0.47
1:A:368:TYR:CD1	1:A:368:TYR:N	2.83	0.47
1:A:140:CYS:O	1:A:141:ASP:HB2	2.14	0.47
1:A:171:LYS:HG2	1:A:205:GLU:HB2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:306:GLN:O	1:B:310:GLU:HG3	2.14	0.47
1:A:397:LYS:HE3	5:A:819:HOH:O	2.15	0.47
1:B:130:TRP:CZ2	1:B:132:ASN:HB3	2.51	0.46
1:B:140:CYS:O	1:B:141[A]:ASP:HB2	2.15	0.46
1:B:246:LYS:CE	4:B:405:PMP:N4A	2.75	0.46
1:B:76:LYS:HE2	5:B:726:HOH:O	2.15	0.46
1:A:246:LYS:HZ1	4:A:409:PMP:H4A2	1.77	0.46
1:A:157:ILE:HD12	1:A:189:LEU:HD23	1.99	0.46
1:B:34:GLY:HA3	3:B:402:NO3:O1	2.16	0.46
1:A:63:ARG:HG2	1:B:253:GLU:HG2	1.99	0.45
1:B:179:PRO:HG2	1:B:212:ILE:HB	1.99	0.45
1:B:311:VAL:HA	1:B:314:MET:CE	2.47	0.45
1:B:337:ASN:ND2	5:B:718:HOH:O	2.50	0.45
1:A:333:ILE:HD11	1:A:393:VAL:HA	1.99	0.45
4:A:409:PMP:O4P	4:A:409:PMP:H4A1	2.16	0.45
1:A:17:VAL:HG22	1:A:30:ASN:HD21	1.82	0.45
1:A:347:MET:CE	1:A:378:ALA:CB	2.95	0.45
1:B:73:GLY:HA3	1:B:295:ASP:OD1	2.16	0.45
1:A:362:GLN:HB3	5:A:836:HOH:O	2.17	0.44
1:A:246:LYS:HZ1	4:A:409:PMP:C4A	2.30	0.43
1:A:60:ILE:HG23	1:B:53:GLU:OE1	2.18	0.43
1:A:328:VAL:HG12	1:A:389:ALA:HB1	2.01	0.43
1:A:368:TYR:HD1	1:A:368:TYR:N	2.17	0.43
1:A:68:MET:HG2	1:A:284:SER:O	2.19	0.43
1:B:35:ILE:HG21	1:B:43:MET:HE2	1.98	0.43
1:B:13:ILE:C	1:B:13:ILE:HD12	2.39	0.43
1:B:248:LEU:HB3	1:B:250:LEU:HB2	2.01	0.42
1:B:311:VAL:HA	1:B:314:MET:HE3	2.01	0.42
1:A:5:ILE:HG23	1:B:274:GLN:HG3	2.01	0.42
1:A:246:LYS:HZ3	4:A:409:PMP:H4A2	1.82	0.42
1:B:271:VAL:O	1:B:275:LEU:HG	2.19	0.42
1:A:19[B]:LYS:HZ2	1:A:362:GLN:HE21	1.68	0.42
1:A:130:TRP:CH2	1:A:132:ASN:HB3	2.55	0.42
1:A:130:TRP:CE3	1:A:133:HIS:HD2	2.37	0.41
1:A:336:ARG:HG3	5:A:872:HOH:O	2.20	0.41
1:B:14:LEU:HG	1:B:17:VAL:HG11	2.01	0.41
1:A:183:ASN:HA	1:A:184:PRO:HA	1.80	0.41
4:A:409:PMP:O1P	1:B:65:TYR:OH	2.31	0.41
1:A:354:THR:OG1	1:A:357:GLN:CG	2.68	0.41
1:B:12:PRO:HD2	5:B:862:HOH:O	2.20	0.41
1:B:244:PHE:HB2	1:B:255:VAL:HG23	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:336:ARG:HD3	1:A:338:PHE:CZ	2.54	0.41
1:B:83:PHE:CE2	1:B:95:VAL:HG11	2.56	0.41
1:A:133:HIS:CG	1:A:176:LEU:HD21	2.56	0.41
1:A:33:ILE:CG1	1:A:34:GLY:H	2.34	0.41
1:B:100:THR:HG21	1:B:106:ALA:HA	2.03	0.41
1:B:176:LEU:HA	1:B:176:LEU:HD12	1.88	0.41
1:A:330:GLU:HG3	1:A:338:PHE:HD2	1.85	0.41
1:A:254:ARG:NH1	1:A:254:ARG:HA	2.35	0.40
1:A:19[B]:LYS:HZ2	1:A:362:GLN:NE2	2.20	0.40
1:A:127:ASP:HA	1:A:128:PRO:HA	1.86	0.40
3:B:403:NO3:O3	5:B:771:HOH:O	2.22	0.40
1:A:364:GLU:HB2	1:A:365:PHE:CD2	2.56	0.40
1:B:35:ILE:CG2	1:B:43:MET:CE	2.97	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	398/398 (100%)	379 (95%)	19 (5%)	0	100	100
1	B	401/398 (101%)	391 (98%)	10 (2%)	0	100	100
All	All	799/796 (100%)	770 (96%)	29 (4%)	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	339/337 (101%)	330 (97%)	9 (3%)	50	62
1	B	342/337 (102%)	337 (98%)	5 (2%)	70	82
All	All	681/674 (101%)	667 (98%)	14 (2%)	59	72

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	143	GLU
1	A	184	PRO
1	A	209	PHE
1	A	336	ARG
1	A	350	PHE
1	A	359	GLU
1	A	362	GLN
1	A	363	SER
1	A	368	TYR
1	B	33	ILE
1	B	184	PRO
1	B	209	PHE
1	B	350	PHE
1	B	362	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	345	ASN
1	A	362	GLN
1	B	133	HIS
1	B	362	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 2 are monoatomic - leaving 12 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	NO3	A	402	-	1,3,3	0.40	0	0,3,3	0.00	-
3	NO3	A	403	-	1,3,3	0.17	0	0,3,3	0.00	-
3	NO3	A	404	-	1,3,3	0.39	0	0,3,3	0.00	-
3	NO3	A	405	-	1,3,3	0.61	0	0,3,3	0.00	-
3	NO3	A	406	-	1,3,3	0.18	0	0,3,3	0.00	-
3	NO3	A	407	-	1,3,3	0.39	0	0,3,3	0.00	-
3	NO3	A	408	-	1,3,3	0.84	0	0,3,3	0.00	-
4	PMP	A	409	-	16,16,16	4.52	6 (37%)	20,23,23	2.56	7 (35%)
3	NO3	B	402	-	1,3,3	0.52	0	0,3,3	0.00	-
3	NO3	B	403	-	1,3,3	0.09	0	0,3,3	0.00	-
3	NO3	B	404	-	1,3,3	0.26	0	0,3,3	0.00	-
4	PMP	B	405	-	16,16,16	4.32	4 (25%)	20,23,23	2.57	8 (40%)

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	NO3	A	402	-	-	0/0/0/0	0/0/0/0
3	NO3	A	403	-	-	0/0/0/0	0/0/0/0
3	NO3	A	404	-	-	0/0/0/0	0/0/0/0
3	NO3	A	405	-	-	0/0/0/0	0/0/0/0
3	NO3	A	406	-	-	0/0/0/0	0/0/0/0
3	NO3	A	407	-	-	0/0/0/0	0/0/0/0
3	NO3	A	408	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	PMP	A	409	-	-	0/8/8/8	0/1/1/1
3	NO3	B	402	-	-	0/0/0/0	0/0/0/0
3	NO3	B	403	-	-	0/0/0/0	0/0/0/0
3	NO3	B	404	-	-	0/0/0/0	0/0/0/0
4	PMP	B	405	-	-	0/8/8/8	0/1/1/1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	409	PMP	P-O1P	-2.63	1.41	1.50
4	B	405	PMP	C2A-C2	2.89	1.55	1.50
4	A	409	PMP	C2-N1	2.92	1.39	1.33
4	A	409	PMP	C2A-C2	3.31	1.56	1.50
4	B	405	PMP	C3-C4	6.62	1.50	1.40
4	A	409	PMP	C5-C4	7.27	1.50	1.40
4	B	405	PMP	C5-C4	7.30	1.50	1.40
4	A	409	PMP	C3-C4	7.62	1.52	1.40
4	B	405	PMP	C3-C2	13.36	1.50	1.40
4	A	409	PMP	C3-C2	13.44	1.50	1.40

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	409	PMP	C3-C2-N1	-3.88	115.65	120.75
4	B	405	PMP	C3-C2-N1	-3.41	116.27	120.75
4	B	405	PMP	C4-C4A-N4A	-3.06	98.34	115.56
4	B	405	PMP	C5A-C5-C6	-3.00	114.18	119.33
4	B	405	PMP	C3-C4-C5	-2.64	116.11	118.71
4	A	409	PMP	C4-C4A-N4A	-2.26	102.88	115.56
4	A	409	PMP	C2A-C2-C3	-2.04	118.53	120.96
4	A	409	PMP	O4P-P-O1P	-2.03	100.79	106.47
4	B	405	PMP	O3P-P-O2P	2.27	116.76	107.61
4	B	405	PMP	C2A-C2-N1	3.18	124.25	117.89
4	A	409	PMP	C2A-C2-N1	3.96	125.80	117.89
4	B	405	PMP	C6-N1-C2	4.18	127.31	119.26
4	A	409	PMP	C6-N1-C2	4.77	128.44	119.26
4	A	409	PMP	O4P-C5A-C5	6.46	122.31	109.32
4	B	405	PMP	O4P-C5A-C5	7.14	123.67	109.32

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	409	PMP	8	0
3	B	402	NO3	1	0
3	B	403	NO3	1	0
4	B	405	PMP	9	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	398/398 (100%)	-0.38	8 (2%) 65 63	10, 20, 57, 95	0
1	B	398/398 (100%)	-0.42	5 (1%) 77 75	10, 20, 42, 76	0
All	All	796/796 (100%)	-0.40	13 (1%) 72 70	10, 20, 51, 95	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	15	GLY	3.9
1	A	398	ASP	3.5
1	B	16	LEU	3.5
1	B	13	ILE	3.1
1	A	20	PHE	3.1
1	A	394	ASP	3.0
1	A	26	PRO	3.0
1	B	398	ASP	2.7
1	A	395	VAL	2.6
1	B	14	LEU	2.6
1	A	22	ALA	2.5
1	A	393	VAL	2.4
1	A	333	ILE	2.1

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 carbohydrates in this entry.

6.4 Ligands

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	NO3	B	404	4/4	0.95	0.21	13.19	41,46,54,54	0
3	NO3	A	403	4/4	0.98	0.16	6.49	34,36,40,40	0
3	NO3	B	403	4/4	0.92	0.14	4.70	31,37,38,39	0
4	PMP	A	409	16/16	0.95	0.17	3.48	18,25,28,28	0
3	NO3	B	402	4/4	0.92	0.23	3.03	68,71,74,80	0
3	NO3	A	406	4/4	0.98	0.15	2.12	34,37,39,41	0
4	PMP	B	405	16/16	0.96	0.14	1.77	19,26,32,32	0
3	NO3	A	404	4/4	0.98	0.10	1.69	33,38,39,40	0
2	MG	B	401	1/1	0.98	0.08	-0.01	17,17,17,17	0
3	NO3	A	405	4/4	0.98	0.10	-0.59	30,33,36,38	0
3	NO3	A	402	4/4	0.95	0.10	-0.64	42,42,48,48	0
3	NO3	A	407	4/4	0.90	0.12	-	54,56,60,62	0
3	NO3	A	408	4/4	0.89	0.38	-	35,37,37,39	0
2	MG	A	401	1/1	0.94	0.09	-	37,37,37,37	0

6.5 Other polymers

There are no such residues in this entry.