Full wwPDB X-ray Structure Validation Report

Jan 31, 2016 – 10:34 PM GMT

PDB ID	:	1U7Z
Title	:	Phosphopantothenoylcysteine synthetase from E. coli, 4'-phosphopantothenoyl-CMP complex
Authors	:	Stanitzek, S.; Augustin, M.A.; Huber, R.; Kupke, T.; Steinbacher, S.
Deposited on	:	2004-08-04
Resolution	:	2.30 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

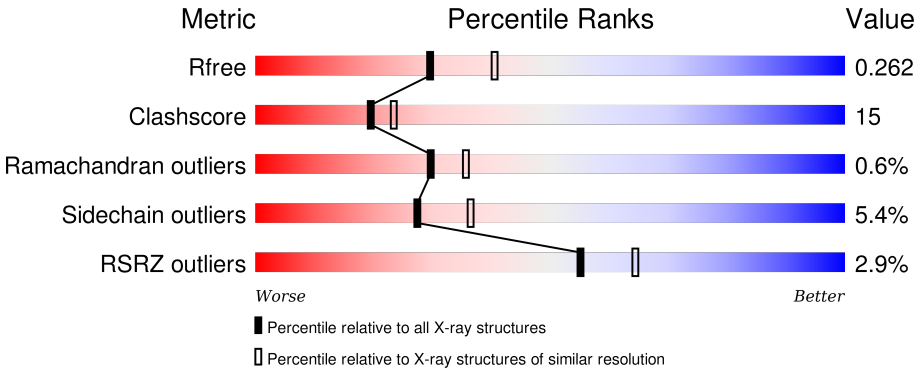
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

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 2.30 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}	91344	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

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 <=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	226	4% 69% 24%
1	B	226	2% 74% 20%
1	C	226	3% 68% 26%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5413 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.

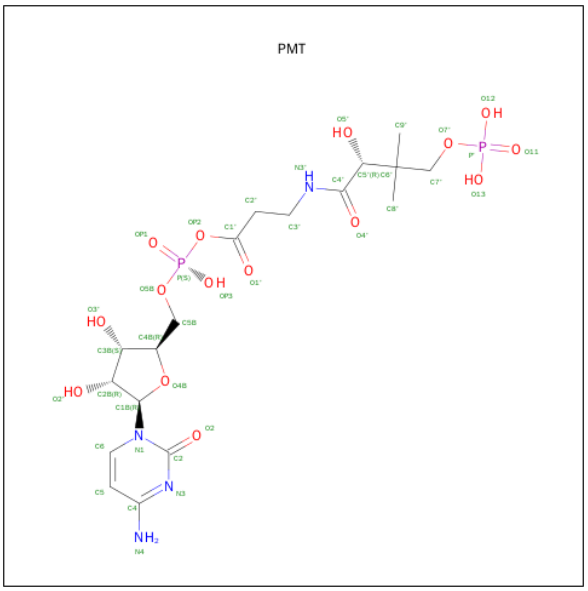
- Molecule 1 is a protein called Coenzyme A biosynthesis bifunctional protein coaBC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	216	Total	C	N	O	S	0	0	0
			1666	1046	298	315	7			
1	B	218	Total	C	N	O	S	0	0	0
			1683	1056	303	317	7			
1	C	219	Total	C	N	O	S	0	0	0
			1689	1062	303	317	7			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	210	ASP	ASN	ENGINEERED	UNP P0ABQ0
B	210	ASP	ASN	ENGINEERED	UNP P0ABQ0
C	210	ASP	ASN	ENGINEERED	UNP P0ABQ0

- Molecule 2 is PHOSPHORIC ACID MONO-[3-(3-{[5-(4-AMINO-2-OXO-2H-PYRIMIDIN-1-YL)-3,4- DIHYDROXY-TETRAHYDRO-FURAN-2- YLMETHOXY]-HYDROXY-PHOSPHORYLOXY}-3-OXO-PROPYLCARBAMOYL)-3-HYDROXY-2,2-DIMETHYL-PROPYL] ESTER (three-letter code: PMT) (formula: $C_{18}H_{30}N_4O_{15}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			39	18	4	15	2		
2	B	1	Total	C	N	O	P	0	0
			39	18	4	15	2		
2	C	1	Total	C	N	O	P	0	0
			39	18	4	15	2		

- Molecule 3 is water.

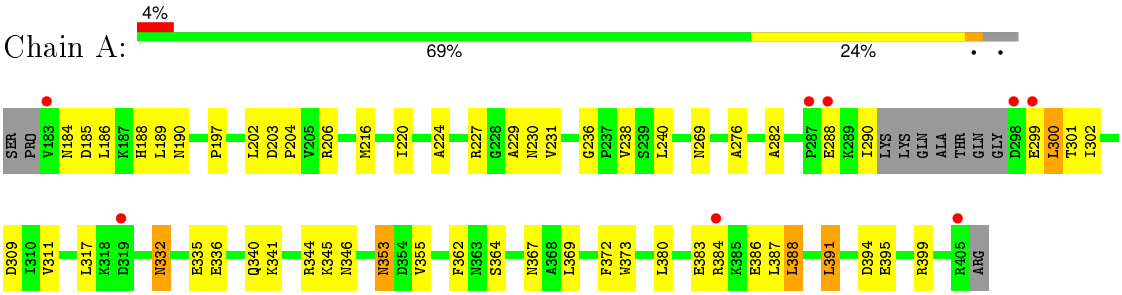
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	77	Total	O	0	0
			77	77		
3	B	97	Total	O	0	0
			97	97		
3	C	84	Total	O	0	0
			84	84		

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 errors 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.

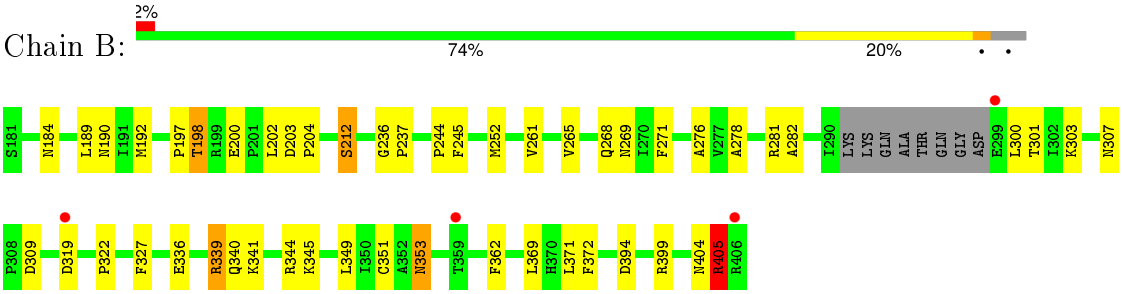
- Molecule 1: Coenzyme A biosynthesis bifunctional protein coaBC

Chain A:



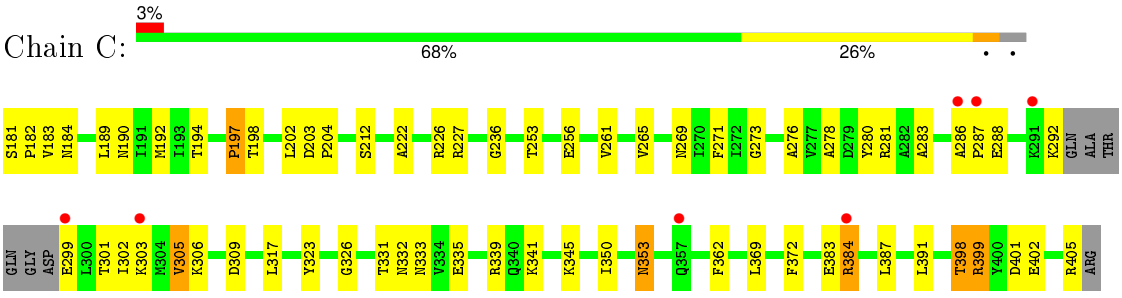
- Molecule 1: Coenzyme A biosynthesis bifunctional protein coaBC

Chain B:



- Molecule 1: Coenzyme A biosynthesis bifunctional protein coaBC

Chain C:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	43.63Å 142.58Å 244.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.30 19.74 – 2.30	Depositor EDS
% Data completeness (in resolution range)	93.4 (20.00-2.30) 94.0 (19.74-2.30)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.95 (at 2.30Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.196 , 0.266 0.196 , 0.262	Depositor DCC
R_{free} test set	1603 reflections (4.96%)	DCC
Wilson B-factor (Å^2)	37.5	Xtriage
Anisotropy	0.292	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 45.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Outliers	1 of 32347 reflections (0.003%)	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	5413	wwPDB-VP
Average B, all atoms (Å^2)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.16% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: PMT

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	0.49	0/1693	0.75	0/2298
1	B	0.54	0/1711	0.76	0/2321
1	C	0.48	0/1717	0.76	0/2329
All	All	0.51	0/5121	0.76	0/6948

There are no bond length outliers.

There are no bond angle outliers.

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	1666	0	1682	41	0
1	B	1683	0	1703	60	0
1	C	1689	0	1716	61	1
2	A	39	0	28	4	0
2	B	39	0	28	3	0
2	C	39	0	28	3	0
3	A	77	0	0	7	0
3	B	97	0	0	6	0
3	C	84	0	0	6	0
All	All	5413	0	5185	155	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 15.

All (155) 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:319:ASP:HB3	3:B:1517:HOH:O	1.61	1.00
1:B:405:ARG:HH21	1:B:405:ARG:HB2	1.24	0.98
1:B:192:MET:HE1	1:B:261:VAL:HG13	1.45	0.95
1:A:190:ASN:H	1:A:269:ASN:HD22	1.05	0.94
2:A:500:PMT:H6	2:A:500:PMT:H5'1	1.45	0.94
2:C:2500:PMT:H5'1	2:C:2500:PMT:H6	1.56	0.88
1:B:190:ASN:H	1:B:269:ASN:HD22	1.21	0.86
1:C:192:MET:HE1	1:C:265:VAL:HB	1.62	0.82
1:A:190:ASN:H	1:A:269:ASN:ND2	1.79	0.80
1:C:190:ASN:H	1:C:269:ASN:HD22	1.29	0.80
1:B:192:MET:CE	1:B:261:VAL:HG13	2.13	0.77
1:C:198:THR:CG2	1:C:278:ALA:H	1.98	0.76
1:C:198:THR:HG22	1:C:278:ALA:H	1.54	0.72
1:A:206:ARG:HH11	1:A:290:ILE:HD12	1.55	0.70
1:B:341:LYS:NZ	2:B:1500:PMT:OP1	2.25	0.69
1:C:181:SER:N	1:C:182:PRO:HD2	2.09	0.68
1:B:344:ARG:NH2	1:C:402:GLU:HA	2.09	0.67
1:B:405:ARG:NH2	1:B:405:ARG:HB2	2.04	0.67
1:A:335:GLU:HG2	1:A:372:PHE:HZ	1.59	0.67
1:C:339:ARG:NH2	3:C:2527:HOH:O	2.27	0.67
1:A:190:ASN:N	1:A:269:ASN:HD22	1.87	0.66
1:A:335:GLU:HG2	1:A:372:PHE:CZ	2.31	0.66
1:C:292:LYS:H	1:C:292:LYS:HD2	1.60	0.66
1:B:300:LEU:HG	1:B:301:THR:N	2.13	0.64
1:C:192:MET:HE3	1:C:271:PHE:CE1	2.31	0.64
1:A:309:ASP:OD2	1:A:345:LYS:HE2	1.98	0.64
1:A:384:ARG:HD3	3:A:575:HOH:O	1.96	0.64
1:B:198:THR:HG23	1:B:200:GLU:OE2	1.99	0.63
1:C:190:ASN:H	1:C:269:ASN:ND2	1.96	0.62
1:A:341:LYS:HE2	3:A:539:HOH:O	1.98	0.62
1:B:190:ASN:H	1:B:269:ASN:ND2	1.94	0.62
1:B:192:MET:HE3	1:B:271:PHE:HE1	1.65	0.62
1:B:344:ARG:HG2	1:C:398:THR:CG2	2.29	0.62
1:C:353:ASN:HB3	1:C:369:LEU:HD23	1.82	0.61
1:C:192:MET:HE3	1:C:271:PHE:CD1	2.37	0.60
1:C:222:ALA:HB1	1:C:226:ARG:NH2	2.17	0.59
1:A:387:LEU:HG	1:A:391:LEU:HD22	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:344:ARG:NE	3:B:1532:HOH:O	2.35	0.59
1:C:194:THR:OG1	1:C:273:GLY:HA2	2.02	0.59
1:A:395:GLU:HB3	3:A:547:HOH:O	2.02	0.59
1:A:353:ASN:HB3	1:A:369:LEU:HD23	1.85	0.58
1:B:200:GLU:OE1	1:B:281:ARG:HB3	2.04	0.57
1:B:184:ASN:ND2	3:B:1506:HOH:O	2.38	0.57
1:B:300:LEU:HG	1:B:301:THR:H	1.70	0.57
1:B:265:VAL:HA	1:B:268:GLN:HG2	1.86	0.56
1:B:281:ARG:HH11	1:B:307:ASN:HD22	1.53	0.56
1:B:197:PRO:O	1:B:236:GLY:HA3	2.05	0.56
2:A:500:PMT:C6	2:A:500:PMT:H5'1	2.28	0.56
1:C:198:THR:HG21	1:C:278:ALA:H	1.71	0.56
1:B:344:ARG:NH2	3:B:1532:HOH:O	2.37	0.56
1:C:281:ARG:HG3	1:C:281:ARG:HH11	1.70	0.56
1:B:344:ARG:CZ	3:B:1532:HOH:O	2.54	0.55
1:B:344:ARG:HH21	1:C:402:GLU:HA	1.70	0.55
1:B:192:MET:HE3	1:B:261:VAL:HG22	1.89	0.55
1:B:339:ARG:HG3	1:B:339:ARG:HH11	1.71	0.55
1:C:181:SER:N	3:C:2522:HOH:O	2.40	0.55
1:B:202:LEU:CD2	1:B:282:ALA:HB2	2.36	0.55
1:A:206:ARG:HH11	1:A:290:ILE:CD1	2.21	0.54
1:C:181:SER:N	1:C:182:PRO:CD	2.71	0.54
1:C:283:ALA:HA	1:C:305:VAL:CG2	2.37	0.54
1:C:276:ALA:HA	2:C:2500:PMT:H2'1	1.90	0.53
1:A:276:ALA:HA	2:A:500:PMT:H2'1	1.89	0.52
1:C:227:ARG:HD2	3:C:2517:HOH:O	2.09	0.52
1:B:202:LEU:HD23	1:B:282:ALA:HB2	1.89	0.52
1:B:344:ARG:HH21	1:C:402:GLU:CA	2.23	0.52
1:A:364:SER:N	3:A:568:HOH:O	2.42	0.52
1:A:197:PRO:O	1:A:236:GLY:HA3	2.10	0.52
1:C:203:ASP:HB2	1:C:204:PRO:CD	2.41	0.51
1:C:253:THR:OG1	1:C:256:GLU:HG3	2.10	0.51
1:C:299:GLU:N	3:C:2559:HOH:O	2.44	0.51
1:B:192:MET:HE3	1:B:271:PHE:CE1	2.43	0.51
1:C:192:MET:CE	1:C:261:VAL:HG13	2.42	0.50
1:A:299:GLU:CD	1:B:303:LYS:HE3	2.31	0.50
1:A:373:TRP:CE2	1:A:399:ARG:NH1	2.79	0.50
1:C:280:TYR:CE1	1:C:306:LYS:HG3	2.46	0.50
1:C:192:MET:CE	1:C:271:PHE:CD1	2.95	0.49
1:B:203:ASP:HB2	1:B:204:PRO:HD3	1.94	0.49
1:C:192:MET:CE	1:C:271:PHE:HD1	2.25	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:344:ARG:HG2	1:C:398:THR:HG22	1.95	0.49
1:C:281:ARG:HB2	3:C:2514:HOH:O	2.12	0.48
1:A:341:LYS:CE	3:A:539:HOH:O	2.57	0.48
1:C:283:ALA:CB	1:C:303:LYS:HB3	2.43	0.48
1:B:344:ARG:NH2	1:C:402:GLU:CA	2.76	0.48
1:C:383:GLU:CD	1:C:387:LEU:HD23	2.34	0.48
1:A:185:ASP:OD2	1:A:185:ASP:N	2.47	0.48
1:B:344:ARG:NH2	1:C:402:GLU:HB2	2.28	0.48
1:B:203:ASP:HB2	1:B:204:PRO:CD	2.44	0.47
1:A:202:LEU:HD23	1:A:282:ALA:HB2	1.95	0.47
1:B:327:PHE:O	2:B:1500:PMT:H5"	2.14	0.47
1:B:309:ASP:OD2	1:B:345:LYS:HE2	2.14	0.47
1:B:405:ARG:HD3	3:B:1556:HOH:O	2.14	0.47
1:B:268:GLN:O	1:B:322:PRO:HB3	2.14	0.47
1:B:351:CYS:SG	1:B:371:LEU:HD22	2.55	0.47
1:A:344:ARG:HD3	3:A:558:HOH:O	2.14	0.47
1:B:404:ASN:O	1:B:405:ARG:HB2	2.15	0.47
1:A:344:ARG:NH2	3:A:534:HOH:O	2.47	0.47
1:A:367:ASN:HB3	1:A:388:LEU:HD12	1.96	0.47
1:B:336:GLU:O	1:B:340:GLN:HG3	2.16	0.46
1:A:204:PRO:HG2	1:A:288:GLU:HA	1.97	0.46
1:B:353:ASN:HB3	1:B:369:LEU:HD23	1.97	0.46
1:A:185:ASP:O	1:A:188:HIS:HE1	1.99	0.46
1:C:405:ARG:HD2	1:C:405:ARG:N	2.30	0.46
1:A:383:GLU:HG3	1:A:384:ARG:N	2.31	0.45
1:A:186:LEU:O	1:A:229:ALA:HA	2.16	0.45
1:B:404:ASN:O	1:B:405:ARG:CB	2.65	0.45
1:B:405:ARG:HH21	1:B:405:ARG:CB	2.13	0.45
1:C:192:MET:HE2	1:C:265:VAL:HG23	1.98	0.45
1:B:192:MET:HE2	1:B:271:PHE:CD1	2.52	0.45
1:A:189:LEU:HA	1:A:269:ASN:ND2	2.32	0.45
1:C:287:PRO:O	1:C:288:GLU:HG3	2.17	0.45
1:B:244:PRO:O	1:B:245:PHE:HB2	2.17	0.44
1:B:190:ASN:N	1:B:269:ASN:HD22	2.02	0.44
1:C:204:PRO:HD3	1:C:286:ALA:O	2.16	0.44
1:A:336:GLU:O	1:A:340:GLN:HG3	2.18	0.44
1:C:192:MET:HE2	1:C:271:PHE:HD1	1.82	0.44
1:A:332:ASN:HD22	1:A:332:ASN:N	2.16	0.44
1:A:216:MET:O	1:A:220:ILE:HG13	2.19	0.43
1:C:283:ALA:HB3	1:C:303:LYS:HB3	2.01	0.43
1:A:227:ARG:NH1	1:A:394:ASP:OD2	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:197:PRO:O	1:C:236:GLY:HA3	2.19	0.43
1:C:323:TYR:OH	1:C:399:ARG:HB3	2.18	0.43
1:C:202:LEU:HD13	1:C:302:ILE:HD13	2.00	0.43
1:A:203:ASP:OD1	1:A:290:ILE:HG13	2.19	0.43
1:B:192:MET:HB2	1:B:268:GLN:HG3	2.01	0.43
1:C:401:ASP:HA	1:C:405:ARG:HH21	1.84	0.43
1:B:276:ALA:HA	2:B:1500:PMT:H2'1	2.01	0.43
1:B:198:THR:CG2	1:B:278:ALA:H	2.32	0.43
1:A:373:TRP:CZ2	1:A:399:ARG:NH1	2.87	0.43
1:B:281:ARG:HH11	1:B:307:ASN:ND2	2.15	0.42
1:C:192:MET:HE3	1:C:271:PHE:HE1	1.81	0.42
1:C:292:LYS:H	1:C:292:LYS:CD	2.29	0.42
1:B:197:PRO:HD3	1:B:212:SER:O	2.18	0.42
1:C:384:ARG:NH1	3:C:2557:HOH:O	2.51	0.42
1:B:349:LEU:HD12	1:B:372:PHE:O	2.20	0.42
1:A:300:LEU:HD12	1:A:301:THR:N	2.35	0.42
1:C:331:THR:OG1	1:C:332:ASN:ND2	2.53	0.42
1:A:202:LEU:HD22	1:A:302:ILE:HG21	2.02	0.41
1:C:192:MET:HE1	1:C:265:VAL:CB	2.41	0.41
1:C:192:MET:HE3	1:C:261:VAL:HG13	2.02	0.41
1:B:344:ARG:NH2	1:C:402:GLU:CB	2.83	0.41
1:A:355:VAL:HB	1:A:362:PHE:CE1	2.55	0.41
1:C:326:GLY:O	1:C:350:ILE:HA	2.20	0.41
1:C:341:LYS:NZ	2:C:2500:PMT:OP1	2.54	0.41
1:C:309:ASP:OD2	1:C:345:LYS:HE2	2.19	0.41
1:C:192:MET:HE1	1:C:261:VAL:HG13	2.02	0.41
1:A:224:ALA:HB3	1:A:231:VAL:HG21	2.01	0.41
1:B:237:PRO:HB3	1:B:252:MET:CE	2.51	0.41
1:B:198:THR:HG22	1:B:278:ALA:H	1.86	0.41
1:B:192:MET:CB	1:B:268:GLN:HG3	2.51	0.41
1:C:335:GLU:HG3	1:C:372:PHE:CE2	2.55	0.41
1:A:311:VAL:HG11	2:A:500:PMT:O4B	2.22	0.40
1:B:344:ARG:CZ	1:C:402:GLU:HB2	2.52	0.40
1:B:339:ARG:HG3	1:B:339:ARG:NH1	2.35	0.40
1:A:238:VAL:HG23	1:A:240:LEU:H	1.86	0.40
1:C:183:VAL:HG12	1:C:184:ASN:N	2.37	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)
1:C:301:THR:CG2	1:C:301:THR:CG2[3_655]	1.91	0.29

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	212/226 (94%)	202 (95%)	9 (4%)	1 (0%)	34	41
1	B	214/226 (95%)	205 (96%)	7 (3%)	2 (1%)	21	24
1	C	215/226 (95%)	206 (96%)	8 (4%)	1 (0%)	34	41
All	All	641/678 (94%)	613 (96%)	24 (4%)	4 (1%)	30	36

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	405	ARG
1	A	300	LEU
1	B	212	SER
1	C	212	SER

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	179/187 (96%)	169 (94%)	10 (6%)	26	35
1	B	181/187 (97%)	173 (96%)	8 (4%)	35	46
1	C	182/187 (97%)	171 (94%)	11 (6%)	24	31

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	542/561 (97%)	513 (95%)	29 (5%)	27 36

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	184	ASN
1	A	230	ASN
1	A	317	LEU
1	A	332	ASN
1	A	346	ASN
1	A	353	ASN
1	A	380	LEU
1	A	386	GLU
1	A	388	LEU
1	A	391	LEU
1	B	189	LEU
1	B	198	THR
1	B	339	ARG
1	B	353	ASN
1	B	362	PHE
1	B	394	ASP
1	B	399	ARG
1	B	405	ARG
1	C	189	LEU
1	C	197	PRO
1	C	305	VAL
1	C	317	LEU
1	C	333	ASN
1	C	353	ASN
1	C	362	PHE
1	C	384	ARG
1	C	391	LEU
1	C	398	THR
1	C	399	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	230	ASN
1	A	269	ASN
1	A	307	ASN

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Mol	Chain	Res	Type
1	A	332	ASN
1	A	346	ASN
1	B	184	ASN
1	B	230	ASN
1	B	269	ASN
1	B	307	ASN
1	B	332	ASN
1	B	333	ASN
1	B	340	GLN
1	B	346	ASN
1	B	404	ASN
1	C	184	ASN
1	C	230	ASN
1	C	262	ASN
1	C	269	ASN
1	C	307	ASN
1	C	332	ASN
1	C	340	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

There are no carbohydrates in this entry.

5.6 Ligand geometry

3 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	$\#\|Z\| > 2$
2	PMT	A	500	-	31,40,40	1.34	5 (16%)	42,60,60	1.33	5 (11%)
2	PMT	B	1500	-	31,40,40	1.34	5 (16%)	42,60,60	1.20	4 (9%)
2	PMT	C	2500	-	31,40,40	1.35	5 (16%)	42,60,60	1.18	3 (7%)

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
2	PMT	A	500	-	-	0/32/54/54	0/2/2/2
2	PMT	B	1500	-	-	0/32/54/54	0/2/2/2
2	PMT	C	2500	-	-	0/32/54/54	0/2/2/2

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	500	PMT	O4B-C1B	2.28	1.44	1.41
2	B	1500	PMT	O4B-C1B	2.37	1.44	1.41
2	C	2500	PMT	O4B-C1B	2.44	1.44	1.41
2	A	500	PMT	C4-N3	2.66	1.40	1.35
2	B	1500	PMT	C4-N3	2.70	1.40	1.35
2	C	2500	PMT	C4-N3	2.75	1.40	1.35
2	C	2500	PMT	P-OP1	2.76	1.61	1.51
2	A	500	PMT	P-OP1	2.77	1.61	1.51
2	B	1500	PMT	P-OP1	2.82	1.61	1.51
2	A	500	PMT	P'-O11	3.11	1.61	1.51
2	B	1500	PMT	P'-O11	3.12	1.61	1.51
2	C	2500	PMT	P'-O11	3.13	1.61	1.51
2	C	2500	PMT	C6-N1	3.46	1.40	1.35
2	A	500	PMT	C6-N1	3.47	1.40	1.35
2	B	1500	PMT	C6-N1	3.47	1.40	1.35

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	500	PMT	O5B-P-OP1	-2.40	100.29	109.62
2	A	500	PMT	C4B-O4B-C1B	-2.23	107.27	109.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	1500	PMT	OP2-C1'-O1'	2.04	125.99	121.67
2	C	2500	PMT	O13-P'-O7'	2.15	112.74	106.56
2	A	500	PMT	O13-P'-O7'	2.52	113.83	106.56
2	B	1500	PMT	O13-P'-O7'	2.62	114.09	106.56
2	B	1500	PMT	OP3-P-OP2	2.95	113.29	104.16
2	C	2500	PMT	C2-N3-C4	3.06	119.92	115.61
2	A	500	PMT	C2-N3-C4	3.33	120.31	115.61
2	C	2500	PMT	OP3-P-OP2	3.52	115.04	104.16
2	B	1500	PMT	C2-N3-C4	3.56	120.64	115.61
2	A	500	PMT	OP3-P-OP2	3.77	115.81	104.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	500	PMT	4	0
2	B	1500	PMT	3	0
2	C	2500	PMT	3	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

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	216/226 (95%)	-0.16	8 (3%) 45 54	19, 35, 66, 99	0
1	B	218/226 (96%)	-0.36	4 (1%) 71 78	21, 33, 60, 82	0
1	C	219/226 (96%)	-0.10	7 (3%) 51 60	24, 38, 73, 98	0
All	All	653/678 (96%)	-0.21	19 (2%) 55 64	19, 36, 66, 99	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	405	ARG	4.3
1	C	291	LYS	4.3
1	B	406	ARG	4.1
1	C	299	GLU	4.0
1	A	183	VAL	3.9
1	A	299	GLU	3.7
1	A	287	PRO	3.6
1	C	287	PRO	3.5
1	A	288	GLU	3.5
1	A	384	ARG	3.1
1	C	303	LYS	3.1
1	A	319	ASP	2.7
1	B	319	ASP	2.6
1	C	286	ALA	2.4
1	C	357	GLN	2.3
1	C	384	ARG	2.2
1	A	298	ASP	2.2
1	B	359	THR	2.1
1	B	299	GLU	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 (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. 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, 95^{th} 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
2	PMT	A	500	39/39	0.97	0.13	0.56	21,29,41,46	0
2	PMT	C	2500	39/39	0.96	0.12	0.05	21,30,49,53	0
2	PMT	B	1500	39/39	0.97	0.10	-0.52	19,30,40,47	0

6.5 Other polymers (i)

There are no such residues in this entry.