



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:53 AM GMT

PDB ID : 2J5C
Title : RATIONAL CONVERSION OF SUBSTRATE AND PRODUCT SPECIFICITY IN A MONOTERPENE SYNTHASE. STRUCTURAL INSIGHTS INTO THE MOLECULAR BASIS OF RAPID EVOLUTION.
Authors : Kampranis, S.C.; Ioannidis, D.; Purvis, A.; Mahrez, W.; Ninga, E.; Katerelos, N.A.; Anssour, S.; Dunwell, J.M.; Makris, A.M.; Goodenough, P.W.; Johnson, C.B.
Deposited on : 2006-09-14
Resolution : 1.95 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 (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

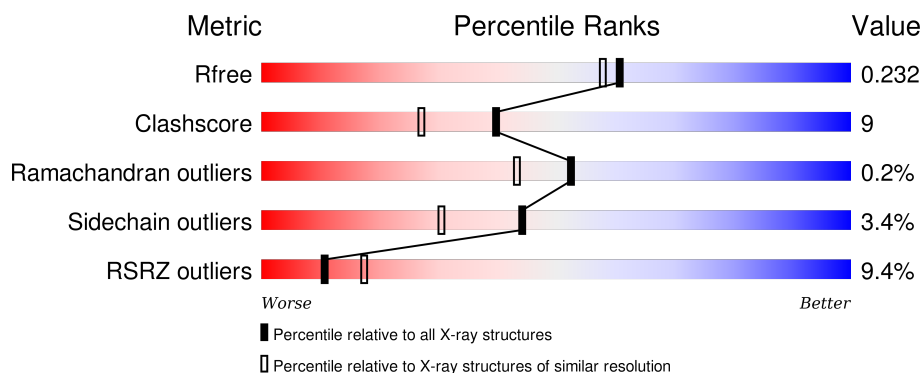
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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	1833 (1.96-1.96)
Clashscore	102246	1953 (1.96-1.96)
Ramachandran outliers	100387	1936 (1.96-1.96)
Sidechain outliers	100360	1936 (1.96-1.96)
RSRZ outliers	91569	1835 (1.96-1.96)

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	569	<div> <div>8%</div> <div>65%</div> <div>19%</div> <div>•</div> <div>15%</div> </div>
1	B	569	<div> <div>8%</div> <div>68%</div> <div>17%</div> <div>•</div> <div>14%</div> </div>

2 Entry composition [i](#)

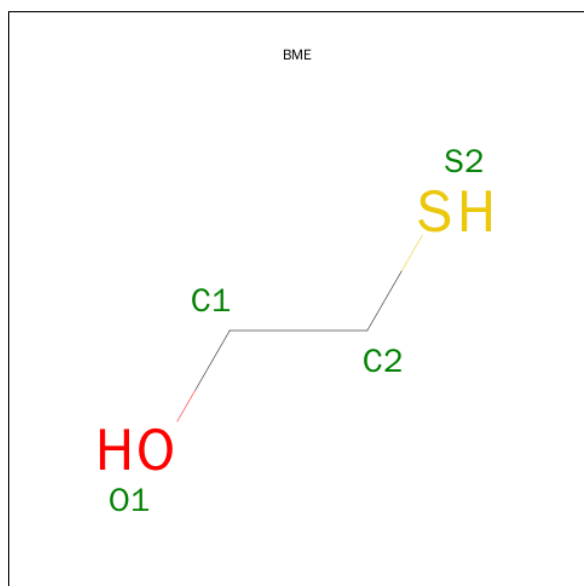
There are 3 unique types of molecules in this entry. The entry contains 8468 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 1,8-CINEOLE SYNTHASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	485	Total	C	N	O	S	0	0	0
			3959	2523	673	738	25			
1	B	491	Total	C	N	O	S	0	0	0
			4034	2575	682	751	26			

- Molecule 2 is BETA-MERCAPTOETHANOL (three-letter code: BME) (formula: C₂H₆OS).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	S	0	0
			4	2	1	1		
2	A	1	Total	C	O	S	0	0
			4	2	1	1		
2	B	1	Total	C	O	S	0	0
			4	2	1	1		
2	B	1	Total	C	O	S	0	0
			4	2	1	1		

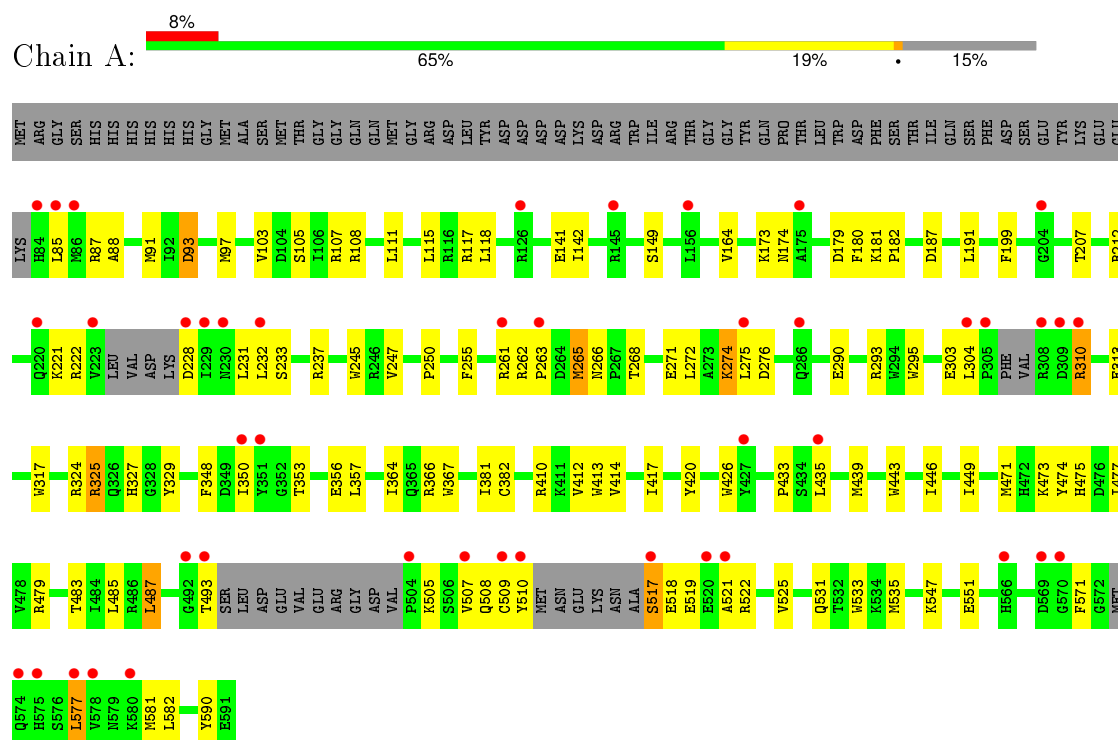
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	221	Total 221	O 221	0	0
3	B	238	Total 238	O 238	0	0

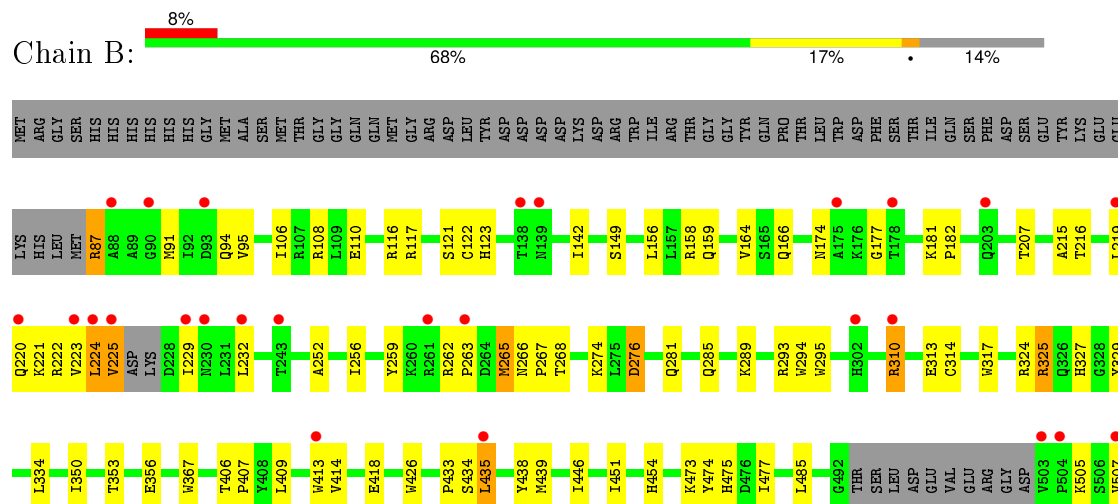
3 Residue-property plots

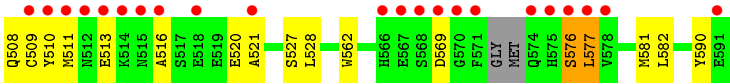
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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: 1,8-CINEOLE SYNTHASE



• Molecule 1: 1,8-CINEOLE SYNTHASE





4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	124.55Å 171.15Å 123.81Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.70 – 1.95 29.70 – 1.95	Depositor EDS
% Data completeness (in resolution range)	99.4 (29.70-1.95) 99.6 (29.70-1.95)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.49 (at 1.95Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.218 , 0.235 0.214 , 0.232	Depositor DCC
R_{free} test set	4786 reflections (5.00%)	DCC
Wilson B-factor (Å ²)	26.4	Xtriage
Anisotropy	0.678	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 60.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 95726 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8468	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.96% 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, 0.375 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: BME

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	0.72	7/4042 (0.2%)	0.92	1/5458 (0.0%)
1	B	0.72	6/4121 (0.1%)	0.92	2/5568 (0.0%)
All	All	0.72	13/8163 (0.2%)	0.92	3/11026 (0.0%)

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

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	245	TRP	NE1-CE2	8.92	1.49	1.37
1	A	413	TRP	NE1-CE2	8.78	1.49	1.37
1	B	294	TRP	NE1-CE2	8.75	1.49	1.37
1	A	443	TRP	NE1-CE2	8.71	1.48	1.37
1	A	367	TRP	NE1-CE2	8.70	1.48	1.37
1	B	413	TRP	NE1-CE2	8.54	1.48	1.37
1	B	317	TRP	NE1-CE2	8.53	1.48	1.37
1	B	562	TRP	NE1-CE2	8.48	1.48	1.37
1	B	367	TRP	NE1-CE2	8.48	1.48	1.37
1	A	533	TRP	NE1-CE2	8.44	1.48	1.37
1	B	295	TRP	NE1-CE2	8.42	1.48	1.37
1	A	317	TRP	NE1-CE2	8.18	1.48	1.37
1	A	295	TRP	NE1-CE2	7.46	1.47	1.37

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	325	ARG	NE-CZ-NH2	-6.39	117.10	120.30
1	B	87	ARG	CD-NE-CZ	-5.22	116.29	123.60
1	A	325	ARG	CD-NE-CZ	-5.19	116.34	123.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	518	GLU	Peptide

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	3959	0	3816	70	0
1	B	4034	0	3914	69	0
2	A	8	0	10	3	0
2	B	8	0	10	3	0
3	A	221	0	0	1	0
3	B	238	0	0	1	0
All	All	8468	0	7750	139	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 (139) 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:225:VAL:O	1:B:225:VAL:HG12	1.62	0.99
1:B:225:VAL:O	1:B:225:VAL:CG1	2.11	0.98
1:B:475:HIS:HD2	1:B:477:ILE:H	1.28	0.82
1:B:142:ILE:HG23	1:B:149:SER:HB3	1.65	0.77
1:B:310:ARG:HG2	1:B:310:ARG:O	1.86	0.76
1:A:88:ALA:HB2	1:A:275:LEU:HD21	1.70	0.74
1:A:310:ARG:HG2	2:A:1593:BME:C1	2.17	0.74
1:A:577:LEU:O	1:A:581:MET:HG3	1.88	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:272:LEU:O	1:A:276:ASP:HB2	1.90	0.72
1:A:142:ILE:HG23	1:A:149:SER:HB3	1.74	0.70
1:A:475:HIS:HD2	1:A:477:ILE:H	1.41	0.69
1:A:310:ARG:HG2	2:A:1593:BME:H11	1.73	0.68
1:B:156:LEU:HD23	1:B:159:GLN:NE2	2.08	0.68
1:A:247:VAL:HG21	1:A:250:PRO:HG2	1.79	0.65
1:A:505:LYS:HG2	1:A:508:GLN:CB	2.27	0.65
1:A:446:ILE:HG12	1:A:485:LEU:HG	1.81	0.63
1:B:310:ARG:CG	1:B:310:ARG:O	2.46	0.63
1:A:93:ASP:O	1:A:97:MET:HG3	1.99	0.62
1:B:281:GLN:O	1:B:285:GLN:HG3	2.00	0.62
1:B:325:ARG:HD2	2:B:1592:BME:H12	1.80	0.62
1:B:510:TYR:CD2	1:B:521:ALA:HA	2.36	0.61
1:B:221:LYS:O	1:B:222:ARG:HG3	2.00	0.60
1:A:232:LEU:HD13	1:A:232:LEU:C	2.22	0.60
1:B:289:LYS:HE3	1:B:293:ARG:NH2	2.16	0.60
1:B:156:LEU:HD23	1:B:159:GLN:HE22	1.65	0.60
1:B:224:LEU:HD13	1:B:232:LEU:HD12	1.83	0.60
1:A:221:LYS:O	1:A:222:ARG:HG3	2.02	0.59
1:A:304:LEU:HD11	1:A:382:CYS:SG	2.44	0.58
1:B:353:THR:OG1	1:B:356:GLU:HG3	2.04	0.58
1:A:435:LEU:HD23	1:A:439:MET:HG2	1.86	0.57
1:A:303:GLU:HG3	1:A:381:ILE:HD13	1.87	0.57
1:B:516:ALA:HB1	1:B:520:GLU:OE1	2.04	0.57
1:A:531:GLN:O	1:A:535:MET:HG3	2.05	0.56
1:A:410:ARG:O	1:A:414:VAL:HG13	2.05	0.56
1:B:225:VAL:O	1:B:225:VAL:HG13	2.02	0.56
1:A:199:PHE:HA	1:A:212:ARG:HH21	1.71	0.56
1:B:334:LEU:HD13	1:B:451:ILE:HG23	1.88	0.55
1:B:224:LEU:HD13	1:B:232:LEU:CD1	2.36	0.54
1:A:199:PHE:HA	1:A:212:ARG:NH2	2.23	0.54
1:A:473:LYS:N	1:A:474:TYR:HA	2.22	0.54
1:B:252:ALA:O	1:B:256:ILE:HG13	2.07	0.54
1:B:438:TYR:CE2	1:B:439:MET:HE2	2.42	0.54
1:B:324:ARG:HB2	1:B:327:HIS:ND1	2.22	0.54
1:A:547:LYS:O	1:A:551:GLU:HG3	2.08	0.54
1:B:216:THR:O	1:B:220:GLN:HG3	2.08	0.53
1:A:310:ARG:O	1:A:313:GLU:HB2	2.08	0.53
1:B:473:LYS:N	1:B:474:TYR:HA	2.23	0.53
1:A:521:ALA:O	1:A:525:VAL:HG23	2.09	0.52
1:A:111:LEU:O	1:A:115:LEU:HG	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:569:ASP:C	1:B:569:ASP:OD1	2.47	0.52
1:B:117:ARG:HD3	3:B:2068:HOH:O	2.09	0.52
1:B:406:THR:N	1:B:407:PRO:HD2	2.25	0.52
1:A:266:ASN:C	1:A:266:ASN:OD1	2.49	0.51
1:B:223:VAL:HG22	1:B:224:LEU:H	1.76	0.51
1:A:353:THR:OG1	1:A:356:GLU:HG3	2.11	0.51
1:A:366:ARG:NE	1:A:366:ARG:HA	2.26	0.50
1:A:582:LEU:C	1:A:582:LEU:HD23	2.31	0.50
1:A:228:ASP:HB2	1:A:231:LEU:HB2	1.92	0.50
1:A:348:PHE:CD2	1:A:420:TYR:HB3	2.47	0.50
1:B:266:ASN:C	1:B:266:ASN:OD1	2.50	0.49
1:B:475:HIS:CD2	1:B:477:ILE:H	2.18	0.49
1:A:91:MET:SD	1:A:271:GLU:HB3	2.52	0.49
1:A:412:VAL:HB	1:A:449:ILE:HG22	1.93	0.49
1:B:406:THR:OG1	1:B:407:PRO:HD3	2.13	0.49
1:B:507:VAL:HG12	1:B:511:MET:HE2	1.95	0.48
1:B:329:TYR:C	1:B:329:TYR:CD1	2.86	0.48
1:A:187:ASP:O	1:A:191:LEU:HG	2.13	0.48
1:A:87:ARG:O	1:A:91:MET:HG3	2.13	0.48
1:A:505:LYS:CG	1:A:508:GLN:H	2.27	0.48
1:B:289:LYS:HE3	1:B:293:ARG:HH21	1.77	0.48
1:B:215:ALA:O	1:B:219:LEU:HG	2.14	0.48
1:B:314:CYS:HA	2:B:1593:BME:H22	1.96	0.48
1:B:91:MET:O	1:B:95:VAL:HG23	2.14	0.47
1:B:334:LEU:CD1	1:B:451:ILE:HG23	2.44	0.47
1:B:582:LEU:HD23	1:B:582:LEU:C	2.35	0.47
1:B:505:LYS:O	1:B:509:CYS:HB2	2.14	0.47
1:B:123:HIS:NE2	1:B:276:ASP:OD2	2.48	0.47
1:A:483:THR:HG22	1:A:487:LEU:HD22	1.97	0.47
1:B:507:VAL:HG12	1:B:511:MET:CE	2.45	0.47
1:A:173:LYS:HA	1:A:180:PHE:HA	1.97	0.47
1:B:435:LEU:O	1:B:435:LEU:HD22	2.15	0.46
1:B:426:TRP:CE3	1:B:433:PRO:HG3	2.50	0.46
1:B:508:GLN:HA	1:B:511:MET:HE2	1.97	0.46
1:A:329:TYR:CD1	1:A:329:TYR:C	2.88	0.46
1:B:174:ASN:OD1	1:B:177:GLY:N	2.49	0.46
1:A:117:ARG:HD2	1:A:255:PHE:CE1	2.51	0.46
1:B:266:ASN:OD1	1:B:268:THR:N	2.49	0.46
1:A:290:GLU:HA	1:A:293:ARG:NH1	2.31	0.45
1:A:232:LEU:HD13	1:A:232:LEU:O	2.17	0.45
1:B:274:LYS:HG2	1:B:590:TYR:CD1	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:106:ILE:O	1:B:110:GLU:HG3	2.17	0.45
1:B:116:ARG:HA	1:B:121:SER:HB3	1.96	0.45
1:A:364:ILE:HG22	1:A:414:VAL:HG12	1.99	0.45
1:A:233:SER:OG	1:A:237:ARG:NH1	2.50	0.45
1:B:576:SER:OG	1:B:577:LEU:N	2.50	0.45
1:B:122:CYS:HB2	2:B:1592:BME:H22	1.84	0.45
1:B:166:GLN:OE1	1:B:207:THR:HB	2.17	0.44
1:A:173:LYS:HE3	1:A:207:THR:HG23	2.00	0.44
1:A:274:LYS:HD2	1:A:590:TYR:CE1	2.53	0.44
1:B:414:VAL:O	1:B:418:GLU:HG3	2.18	0.44
1:B:446:ILE:HG12	1:B:485:LEU:HG	1.99	0.44
1:A:107:ARG:HD3	1:A:107:ARG:HH11	1.64	0.44
1:A:426:TRP:CZ3	1:A:433:PRO:HG3	2.53	0.43
1:B:266:ASN:HA	1:B:267:PRO:HD2	1.88	0.43
1:A:507:VAL:HG12	1:A:517:SER:HB2	2.00	0.43
1:B:158:ARG:HG3	1:B:164:VAL:CG1	2.48	0.43
1:A:181:LYS:HA	1:A:182:PRO:HD3	1.89	0.43
1:B:108:ARG:HH11	1:B:108:ARG:HD2	1.63	0.43
1:A:417:ILE:O	1:A:420:TYR:HB2	2.18	0.43
1:A:103:VAL:HG22	3:A:2005:HOH:O	2.18	0.43
1:A:266:ASN:OD1	1:A:268:THR:N	2.52	0.43
1:A:265:MET:C	1:A:265:MET:SD	2.97	0.43
1:B:142:ILE:CG2	1:B:149:SER:HB3	2.43	0.43
1:A:274:LYS:HD2	1:A:590:TYR:HE1	1.84	0.43
1:B:259:TYR:HA	1:B:262:ARG:HD3	2.00	0.42
1:A:505:LYS:O	1:A:509:CYS:HB2	2.18	0.42
1:A:510:TYR:CD2	1:A:521:ALA:HA	2.54	0.42
1:B:293:ARG:HB2	1:B:293:ARG:HE	1.69	0.42
1:B:310:ARG:HG3	1:B:313:GLU:HB2	2.01	0.42
1:B:507:VAL:HG13	1:B:521:ALA:HB3	2.02	0.42
1:A:479:ARG:HH11	1:A:479:ARG:HD2	1.60	0.42
1:A:353:THR:O	1:A:357:LEU:HG	2.20	0.42
1:A:108:ARG:HH11	1:A:108:ARG:HD2	1.59	0.42
1:B:508:GLN:HA	1:B:511:MET:CE	2.50	0.42
1:A:324:ARG:HB2	1:A:327:HIS:ND1	2.34	0.42
1:B:409:LEU:HD22	1:B:454:HIS:CE1	2.55	0.42
1:A:313:GLU:HG2	1:A:571:PHE:CZ	2.55	0.42
1:B:577:LEU:O	1:B:581:MET:HG3	2.18	0.41
1:A:324:ARG:HB2	1:A:327:HIS:HD1	1.86	0.41
1:A:105:SER:HB3	1:A:141:GLU:OE1	2.19	0.41
1:B:262:ARG:HA	1:B:263:PRO:HD3	1.94	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:446:ILE:O	1:A:446:ILE:HG13	2.21	0.41
1:A:310:ARG:HG2	2:A:1593:BME:H12	1.99	0.41
1:B:181:LYS:HA	1:B:182:PRO:HD3	1.93	0.41
1:A:261:ARG:HD3	1:A:261:ARG:HH11	1.68	0.40
1:A:262:ARG:HA	1:A:263:PRO:HD3	1.93	0.40
1:A:118:LEU:HD23	1:A:255:PHE:HD2	1.87	0.40
1:A:174:ASN:N	1:A:179:ASP:O	2.49	0.40
1:B:265:MET:HG3	1:B:265:MET:O	2.21	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	473/569 (83%)	459 (97%)	13 (3%)	1 (0%)	52	43
1	B	483/569 (85%)	466 (96%)	16 (3%)	1 (0%)	52	43
All	All	956/1138 (84%)	925 (97%)	29 (3%)	2 (0%)	52	43

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	519	GLU
1	B	350	ILE

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	422/515 (82%)	408 (97%)	14 (3%)	45	32
1	B	435/515 (84%)	420 (97%)	15 (3%)	44	30
All	All	857/1030 (83%)	828 (97%)	29 (3%)	44	30

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

Mol	Chain	Res	Type
1	A	85	LEU
1	A	93	ASP
1	A	164	VAL
1	A	265	MET
1	A	274	LYS
1	A	310	ARG
1	A	325	ARG
1	A	350	ILE
1	A	471	MET
1	A	487	LEU
1	A	493	THR
1	A	517	SER
1	A	522	ARG
1	A	577	LEU
1	B	87	ARG
1	B	94	GLN
1	B	224	LEU
1	B	225	VAL
1	B	229	ILE
1	B	265	MET
1	B	276	ASP
1	B	310	ARG
1	B	434	SER
1	B	435	LEU
1	B	513	GLU
1	B	527	SER
1	B	528	LEU
1	B	576	SER
1	B	577	LEU

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

Mol	Chain	Res	Type
1	A	100	GLN
1	A	159	GLN
1	A	220	GLN
1	A	286	GLN
1	A	475	HIS
1	A	531	GLN
1	B	159	GLN
1	B	475	HIS
1	B	531	GLN
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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

4 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	BME	A	1592	1	3,3,3	0.36	0	2,2,2	0.46	0
2	BME	A	1593	1	3,3,3	0.35	0	2,2,2	0.46	0
2	BME	B	1592	1	3,3,3	0.35	0	2,2,2	0.46	0
2	BME	B	1593	1	3,3,3	0.35	0	2,2,2	0.45	0

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	BME	A	1592	1	-	0/1/1/1	0/0/0/0
2	BME	A	1593	1	-	0/1/1/1	0/0/0/0
2	BME	B	1592	1	-	0/1/1/1	0/0/0/0
2	BME	B	1593	1	-	0/1/1/1	0/0/0/0

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.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1593	BME	3	0
2	B	1592	BME	2	0
2	B	1593	BME	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 ⓘ

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, 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	485/569 (85%)	0.56	44 (9%)	11 18	16, 30, 56, 65	0
1	B	491/569 (86%)	0.64	48 (9%)	10 15	14, 30, 57, 73	0
All	All	976/1138 (85%)	0.60	92 (9%)	11 17	14, 30, 57, 73	0

All (92) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	225	VAL	8.8
1	A	493	THR	6.6
1	B	229	ILE	6.4
1	B	223	VAL	6.3
1	B	224	LEU	6.0
1	B	503	VAL	5.6
1	A	229	ILE	4.9
1	B	515	ASN	4.9
1	B	507	VAL	4.9
1	B	569	ASP	4.7
1	A	84	HIS	4.6
1	B	88	ALA	4.5
1	A	85	LEU	4.4
1	A	517	SER	4.4
1	A	577	LEU	4.3
1	B	232	LEU	4.3
1	B	90	GLY	4.3
1	A	305	PRO	4.2
1	A	520	GLU	4.1
1	A	228	ASP	4.1
1	A	308	ARG	4.1
1	A	232	LEU	4.1
1	B	576	SER	4.1
1	A	351	TYR	4.0

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Mol	Chain	Res	Type	RSRZ
1	A	175	ALA	4.0
1	A	509	CYS	3.9
1	B	261	ARG	3.9
1	B	511	MET	3.9
1	B	512	ASN	3.8
1	B	521	ALA	3.8
1	A	570	GLY	3.7
1	A	223	VAL	3.6
1	B	220	GLN	3.6
1	A	427	TYR	3.6
1	A	510	TYR	3.6
1	B	577	LEU	3.6
1	A	350	ILE	3.6
1	B	591	GLU	3.5
1	A	263	PRO	3.5
1	B	435	LEU	3.5
1	B	138	THR	3.4
1	B	570	GLY	3.4
1	A	435	LEU	3.4
1	B	504	PRO	3.3
1	A	569	ASP	3.1
1	A	521	ALA	3.1
1	B	175	ALA	3.0
1	B	310	ARG	2.9
1	A	304	LEU	2.9
1	B	571	PHE	2.9
1	B	516	ALA	2.9
1	B	93	ASP	2.9
1	A	230	ASN	2.8
1	B	510	TYR	2.8
1	B	566	HIS	2.8
1	A	507	VAL	2.7
1	B	230	ASN	2.7
1	B	578	VAL	2.7
1	B	575	HIS	2.7
1	B	513	GLU	2.7
1	A	504	PRO	2.7
1	A	156	LEU	2.7
1	B	567	GLU	2.6
1	B	568	SER	2.6
1	A	261	ARG	2.6
1	B	518	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	219	LEU	2.6
1	A	275	LEU	2.5
1	B	509	CYS	2.5
1	A	309	ASP	2.5
1	A	204	GLY	2.5
1	B	178	THR	2.5
1	A	578	VAL	2.4
1	A	574	GLN	2.4
1	A	580	LYS	2.4
1	A	126	ARG	2.3
1	B	514	LYS	2.3
1	A	86	MET	2.3
1	A	310	ARG	2.2
1	B	574	GLN	2.2
1	B	139	ASN	2.2
1	B	263	PRO	2.2
1	A	145	ARG	2.2
1	A	575	HIS	2.2
1	A	286	GLN	2.1
1	B	243	THR	2.1
1	B	302	HIS	2.1
1	B	203	GLN	2.1
1	A	492	GLY	2.1
1	A	220	GLN	2.1
1	A	566	HIS	2.0
1	B	413	TRP	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 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, 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(\AA^2)	Q<0.9
2	BME	A	1593	4/4	0.90	0.21	1.38	41,45,46,51	0
2	BME	B	1593	4/4	0.90	0.20	0.64	41,44,46,50	0
2	BME	B	1592	4/4	0.88	0.24	-	77,77,78,79	0
2	BME	A	1592	4/4	0.91	0.32	-	45,48,51,56	0

6.5 Other polymers [i](#)

There are no such residues in this entry.