



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 10:43 AM GMT

PDB ID : 3MV6
Title : Axial Ligand Swapping In Double Mutant Maintains Intradiol-cleavage Chemistry in Protocatechuate 3,4-Dioxygenase
Authors : Purpero, V.M.; Lipscomb, J.D.
Deposited on : 2010-05-03
Resolution : 1.86 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

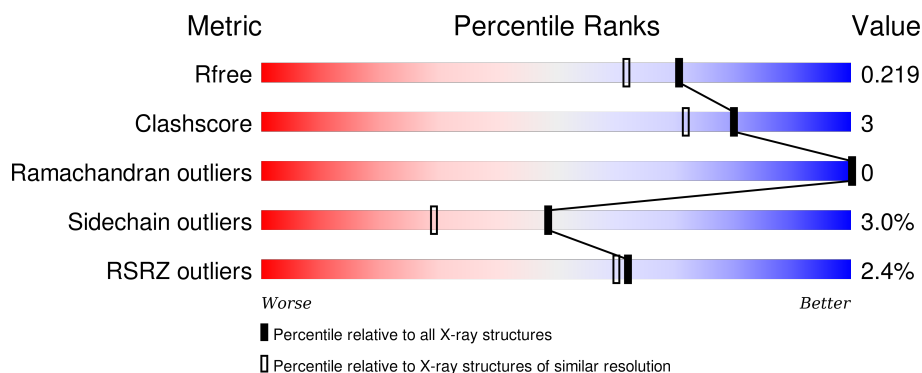
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.86 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	1745 (1.86-1.86)
Clashscore	102246	1898 (1.86-1.86)
Ramachandran outliers	100387	1875 (1.86-1.86)
Sidechain outliers	100360	1875 (1.86-1.86)
RSRZ outliers	91569	1747 (1.86-1.86)

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	200	<div> <div>4%</div> <div>92%</div> <div>9%</div> </div>
1	B	200	<div> <div>%</div> <div>92%</div> <div>8%</div> </div>
1	C	200	<div> <div>6%</div> <div>90%</div> <div>10%</div> </div>
2	M	238	<div> <div>%</div> <div>91%</div> <div>8%</div> </div>
2	N	238	<div> <div>2%</div> <div>92%</div> <div>6%</div> </div>

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Mol	Chain	Length	Quality of chain
2	O	238	

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
4	GOL	A	203[B]	-	-	X	-
4	GOL	C	203	-	-	-	X
5	BME	B	204	-	-	X	X
5	BME	N	1	-	-	-	X
5	BME	N	539	-	-	-	X
7	DHB	M	539	-	-	-	X
7	DHB	N	540	-	-	-	X
7	DHB	O	539	-	-	-	X

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 11533 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 Protocatechuate 3,4-dioxygenase alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	200	Total	C	N	O	S	0	4	0
			1594	1010	277	304	3			
1	B	200	Total	C	N	O	S	0	6	0
			1608	1021	280	304	3			
1	C	200	Total	C	N	O	S	0	6	0
			1608	1023	282	300	3			

- Molecule 2 is a protein called Protocatechuate 3,4-dioxygenase beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	M	238	Total	C	N	O	S	0	2	0
			1891	1200	344	339	8			
2	N	238	Total	C	N	O	S	0	1	0
			1886	1195	344	339	8			
2	O	238	Total	C	N	O	S	0	0	0
			1883	1193	344	338	8			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	447	HIS	TYR	engineered	UNP P00437
M	462	TYR	HIS	engineered	UNP P00437
N	447	HIS	TYR	engineered	UNP P00437
N	462	TYR	HIS	engineered	UNP P00437
O	447	HIS	TYR	engineered	UNP P00437
O	462	TYR	HIS	engineered	UNP P00437

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



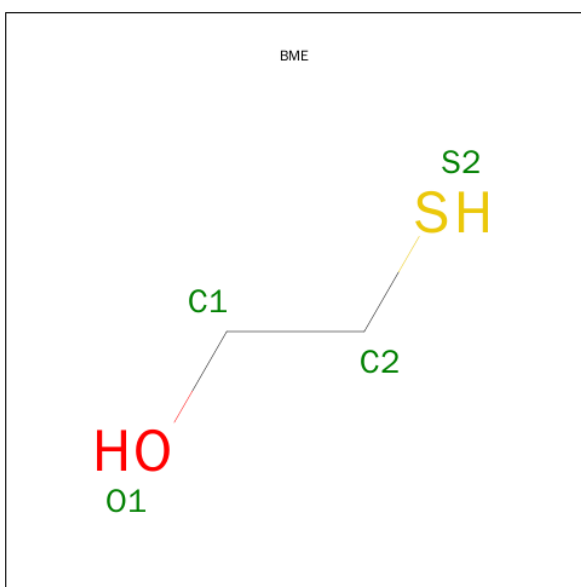
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	N	1	Total	O	S	0	0
			5	4	1		
3	O	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	1
			12	6	6		
4	C	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is BETA-MERCAPTOETHANOL (three-letter code: BME) (formula: C_2H_6OS).



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

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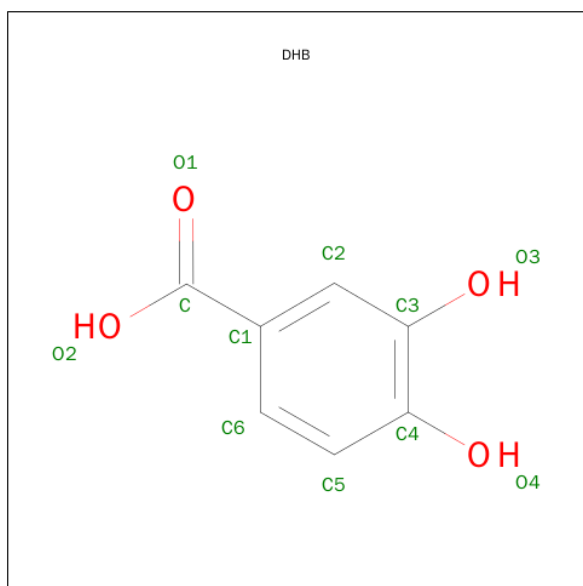
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	C	O	S	0	0
			4	2	1	1		
5	M	1	Total	C	O	S	0	0
			4	2	1	1		
5	N	1	Total	C	O	S	0	0
			4	2	1	1		
5	N	1	Total	C	O	S	0	0
			4	2	1	1		
5	N	1	Total	C	O	S	0	0
			4	2	1	1		

- Molecule 6 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	O	1	Total	Fe	0	0
			1	1		
6	N	1	Total	Fe	0	0
			1	1		
6	M	1	Total	Fe	0	0
			1	1		

- Molecule 7 is 3,4-DIHYDROXYBENZOIC ACID (three-letter code: DHB) (formula: C₇H₆O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	M	1	Total	C	O	0	0
			11	7	4		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	N	1	Total	C	O	0	0
			11	7	4		
7	O	1	Total	C	O	0	0
			11	7	4		

- Molecule 8 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	O	1	Total	Cl	0	0
			1	1		

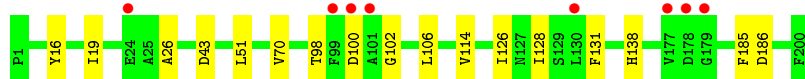
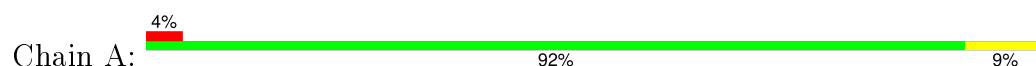
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	130	Total	O	0	3
			133	133		
9	B	139	Total	O	0	1
			140	140		
9	C	109	Total	O	0	1
			110	110		
9	M	191	Total	O	0	1
			192	192		
9	N	196	Total	O	0	1
			197	197		
9	O	171	Total	O	0	0
			171	171		

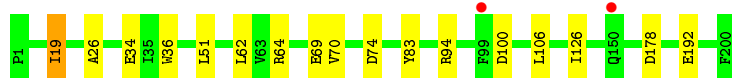
3 Residue-property plots [i](#)

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 ($\text{RSRZ} > 2$). 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.

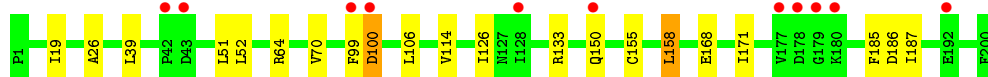
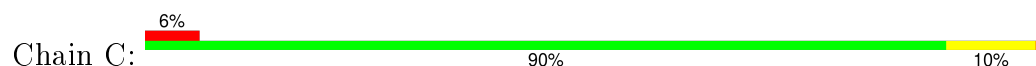
- Molecule 1: Protocatechuate 3,4-dioxygenase alpha chain



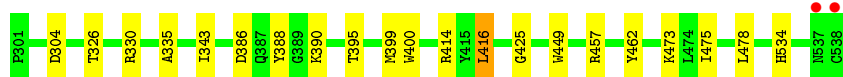
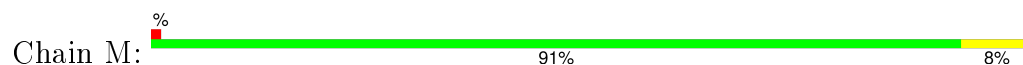
- Molecule 1: Protocatechuate 3,4-dioxygenase alpha chain



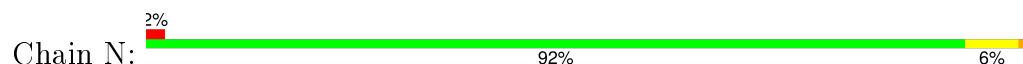
- Molecule 1: Protocatechuate 3,4-dioxygenase alpha chain



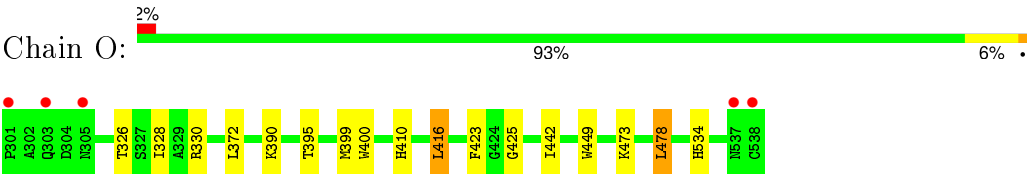
- Molecule 2: Protocatechuate 3,4-dioxygenase beta chain



- Molecule 2: Protocatechuate 3,4-dioxygenase beta chain



- Molecule 2: Protocatechuate 3,4-dioxygenase beta chain



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	128.14Å 140.83Å 167.83Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.09 – 1.86 27.27 – 1.86	Depositor EDS
% Data completeness (in resolution range)	94.7 (29.09-1.86) 94.7 (27.27-1.86)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.96 (at 1.85Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.181 , 0.219 0.182 , 0.219	Depositor DCC
R_{free} test set	6067 reflections (5.31%)	DCC
Wilson B-factor (Å ²)	20.8	Xtriage
Anisotropy	0.171	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 63.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 120246 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	11533	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 2.82% 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: GOL, CL, BME, DHB, SO4, FE

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	0.71	0/1646	0.69	0/2241
1	B	0.68	0/1666	0.71	1/2267 (0.0%)
1	C	0.67	0/1667	0.66	0/2269
2	M	0.72	0/1953	0.75	2/2657 (0.1%)
2	N	0.73	0/1945	0.73	2/2646 (0.1%)
2	O	0.69	0/1939	0.70	1/2638 (0.0%)
All	All	0.70	0/10816	0.71	6/14718 (0.0%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	N	522	ARG	NE-CZ-NH2	-6.49	117.06	120.30
2	N	416	LEU	CA-CB-CG	5.63	128.25	115.30
2	O	416	LEU	CA-CB-CG	5.58	128.14	115.30
2	M	416	LEU	CA-CB-CG	5.49	127.94	115.30
1	B	74	ASP	CB-CG-OD1	5.25	123.03	118.30
2	M	386	ASP	CB-CG-OD2	5.12	122.90	118.30

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	1594	0	1536	14	0
1	B	1608	0	1562	14	0
1	C	1608	0	1568	20	0
2	M	1891	0	1853	10	0
2	N	1886	0	1842	11	0
2	O	1883	0	1837	10	0
3	A	10	0	0	0	0
3	B	10	0	0	1	0
3	C	5	0	0	0	0
3	N	5	0	0	0	0
3	O	5	0	0	0	0
4	A	12	0	16	4	0
4	C	12	0	16	4	0
5	B	8	0	12	6	0
5	M	4	0	6	0	0
5	N	12	0	18	1	0
6	M	1	0	0	0	0
6	N	1	0	0	0	0
6	O	1	0	0	0	0
7	M	11	0	3	3	0
7	N	11	0	3	2	0
7	O	11	0	3	1	0
8	O	1	0	0	0	0
9	A	133	0	0	1	0
9	B	140	0	0	0	0
9	C	110	0	0	1	0
9	M	192	0	0	0	0
9	N	197	0	0	0	0
9	O	171	0	0	0	0
All	All	11533	0	10275	71	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 3.

All (71) 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:C:186:ASP:H	4:C:202:GOL:H32	1.24	0.99
1:C:185:PHE:CE2	1:C:187[B]:ILE:HD11	2.12	0.84
1:B:83:TYR:OH	5:B:204:BME:H12	1.84	0.76
1:C:64:ARG:NH2	1:C:100:ASP:O	2.20	0.74
1:A:19[A]:ILE:HG22	1:A:26:ALA:HB1	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:186:ASP:H	4:C:202:GOL:C3	2.03	0.69
1:C:19[B]:ILE:HD12	1:C:26:ALA:HB1	1.78	0.63
1:C:64:ARG:HD3	1:C:99:PHE:O	2.00	0.61
1:C:19[B]:ILE:HD11	2:O:410:HIS:HB2	1.84	0.60
1:C:19[B]:ILE:HD12	1:C:26:ALA:CB	2.32	0.59
1:A:186:ASP:H	4:A:203[B]:GOL:C1	2.15	0.59
2:N:449:TRP:CE3	7:N:540:DHB:H6	2.42	0.55
1:A:98:THR:O	1:A:102:GLY:HA2	2.06	0.55
1:B:34:GLU:O	5:B:204:BME:O1	2.23	0.54
1:B:70:VAL:HG11	1:B:106:LEU:HD11	1.90	0.54
2:M:326:THR:HG22	2:M:330:ARG:HD2	1.88	0.54
1:C:150:GLN:HG3	9:C:428:HOH:O	2.07	0.53
1:C:185:PHE:HA	4:C:202:GOL:H31	1.91	0.53
2:N:457:ARG:HD3	7:N:540:DHB:H5	1.90	0.52
1:C:19[B]:ILE:HD13	2:O:410:HIS:HD2	1.74	0.52
1:A:186:ASP:H	4:A:203[B]:GOL:H12	1.74	0.52
1:B:19[A]:ILE:HD11	2:N:400:TRP:HB2	1.91	0.52
1:B:19[A]:ILE:HG22	1:B:26:ALA:HB1	1.91	0.51
1:A:98:THR:HA	9:A:899:HOH:O	2.10	0.51
1:B:36:TRP:C	5:B:204:BME:H21	2.32	0.51
1:B:69:GLU:HG2	1:B:94:ARG:HG2	1.94	0.50
1:A:186:ASP:H	4:A:203[B]:GOL:H11	1.77	0.49
1:A:19[A]:ILE:HG22	1:A:26:ALA:CB	2.42	0.49
2:N:364:LEU:HD22	2:N:440:ARG:HG2	1.94	0.49
1:A:70:VAL:HG11	1:A:106:LEU:HD11	1.94	0.48
1:B:51:LEU:HD11	1:B:126[B]:ILE:CD1	2.43	0.48
1:B:36:TRP:N	5:B:204:BME:O1	2.47	0.47
2:M:335:ALA:HB2	2:O:328:ILE:HD12	1.97	0.47
1:C:70:VAL:HG11	1:C:106:LEU:HD11	1.97	0.46
2:M:478:LEU:C	2:M:478:LEU:HD23	2.36	0.46
1:C:185:PHE:HE2	1:C:187[B]:ILE:HD11	1.74	0.46
1:C:168:GLU:HA	1:C:171[A]:ILE:HD12	1.97	0.46
1:B:36:TRP:H	5:B:204:BME:C1	2.30	0.45
2:O:449:TRP:CE3	7:O:539:DHB:H6	2.52	0.45
2:N:400:TRP:HA	2:N:425:GLY:O	2.17	0.45
1:C:39:LEU:C	4:C:203:GOL:H11	2.37	0.45
2:N:399:MET:HA	2:N:462:TYR:O	2.17	0.45
2:M:449:TRP:CE3	7:M:539:DHB:H6	2.53	0.44
2:N:359:HIS:HB2	5:N:3:BME:H22	1.98	0.44
2:N:326:THR:HG22	2:N:330:ARG:HD2	1.98	0.44
1:A:70:VAL:HG12	1:A:128:ILE:HG12	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:64:ARG:NH1	1:B:100:ASP:O	2.48	0.44
1:A:51:LEU:HD11	1:A:126:ILE:CD1	2.48	0.43
2:M:304:ASP:HB2	2:M:343:ILE:HB	2.00	0.43
1:C:155:CYS:HB3	1:C:158:LEU:HB2	2.00	0.43
2:M:388:TYR:HB2	2:M:390:LYS:HE3	2.01	0.43
1:A:16:TYR:CE2	7:M:539:DHB:H2	2.54	0.43
2:N:478:LEU:HD23	2:N:478:LEU:C	2.39	0.43
2:O:423:PHE:CE2	2:O:442:ILE:HG13	2.54	0.42
1:C:19[B]:ILE:HD13	2:O:410:HIS:CD2	2.54	0.42
1:B:19[A]:ILE:CD1	2:N:400:TRP:HB2	2.49	0.42
2:O:400:TRP:HA	2:O:425:GLY:O	2.18	0.42
1:C:51:LEU:HD11	1:C:126:ILE:CD1	2.49	0.42
2:O:478:LEU:C	2:O:478:LEU:HD23	2.40	0.42
1:C:19[B]:ILE:CD1	1:C:26:ALA:HB1	2.45	0.42
2:M:400:TRP:HA	2:M:425:GLY:O	2.19	0.42
2:O:326:THR:HG22	2:O:330:ARG:HD2	2.01	0.42
1:A:185:PHE:HA	4:A:203[B]:GOL:H12	2.01	0.41
1:C:133:ARG:HG2	2:O:326:THR:HG21	2.02	0.41
1:A:131:PHE:CD2	2:M:475:ILE:HD12	2.55	0.41
2:M:399:MET:HA	2:M:462:TYR:O	2.20	0.41
2:M:457:ARG:HD3	7:M:539:DHB:H5	2.03	0.41
1:A:131:PHE:CE2	1:A:138:HIS:HB3	2.55	0.41
2:N:493:LYS:HD2	2:N:493:LYS:HA	1.76	0.41
1:B:62:LEU:N	3:B:202:SO4:O1	2.35	0.41
1:B:36:TRP:O	5:B:204:BME:H21	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	202/200 (101%)	195 (96%)	7 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	204/200 (102%)	200 (98%)	4 (2%)	0	100	100
1	C	204/200 (102%)	200 (98%)	4 (2%)	0	100	100
2	M	238/238 (100%)	232 (98%)	6 (2%)	0	100	100
2	N	237/238 (100%)	231 (98%)	6 (2%)	0	100	100
2	O	236/238 (99%)	231 (98%)	5 (2%)	0	100	100
All	All	1321/1314 (100%)	1289 (98%)	32 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	167/163 (102%)	163 (98%)	4 (2%)	57	39
1	B	169/163 (104%)	165 (98%)	4 (2%)	57	39
1	C	169/163 (104%)	165 (98%)	4 (2%)	57	39
2	M	204/202 (101%)	199 (98%)	5 (2%)	55	37
2	N	203/202 (100%)	193 (95%)	10 (5%)	31	12
2	O	202/202 (100%)	194 (96%)	8 (4%)	38	18
All	All	1114/1095 (102%)	1079 (97%)	35 (3%)	48	28

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	43[A]	ASP
1	A	43[B]	ASP
1	A	100	ASP
1	A	114	VAL
1	B	19[A]	ILE
1	B	19[B]	ILE
1	B	178	ASP
1	B	192	GLU

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Mol	Chain	Res	Type
1	C	52	LEU
1	C	100	ASP
1	C	114	VAL
1	C	158	LEU
2	M	395	THR
2	M	414	ARG
2	M	416	LEU
2	M	473	LYS
2	M	534	HIS
2	N	364	LEU
2	N	372	LEU
2	N	395	THR
2	N	399	MET
2	N	411	LYS
2	N	416	LEU
2	N	473	LYS
2	N	478	LEU
2	N	522	ARG
2	N	534	HIS
2	O	372	LEU
2	O	390	LYS
2	O	395	THR
2	O	399	MET
2	O	416	LEU
2	O	473	LYS
2	O	478	LEU
2	O	534	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
2	N	530	GLN
2	O	530	GLN

5.3.3 RNA ⓘ

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](#)

Of 24 ligands modelled in this entry, 4 are monoatomic - leaving 20 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	SO4	A	201	-	4,4,4	0.38	0	6,6,6	0.17	0
3	SO4	A	202	-	4,4,4	0.19	0	6,6,6	0.14	0
4	GOL	A	203[A]	-	5,5,5	0.40	0	5,5,5	0.44	0
4	GOL	A	203[B]	-	5,5,5	0.30	0	5,5,5	0.54	0
3	SO4	B	201	-	4,4,4	0.35	0	6,6,6	0.17	0
3	SO4	B	202	-	4,4,4	0.50	0	6,6,6	0.12	0
5	BME	B	203	-	3,3,3	0.40	0	2,2,2	0.89	0
5	BME	B	204	-	3,3,3	0.26	0	2,2,2	0.64	0
3	SO4	C	201	-	4,4,4	0.32	0	6,6,6	0.17	0
4	GOL	C	202	-	5,5,5	0.35	0	5,5,5	0.83	0
4	GOL	C	203	-	5,5,5	0.33	0	5,5,5	0.60	0
5	BME	M	1	-	3,3,3	0.30	0	2,2,2	0.91	0
7	DHB	M	539	6	8,11,11	1.34	1 (12%)	11,15,15	1.31	2 (18%)
5	BME	N	1	-	3,3,3	0.30	0	2,2,2	0.95	0
5	BME	N	3	-	3,3,3	0.43	0	2,2,2	0.49	0
5	BME	N	539	-	3,3,3	0.52	0	2,2,2	0.82	0
7	DHB	N	540	6	8,11,11	1.59	1 (12%)	11,15,15	1.28	1 (9%)
3	SO4	N	6	-	4,4,4	0.17	0	6,6,6	0.13	0
3	SO4	O	4	-	4,4,4	0.22	0	6,6,6	0.18	0
7	DHB	O	539	6	8,11,11	1.45	1 (12%)	11,15,15	1.29	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
3	SO4	A	201	-	-	0/0/0/0	0/0/0/0
3	SO4	A	202	-	-	0/0/0/0	0/0/0/0
4	GOL	A	203[A]	-	-	0/4/4/4	0/0/0/0
4	GOL	A	203[B]	-	-	0/4/4/4	0/0/0/0
3	SO4	B	201	-	-	0/0/0/0	0/0/0/0
3	SO4	B	202	-	-	0/0/0/0	0/0/0/0
5	BME	B	203	-	-	0/1/1/1	0/0/0/0
5	BME	B	204	-	-	0/1/1/1	0/0/0/0
3	SO4	C	201	-	-	0/0/0/0	0/0/0/0
4	GOL	C	202	-	-	0/4/4/4	0/0/0/0
4	GOL	C	203	-	-	0/4/4/4	0/0/0/0
5	BME	M	1	-	-	0/1/1/1	0/0/0/0
7	DHB	M	539	6	-	0/0/4/4	0/1/1/1
5	BME	N	1	-	-	0/1/1/1	0/0/0/0
5	BME	N	3	-	-	0/1/1/1	0/0/0/0
5	BME	N	539	-	-	0/1/1/1	0/0/0/0
7	DHB	N	540	6	-	0/0/4/4	0/1/1/1
3	SO4	N	6	-	-	0/0/0/0	0/0/0/0
3	SO4	O	4	-	-	0/0/0/0	0/0/0/0
7	DHB	O	539	6	-	0/0/4/4	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	M	539	DHB	C4-C3	3.58	1.46	1.40
7	O	539	DHB	C4-C3	3.87	1.46	1.40
7	N	540	DHB	C4-C3	4.31	1.47	1.40

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	M	539	DHB	C1-C2-C3	-2.64	118.75	120.98
7	M	539	DHB	C6-C1-C2	2.59	121.61	118.17
7	N	540	DHB	C6-C1-C2	2.76	121.82	118.17

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

9 monomers are involved in 22 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	203[B]	GOL	4	0
3	B	202	SO4	1	0
5	B	204	BME	6	0
4	C	202	GOL	3	0
4	C	203	GOL	1	0
7	M	539	DHB	3	0
5	N	3	BME	1	0
7	N	540	DHB	2	0
7	O	539	DHB	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	200/200 (100%)	0.02	8 (4%) 42 39	18, 24, 39, 50	0
1	B	200/200 (100%)	-0.10	2 (1%) 84 84	18, 23, 34, 40	0
1	C	200/200 (100%)	0.26	11 (5%) 29 27	18, 28, 42, 52	1 (0%)
2	M	238/238 (100%)	-0.22	2 (0%) 87 87	17, 21, 31, 41	0
2	N	238/238 (100%)	-0.20	4 (1%) 73 72	18, 22, 30, 38	0
2	O	238/238 (100%)	-0.19	5 (2%) 67 65	18, 23, 32, 45	1 (0%)
All	All	1314/1314 (100%)	-0.09	32 (2%) 62 60	17, 23, 36, 52	2 (0%)

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	43	ASP	4.5
2	O	301	PRO	4.3
1	C	178	ASP	4.1
1	A	178	ASP	3.7
2	O	538	CYS	3.3
1	A	99	PHE	2.9
1	A	177	VAL	2.8
1	C	177	VAL	2.8
1	C	128	ILE	2.8
1	C	100	ASP	2.7
2	N	358	ALA	2.6
2	M	538	CYS	2.6
2	N	532	LYS	2.5
1	C	99	PHE	2.5
1	C	179	GLY	2.4
2	M	537	ASN	2.4
2	N	538	CYS	2.4
1	A	179	GLY	2.4
1	C	192	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	99	PHE	2.3
2	O	303	GLN	2.3
1	C	150	GLN	2.2
1	C	42	PRO	2.2
2	N	537	ASN	2.1
1	B	150	GLN	2.1
1	C	180	LYS	2.1
2	O	305	ASN	2.1
2	O	537	ASN	2.1
1	A	130	LEU	2.0
1	A	100	ASP	2.0
1	A	101	ALA	2.0
1	A	24	GLU	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(Å ²)	Q<0.9
7	DHB	O	539	11/11	0.83	0.26	11.38	33,35,37,39	11
7	DHB	M	539	11/11	0.81	0.21	6.45	23,30,32,33	11
5	BME	B	204	4/4	0.86	0.30	6.20	37,38,38,44	4
7	DHB	N	540	11/11	0.90	0.16	3.58	27,31,36,38	11
5	BME	N	539	4/4	0.94	0.19	3.38	45,48,49,50	0
4	GOL	C	203	6/6	0.80	0.25	2.89	42,43,45,45	0
5	BME	N	1	4/4	0.81	0.14	2.23	60,61,61,62	0
3	SO4	B	201	5/5	0.89	0.16	1.63	48,48,50,50	5

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
5	BME	B	203	4/4	0.83	0.16	1.51	45,50,51,55	0
4	GOL	A	203[A]	6/6	0.88	0.16	1.41	37,39,40,41	6
4	GOL	A	203[B]	6/6	0.88	0.16	1.29	35,37,37,38	6
3	SO4	O	4	5/5	0.92	0.14	0.85	59,59,60,61	5
3	SO4	B	202	5/5	0.90	0.15	0.68	51,53,53,54	5
3	SO4	A	202	5/5	0.92	0.20	0.59	54,54,55,56	5
5	BME	N	3	4/4	0.78	0.15	0.56	43,44,44,47	4
4	GOL	C	202	6/6	0.85	0.12	-0.15	44,46,47,48	0
5	BME	M	1	4/4	0.89	0.24	-	53,53,54,54	0
6	FE	M	600	1/1	0.99	0.04	-	30,30,30,30	1
3	SO4	N	6	5/5	0.92	0.18	-	60,61,61,62	5
8	CL	O	1	1/1	0.85	0.10	-	63,63,63,63	0
3	SO4	A	201	5/5	0.94	0.10	-	47,48,49,50	5
3	SO4	C	201	5/5	0.95	0.11	-	50,50,51,52	5
6	FE	N	600	1/1	0.98	0.05	-	32,32,32,32	1
6	FE	O	600	1/1	0.98	0.06	-	31,31,31,31	1

6.5 Other polymers

There are no such residues in this entry.