



Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 09:02 pm BST

PDB ID : 6B1B
Title : STRUCTURE OF 4 - H Y D R O X Y P H E N Y L A C E T A T E 3-MONOOXYGENASE (HPAB), OXYGENASE COMPONENT FROM ES-CHERICHIA COLI MUTANT XS6 (APO Enzyme)
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Deposited on : 2017-09-18
Resolution : 1.94 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

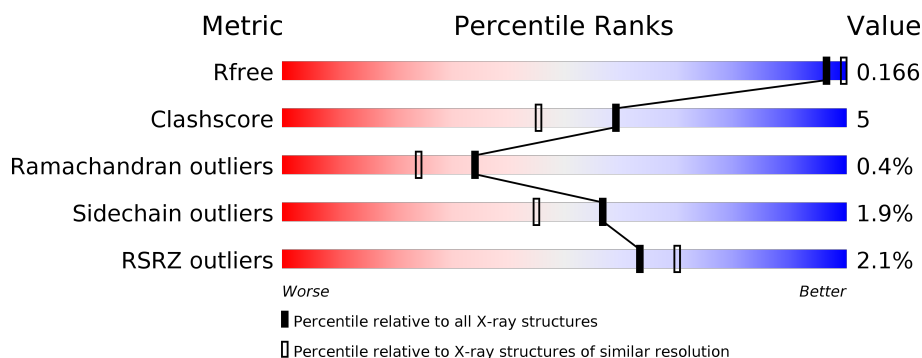
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.94 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4310 (1.96-1.92)
Clashscore	141614	1023 (1.94-1.94)
Ramachandran outliers	138981	1007 (1.94-1.94)
Sidechain outliers	138945	1007 (1.94-1.94)
RSRZ outliers	127900	4250 (1.96-1.92)

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 respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	527	<div> <div>2%</div> <div> <div></div> <div>87%</div> <div>9%</div> <div>..</div> </div> </div>
1	B	527	<div> <div>2%</div> <div> <div></div> <div>84%</div> <div>11%</div> <div>..</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9230 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 4-hydroxyphenylacetate 3-monooxygenase, oxygenase subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	510	Total	C	N	O	S	0	0	0
			4069	2572	708	763	26			
1	B	509	Total	C	N	O	S	0	0	0
			4060	2566	706	762	26			

There are 30 discrepancies between the modelled and reference sequences:

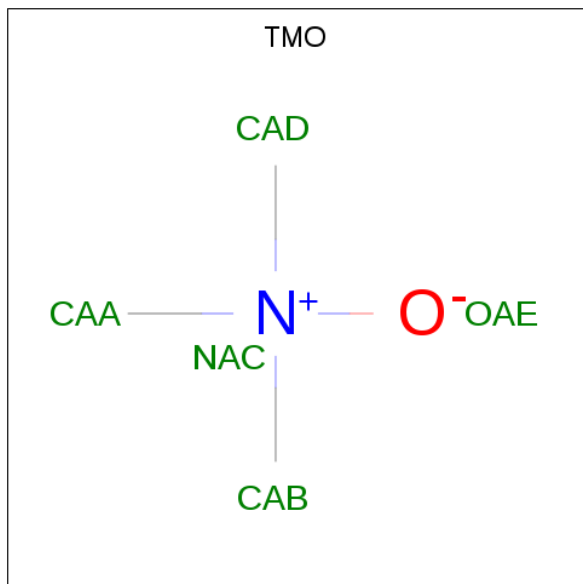
Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	MET	-	initiating methionine	UNP A0A140NG21
A	-5	HIS	-	expression tag	UNP A0A140NG21
A	-4	HIS	-	expression tag	UNP A0A140NG21
A	-3	HIS	-	expression tag	UNP A0A140NG21
A	-2	HIS	-	expression tag	UNP A0A140NG21
A	-1	HIS	-	expression tag	UNP A0A140NG21
A	0	HIS	-	expression tag	UNP A0A140NG21
A	1	HIS	-	expression tag	UNP A0A140NG21
A	208	SER	PHE	engineered mutation	UNP A0A140NG21
A	211	ASP	ALA	engineered mutation	UNP A0A140NG21
A	212	LEU	GLN	engineered mutation	UNP A0A140NG21
A	213	GLY	VAL	engineered mutation	UNP A0A140NG21
A	214	SER	MET	engineered mutation	UNP A0A140NG21
A	216	SER	GLU	engineered mutation	UNP A0A140NG21
A	217	ASP	ASN	engineered mutation	UNP A0A140NG21
B	-6	MET	-	initiating methionine	UNP A0A140NG21
B	-5	HIS	-	expression tag	UNP A0A140NG21
B	-4	HIS	-	expression tag	UNP A0A140NG21
B	-3	HIS	-	expression tag	UNP A0A140NG21
B	-2	HIS	-	expression tag	UNP A0A140NG21
B	-1	HIS	-	expression tag	UNP A0A140NG21
B	0	HIS	-	expression tag	UNP A0A140NG21
B	1	HIS	-	expression tag	UNP A0A140NG21
B	208	SER	PHE	engineered mutation	UNP A0A140NG21
B	211	ASP	ALA	engineered mutation	UNP A0A140NG21

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Chain	Residue	Modelled	Actual	Comment	Reference
B	212	LEU	GLN	engineered mutation	UNP A0A140NG21
B	213	GLY	VAL	engineered mutation	UNP A0A140NG21
B	214	SER	MET	engineered mutation	UNP A0A140NG21
B	216	SER	GLU	engineered mutation	UNP A0A140NG21
B	217	ASP	ASN	engineered mutation	UNP A0A140NG21

- Molecule 2 is trimethylamine oxide (three-letter code: TMO) (formula: C_3H_9NO).



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

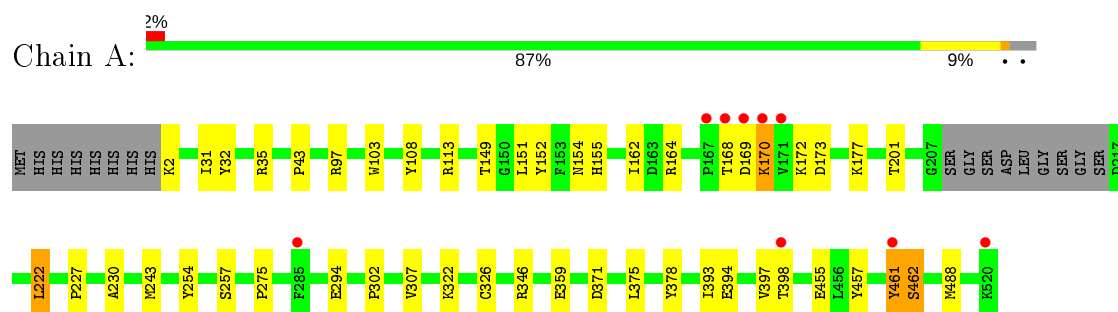
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	537	Total 537	O 537	0	0
3	B	524	Total 524	O 524	0	0

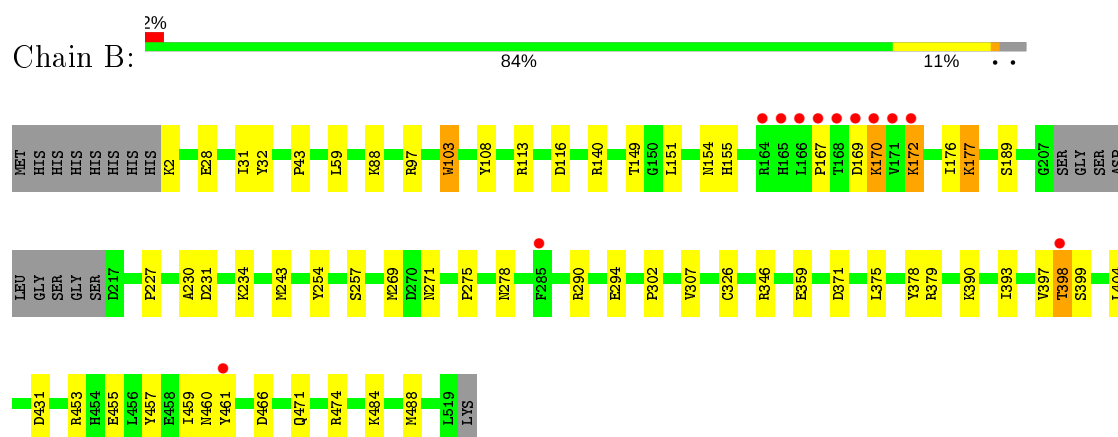
3 Residue-property plots [i](#)

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: 4-hydroxyphenylacetate 3-monooxygenase, oxygenase subunit



- Molecule 1: 4-hydroxyphenylacetate 3-monooxygenase, oxygenase subunit



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 2 2	Depositor
Cell constants a, b, c, α , β , γ	100.45Å 100.45Å 336.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.53 – 1.94 48.96 – 1.94	Depositor EDS
% Data completeness (in resolution range)	99.9 (44.53-1.94) 98.5 (48.96-1.94)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	11.23 (at 1.94Å)	Xtriage
Refinement program	PHENIX 1.12_2829	Depositor
R, R_{free}	0.152 , 0.166 0.152 , 0.166	Depositor DCC
R_{free} test set	2000 reflections (1.57%)	wwPDB-VP
Wilson B-factor (Å ²)	18.4	Xtriage
Anisotropy	0.050	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 57.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9230	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.39% 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: TMO

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	0.38	1/4165 (0.0%)	0.57	1/5644 (0.0%)
1	B	0.39	1/4156 (0.0%)	0.60	3/5633 (0.1%)
All	All	0.38	2/8321 (0.0%)	0.59	4/11277 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	326	CYS	CB-SG	-6.72	1.70	1.82
1	B	326	CYS	CB-SG	-5.07	1.73	1.81

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	170	LYS	CD-CE-NZ	-8.20	92.85	111.70
1	A	222	LEU	CA-CB-CG	6.16	129.46	115.30
1	B	170	LYS	CA-CB-CG	-5.59	101.09	113.40
1	B	170	LYS	CB-CG-CD	5.21	125.15	111.60

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	4069	0	3945	32	0
1	B	4060	0	3932	45	0
2	A	20	0	36	1	0
2	B	20	0	36	3	0
3	A	537	0	0	10	1
3	B	524	0	0	13	2
All	All	9230	0	7949	76	2

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 5.

All (76) 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:140:ARG:NH1	3:B:2101:HOH:O	1.91	0.96
1:B:2:LYS:N	3:B:2104:HOH:O	2.06	0.87
1:A:170:LYS:O	3:A:701:HOH:O	2.04	0.75
1:B:459:ILE:HG22	1:B:460:ASN:HD22	1.51	0.73
1:B:294:GLU:OE2	3:B:2105:HOH:O	2.06	0.72
1:A:162:ILE:O	1:A:164:ARG:NH1	2.24	0.71
1:A:455:GLU:OE1	3:A:702:HOH:O	2.11	0.67
1:B:231:ASP:OD1	3:B:2107:HOH:O	2.15	0.65
1:B:227:PRO:HG2	1:B:230:ALA:HB2	1.80	0.63
1:B:176:ILE:HD12	1:B:269:MET:HE2	1.80	0.63
1:A:172:LYS:N	1:A:172:LYS:HD2	2.14	0.62
1:B:459:ILE:HG22	1:B:460:ASN:ND2	2.14	0.62
1:A:461:TYR:OH	3:A:703:HOH:O	2.13	0.60
1:A:2:LYS:NZ	3:A:708:HOH:O	2.27	0.60
1:A:173:ASP:HA	1:A:177:LYS:HE3	1.83	0.60
1:B:404:LEU:HA	3:B:2118:HOH:O	2.02	0.60
1:B:393:ILE:O	1:B:397:VAL:HG22	2.02	0.59
1:B:466:ASP:OD2	3:B:2108:HOH:O	2.17	0.58
1:B:88:LYS:NZ	2:B:2001:TMO:HADA	2.19	0.58
1:A:294:GLU:OE2	3:A:705:HOH:O	2.17	0.57
1:A:227:PRO:HG2	1:A:230:ALA:HB2	1.87	0.57
1:A:169:ASP:O	1:A:170:LYS:HB3	2.04	0.56
1:A:108:TYR:HD1	1:B:488:MET:HG2	1.71	0.56
1:B:484:LYS:NZ	3:B:2102:HOH:O	1.99	0.55
1:A:113:ARG:HH11	1:A:154:ASN:HD21	1.54	0.55
1:B:302:PRO:HB2	1:B:375:LEU:HD22	1.89	0.54
1:B:379:ARG:NH2	1:B:471:GLN:OE1	2.37	0.54
1:B:275:PRO:HD2	3:B:2112:HOH:O	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:275:PRO:HD2	3:A:746:HOH:O	2.08	0.54
1:B:149:THR:OG1	1:B:151:LEU:HG	2.08	0.54
1:A:149:THR:OG1	1:A:151:LEU:HG	2.08	0.53
1:B:404:LEU:N	3:B:2118:HOH:O	2.42	0.52
1:A:457:TYR:OH	3:A:704:HOH:O	2.17	0.51
1:B:167:PRO:HB2	1:B:169:ASP:O	2.11	0.50
1:A:173:ASP:OD1	1:A:177:LYS:HE3	2.11	0.50
1:B:169:ASP:HA	1:B:172:LYS:NZ	2.27	0.49
2:A:604:TMO:HAB	3:A:1110:HOH:O	2.13	0.49
1:A:302:PRO:HB2	1:A:375:LEU:HD22	1.94	0.49
1:A:394:GLU:O	1:A:398:THR:OG1	2.21	0.49
1:A:488:MET:HG2	1:B:108:TYR:HD1	1.77	0.48
1:B:176:ILE:HD12	1:B:269:MET:CE	2.41	0.48
1:B:177:LYS:HD2	1:B:189:SER:O	2.14	0.48
1:B:97:ARG:HG2	1:B:307:VAL:HG21	1.94	0.47
1:B:278:ASN:ND2	3:B:2112:HOH:O	2.31	0.47
1:B:113:ARG:HD2	1:B:154:ASN:OD1	2.15	0.46
1:B:474:ARG:NH1	3:B:2109:HOH:O	2.21	0.46
1:B:359:GLU:HB2	1:B:371:ASP:HB2	1.97	0.46
1:A:31:ILE:HG12	1:A:32:TYR:CD2	2.51	0.46
1:A:168:THR:O	1:A:172:LYS:HD3	2.16	0.46
1:B:59:LEU:HD21	1:B:103:TRP:CZ2	2.51	0.46
1:A:113:ARG:NH1	1:A:154:ASN:HD21	2.13	0.46
1:A:461:TYR:O	1:A:462:SER:HB2	2.16	0.46
1:B:457:TYR:HD2	1:B:461:TYR:CD1	2.33	0.46
1:A:359:GLU:HB2	1:A:371:ASP:HB2	1.98	0.46
1:A:393:ILE:O	1:A:397:VAL:HG22	2.15	0.46
1:A:322:LYS:NZ	3:A:730:HOH:O	2.48	0.45
1:B:31:ILE:HG12	1:B:32:TYR:CD2	2.51	0.45
1:B:116:ASP:OD1	1:B:116:ASP:N	2.50	0.45
1:A:169:ASP:O	1:A:170:LYS:CB	2.65	0.45
1:A:164:ARG:NH1	3:A:731:HOH:O	2.49	0.45
1:B:88:LYS:HZ3	2:B:2001:TMO:HADA	1.80	0.44
1:B:254:TYR:HB3	1:B:257:SER:HB2	1.98	0.44
1:B:28:GLU:CD	1:B:234:LYS:HG2	2.38	0.44
1:B:404:LEU:CA	3:B:2118:HOH:O	2.63	0.44
1:B:398:THR:HG22	1:B:399:SER:N	2.33	0.43
1:B:379:ARG:NH1	1:B:471:GLN:OE1	2.51	0.43
1:B:43:PRO:HB2	1:B:243:MET:HG3	2.01	0.43
1:B:390:LYS:NZ	1:B:455:GLU:OE1	2.48	0.43
1:A:97:ARG:HG2	1:A:307:VAL:HG21	1.99	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:154:ASN:HB2	1:A:201:THR:HG21	2.01	0.42
1:B:169:ASP:OD1	1:B:172:LYS:NZ	2.51	0.42
1:A:254:TYR:HB3	1:A:257:SER:HB2	2.01	0.42
1:B:88:LYS:CE	2:B:2001:TMO:HADA	2.50	0.41
1:A:43:PRO:HB2	1:A:243:MET:HG3	2.02	0.41
1:B:271:ASN:ND2	3:B:2103:HOH:O	2.04	0.41
1:B:290:ARG:HD2	1:B:294:GLU:OE2	2.22	0.40

All (2) 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)
3:B:2510:HOH:O	3:B:2510:HOH:O[5_555]	2.07	0.13
3:A:783:HOH:O	3:B:2475:HOH:O[7_555]	2.19	0.01

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	506/527 (96%)	493 (97%)	11 (2%)	2 (0%)	34	24
1	B	505/527 (96%)	491 (97%)	12 (2%)	2 (0%)	34	24
All	All	1011/1054 (96%)	984 (97%)	23 (2%)	4 (0%)	34	24

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	462	SER
1	A	170	LYS
1	B	398	THR
1	B	170	LYS

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	429/443 (97%)	421 (98%)	8 (2%)	57	45
1	B	428/443 (97%)	420 (98%)	8 (2%)	57	45
All	All	857/886 (97%)	841 (98%)	16 (2%)	57	45

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	35	ARG
1	A	103	TRP
1	A	152	TYR
1	A	155	HIS
1	A	222	LEU
1	A	346	ARG
1	A	378	TYR
1	A	461	TYR
1	B	103	TRP
1	B	155	HIS
1	B	172	LYS
1	B	177	LYS
1	B	346	ARG
1	B	378	TYR
1	B	431	ASP
1	B	453	ARG

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

Mol	Chain	Res	Type
1	A	154	ASN
1	B	460	ASN

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](#)

8 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	TMO	A	602	-	4,4,4	1.91	1 (25%)	6,6,6	0.18	0
2	TMO	B	2003	-	4,4,4	1.63	0	6,6,6	0.26	0
2	TMO	A	601	-	4,4,4	1.88	1 (25%)	6,6,6	0.25	0
2	TMO	B	2002	-	4,4,4	2.00	2 (50%)	6,6,6	0.19	0
2	TMO	A	604	-	4,4,4	1.77	0	6,6,6	0.19	0
2	TMO	B	2001	-	4,4,4	2.02	1 (25%)	6,6,6	0.27	0
2	TMO	A	603	-	4,4,4	2.08	3 (75%)	6,6,6	0.23	0
2	TMO	B	2004	-	4,4,4	1.95	2 (50%)	6,6,6	0.47	0

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2001	TMO	CAD-NAC	-3.07	1.44	1.48
2	B	2004	TMO	CAD-NAC	-2.60	1.44	1.48
2	B	2002	TMO	CAB-NAC	-2.37	1.45	1.48
2	A	602	TMO	CAA-NAC	-2.34	1.45	1.48
2	A	603	TMO	CAB-NAC	-2.30	1.45	1.48
2	B	2002	TMO	CAD-NAC	-2.27	1.45	1.48
2	A	601	TMO	CAB-NAC	-2.18	1.45	1.48
2	A	603	TMO	CAD-NAC	-2.17	1.45	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	603	TMO	CAA-NAC	-2.13	1.45	1.48
2	B	2004	TMO	CAB-NAC	-2.04	1.45	1.48

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	604	TMO	1	0
2	B	2001	TMO	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 [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	510/527 (96%)	-0.37	9 (1%) 68 74	9, 18, 39, 83	0
1	B	509/527 (96%)	-0.38	12 (2%) 59 66	8, 17, 38, 89	0
All	All	1019/1054 (96%)	-0.37	21 (2%) 63 70	8, 18, 39, 89	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	461	TYR	8.4
1	B	169	ASP	6.2
1	B	170	LYS	5.2
1	B	167	PRO	5.0
1	A	169	ASP	4.8
1	B	168	THR	4.7
1	A	285	PHE	4.0
1	B	166	LEU	3.7
1	A	167	PRO	3.4
1	B	285	PHE	3.2
1	A	168	THR	3.2
1	B	171	VAL	3.1
1	B	165	HIS	3.1
1	B	461	TYR	2.8
1	B	398	THR	2.8
1	A	170	LYS	2.7
1	A	171	VAL	2.3
1	A	398	THR	2.2
1	B	172	LYS	2.1
1	A	520	LYS	2.0
1	B	164	ARG	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no 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. 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	B-factors(\AA^2)	Q<0.9
2	TMO	B	2003	5/5	0.90	0.18	33,39,44,47	0
2	TMO	A	604	5/5	0.90	0.22	35,39,44,54	0
2	TMO	B	2004	5/5	0.90	0.17	25,31,36,37	0
2	TMO	B	2001	5/5	0.91	0.13	14,21,29,40	0
2	TMO	A	603	5/5	0.93	0.20	52,52,53,55	0
2	TMO	A	601	5/5	0.95	0.10	37,38,40,44	0
2	TMO	B	2002	5/5	0.96	0.14	33,34,36,48	0
2	TMO	A	602	5/5	0.97	0.10	29,36,36,44	0

6.5 Other polymers [i](#)

There are no such residues in this entry.