



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 7, 2026 – 01:57 AM UTC

PDB ID : 3LKT / pdb_00003lkt
Title : Tyrosine 447 of Protocatechuate 3,4-Dioxygenase Controls Efficient Progress Through Catalysis
Authors : Lipscomb, J.D.; Purpero, V.M.
Deposited on : 2010-01-27
Resolution : 1.65 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

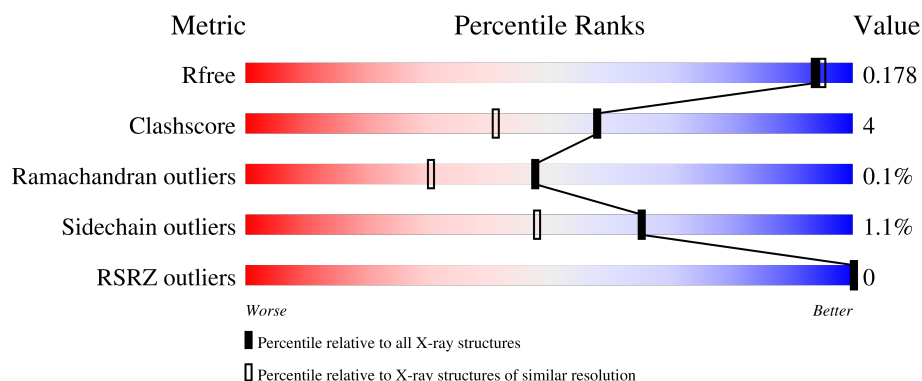
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.65 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.



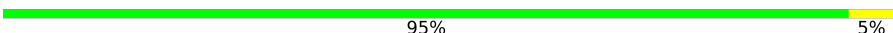
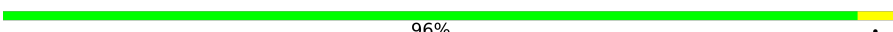
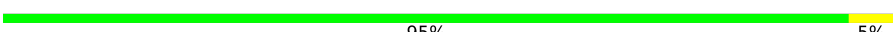
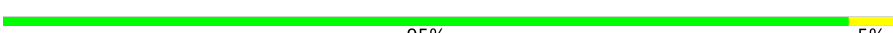
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2563 (1.66-1.66)
Clashscore	190562	2662 (1.66-1.66)
Ramachandran outliers	187476	2621 (1.66-1.66)
Sidechain outliers	187428	2621 (1.66-1.66)
RSRZ outliers	180081	2564 (1.66-1.66)

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 of 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	200	92% 8%
1	B	200	94% 6%
1	C	200	90% 9% .
1	D	200	95% 5%
1	E	200	94% 6%

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Mol	Chain	Length	Quality of chain
1	F	200	 90% 10%
2	M	238	 95% 5%
2	N	238	 96% 4%
2	O	238	 95% 5%
2	P	238	 95% 5%
2	Q	238	 95% 5%
2	R	238	 95% 5%

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	BME	M	21[C]	-	-	X	-
4	BME	N	18	-	-	X	-
4	BME	O	33	-	-	X	-
4	BME	P	22[A]	-	-	X	-
4	BME	Q	19	-	-	X	-
4	BME	R	20	-	-	X	-

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 23995 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	0	0
			1575	996	277	299	3			
1	B	200	Total	C	N	O	S	0	2	0
			1591	1005	282	301	3			
1	C	200	Total	C	N	O	S	0	10	0
			1640	1037	287	313	3			
1	D	200	Total	C	N	O	S	0	1	0
			1586	1002	281	300	3			
1	E	200	Total	C	N	O	S	0	2	0
			1591	1004	280	304	3			
1	F	200	Total	C	N	O	S	0	11	0
			1646	1041	287	315	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	3	0
			1893	1199	347	339	8			
2	N	238	Total	C	N	O	S	0	2	0
			1889	1197	346	338	8			
2	O	238	Total	C	N	O	S	0	1	0
			1885	1193	346	338	8			
2	P	238	Total	C	N	O	S	0	2	0
			1890	1196	347	339	8			
2	Q	238	Total	C	N	O	S	0	3	0
			1904	1203	352	341	8			
2	R	238	Total	C	N	O	S	0	2	0
			1892	1198	347	339	8			

There are 6 discrepancies between the modelled and reference sequences:

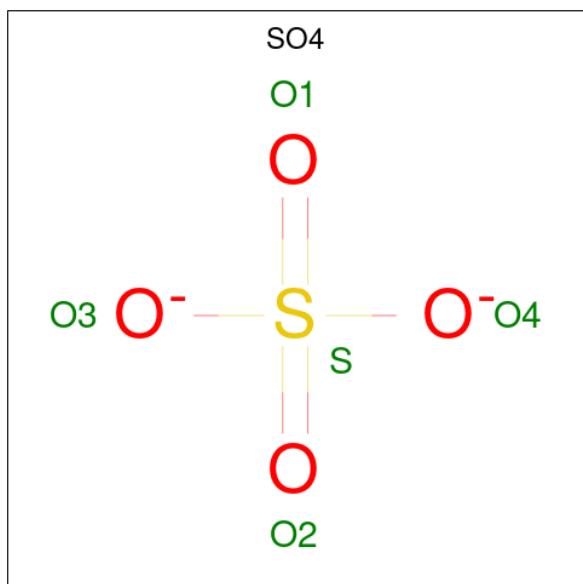
Chain	Residue	Modelled	Actual	Comment	Reference
M	447	HIS	TYR	engineered mutation	UNP P00437

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Chain	Residue	Modelled	Actual	Comment	Reference
N	447	HIS	TYR	engineered mutation	UNP P00437
O	447	HIS	TYR	engineered mutation	UNP P00437
P	447	HIS	TYR	engineered mutation	UNP P00437
Q	447	HIS	TYR	engineered mutation	UNP P00437
R	447	HIS	TYR	engineered mutation	UNP P00437

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	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	D	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is BETA-MERCAPTOETHANOL (CCD ID: BME) (formula: C₂H₆OS).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	O	S	0	0
			4	2	1	1		
4	M	1	Total	C	O	S	0	1
			12	6	3	3		
4	M	1	Total	C	O	S	0	0
			4	2	1	1		
4	M	1	Total	C	O	S	0	0
			4	2	1	1		
4	M	1	Total	C	O	S	0	0
			4	2	1	1		
4	N	1	Total	C	O	S	0	0
			4	2	1	1		
4	N	1	Total	C	O	S	0	1
			8	4	2	2		
4	N	1	Total	C	O	S	0	0
			4	2	1	1		
4	N	1	Total	C	O	S	0	0
			4	2	1	1		
4	C	1	Total	C	O	S	0	0
			4	2	1	1		
4	O	1	Total	C	O	S	0	0
			4	2	1	1		
4	O	1	Total	C	O	S	0	0
			4	2	1	1		
4	O	1	Total	C	O	S	0	0
			4	2	1	1		
4	O	1	Total	C	O	S	0	0
			4	2	1	1		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	O	1	Total 4	C 2	O 1	S 1	0	0
4	O	1	Total 4	C 2	O 1	S 1	0	0
4	P	1	Total 8	C 4	O 2	S 2	0	1
4	P	1	Total 4	C 2	O 1	S 1	0	0
4	P	1	Total 4	C 2	O 1	S 1	0	0
4	P	1	Total 4	C 2	O 1	S 1	0	0
4	P	1	Total 4	C 2	O 1	S 1	0	0
4	P	1	Total 4	C 2	O 1	S 1	0	0
4	P	1	Total 4	C 2	O 1	S 1	0	0
4	P	1	Total 4	C 2	O 1	S 1	0	0
4	Q	1	Total 4	C 2	O 1	S 1	0	0
4	Q	1	Total 4	C 2	O 1	S 1	0	0
4	Q	1	Total 8	C 4	O 2	S 2	0	1
4	Q	1	Total 4	C 2	O 1	S 1	0	0
4	R	1	Total 4	C 2	O 1	S 1	0	0
4	R	1	Total 4	C 2	O 1	S 1	0	0
4	R	1	Total 4	C 2	O 1	S 1	0	0
4	R	1	Total 4	C 2	O 1	S 1	0	0

- Molecule 5 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (CCD ID: TRS) (formula: C₄H₁₂NO₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			8	4	1	3		
5	B	1	Total	C	N	O	0	0
			8	4	1	3		
5	D	1	Total	C	N	O	0	0
			8	4	1	3		
5	E	1	Total	C	N	O	0	0
			8	4	1	3		
5	F	1	Total	C	N	O	0	0
			8	4	1	3		

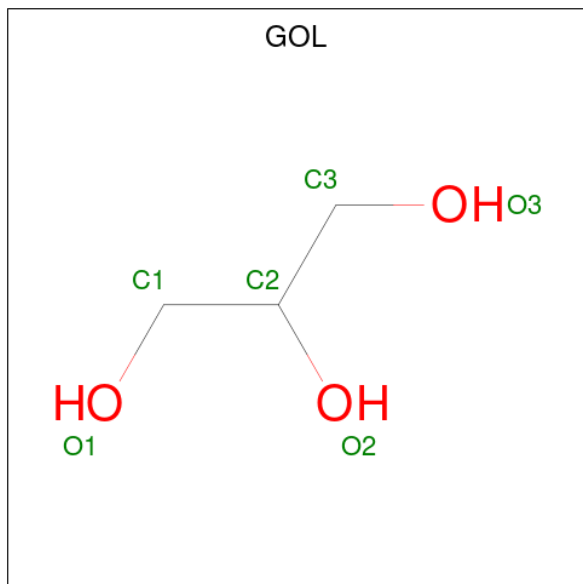
- Molecule 6 is FE (III) ION (CCD ID: FE) (formula: Fe).

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

- Molecule 7 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	M	4	Total Cl 4 4	0	0
7	N	1	Total Cl 1 1	0	0
7	O	1	Total Cl 1 1	0	0
7	P	1	Total Cl 1 1	0	0
7	Q	1	Total Cl 1 1	0	0
7	R	1	Total Cl 1 1	0	0

- Molecule 8 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	M	1	Total C O 6 3 3	0	0
8	C	1	Total C O 6 3 3	0	0

- Molecule 9 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	213	Total O 214 214	0	1
9	M	288	Total O 289 289	0	1

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	B	190	Total 190	O 190	0	0
9	N	264	Total 265	O 265	0	1
9	C	202	Total 203	O 203	0	1
9	O	257	Total 257	O 257	0	0
9	D	191	Total 192	O 192	0	1
9	P	270	Total 271	O 271	0	1
9	E	173	Total 174	O 174	0	1
9	Q	250	Total 251	O 251	0	1
9	F	201	Total 201	O 201	0	0
9	R	260	Total 261	O 261	0	1

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: Protocatechuate 3,4-dioxygenase alpha chain

Chain A:  92% 8%



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

Chain B:  94% 6%

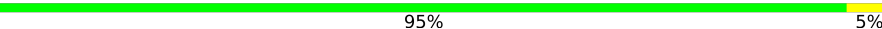


- Molecule 1: Protocatechuate 3,4-dioxygenase alpha chain

Chain C:  90% 9% .

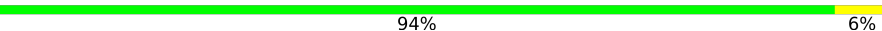


- Molecule 1: Protocatechuate 3,4-dioxygenase alpha chain

Chain D:  95% 5%



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

Chain E:  94% 6%



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

Chain F:  90% 10%



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

Chain M: 95% 5%



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

Chain N: 96% 4%



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

Chain O: 95% 5%



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

Chain P: 95% 5%



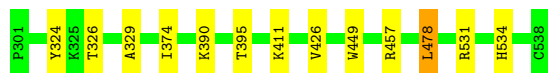
- Molecule 2: Protocatechuate 3,4-dioxygenase beta chain

Chain Q: 95% 5%



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

Chain R: 95% 5%



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	190.31Å 168.04Å 128.16Å 90.00° 132.30° 90.00°	Depositor
Resolution (Å)	29.57 – 1.65 29.57 – 1.65	Depositor EDS
% Data completeness (in resolution range)	98.2 (29.57-1.65) 98.3 (29.57-1.65)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.15 (at 1.65Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.148 , 0.173 0.153 , 0.178	Depositor DCC
R_{free} test set	17717 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	15.7	Xtriage
Anisotropy	0.018	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 34.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.480 for -h-2*k,l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	23995	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.62% 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: FE, BME, SO4, TRS, CL, GOL

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	0.68	0/1615	0.75	0/2199
1	B	0.63	0/1634	0.72	0/2224
1	C	0.65	0/1690	0.79	4/2301 (0.2%)
1	D	0.67	0/1626	0.74	0/2213
1	E	0.63	0/1631	0.72	0/2221
1	F	0.65	0/1699	0.80	0/2313
2	M	0.68	0/1958	0.79	0/2664
2	N	0.68	0/1951	0.79	0/2655
2	O	0.67	0/1944	0.79	0/2645
2	P	0.68	0/1952	0.79	0/2656
2	Q	0.67	0/1963	0.78	0/2670
2	R	0.66	0/1951	0.80	0/2655
All	All	0.66	0/21614	0.77	4/29416 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	102[A]	GLY	CA-C-N	5.03	129.94	123.00
1	C	102[A]	GLY	C-N-CA	5.03	129.94	123.00
1	C	102[B]	GLY	CA-C-N	5.03	129.94	123.00
1	C	102[B]	GLY	C-N-CA	5.03	129.94	123.00

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	1575	0	1510	18	0
1	B	1591	0	1528	15	0
1	C	1640	0	1574	38	0
1	D	1586	0	1522	13	0
1	E	1591	0	1518	11	0
1	F	1646	0	1580	32	0
2	M	1893	0	1856	12	0
2	N	1889	0	1852	6	0
2	O	1885	0	1843	11	0
2	P	1890	0	1849	10	0
2	Q	1904	0	1860	11	0
2	R	1892	0	1851	15	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
3	C	5	0	0	0	0
3	D	5	0	0	0	0
3	E	5	0	0	0	0
3	F	5	0	0	0	0
4	A	4	0	6	2	0
4	C	4	0	6	2	0
4	M	24	0	34	12	0
4	N	20	0	26	14	0
4	O	24	0	34	11	0
4	P	36	0	52	11	0
4	Q	20	0	26	13	0
4	R	16	0	22	14	0
5	A	8	0	12	1	0
5	B	8	0	12	1	0
5	D	8	0	12	4	0
5	E	8	0	12	0	0
5	F	8	0	12	1	0
6	M	1	0	0	0	0
6	N	1	0	0	0	0
6	O	1	0	0	0	0
6	P	1	0	0	0	0
6	Q	1	0	0	0	0
6	R	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	M	4	0	0	1	0
7	N	1	0	0	0	0
7	O	1	0	0	0	0
7	P	1	0	0	0	0
7	Q	1	0	0	0	0
7	R	1	0	0	0	0
8	C	6	0	8	0	0
8	M	6	0	8	1	0
9	A	214	0	0	0	0
9	B	190	0	0	1	0
9	C	203	0	0	3	0
9	D	192	0	0	0	0
9	E	174	0	0	1	0
9	F	201	0	0	2	0
9	M	289	0	0	2	0
9	N	265	0	0	4	0
9	O	257	0	0	3	0
9	P	271	0	0	5	0
9	Q	251	0	0	2	0
9	R	261	0	0	5	0
All	All	23995	0	20625	188	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 4.

The worst 5 of 188 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:99[B]:PHE:HD2	1:C:99[B]:PHE:N	1.25	1.23
1:F:99[A]:PHE:HD1	1:F:99[A]:PHE:N	1.46	1.12
1:C:99[B]:PHE:N	1:C:99[B]:PHE:CD2	2.02	1.10
4:Q:34[B]:BME:H22	9:Q:623:HOH:O	1.55	1.03
1:C:133:ARG:CD	4:O:33:BME:H12	1.93	0.97

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	198/200 (99%)	193 (98%)	5 (2%)	0	100	100
1	B	200/200 (100%)	197 (98%)	3 (2%)	0	100	100
1	C	208/200 (104%)	202 (97%)	6 (3%)	0	100	100
1	D	199/200 (100%)	196 (98%)	3 (2%)	0	100	100
1	E	200/200 (100%)	196 (98%)	4 (2%)	0	100	100
1	F	209/200 (104%)	200 (96%)	5 (2%)	4 (2%)	6	0
2	M	239/238 (100%)	235 (98%)	4 (2%)	0	100	100
2	N	238/238 (100%)	234 (98%)	4 (2%)	0	100	100
2	O	237/238 (100%)	232 (98%)	5 (2%)	0	100	100
2	P	238/238 (100%)	232 (98%)	6 (2%)	0	100	100
2	Q	239/238 (100%)	235 (98%)	4 (2%)	0	100	100
2	R	238/238 (100%)	231 (97%)	7 (3%)	0	100	100
All	All	2643/2628 (101%)	2583 (98%)	56 (2%)	4 (0%)	48	27

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	100[A]	ASP
1	F	100[B]	ASP
1	F	99[A]	PHE
1	F	99[B]	PHE

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	163/163 (100%)	162 (99%)	1 (1%)	78	68
1	B	165/163 (101%)	164 (99%)	1 (1%)	78	68
1	C	171/163 (105%)	165 (96%)	6 (4%)	32	10
1	D	164/163 (101%)	163 (99%)	1 (1%)	78	68
1	E	165/163 (101%)	163 (99%)	2 (1%)	63	45
1	F	172/163 (106%)	169 (98%)	3 (2%)	53	32
2	M	205/202 (102%)	203 (99%)	2 (1%)	68	52
2	N	204/202 (101%)	202 (99%)	2 (1%)	68	52
2	O	203/202 (100%)	201 (99%)	2 (1%)	68	52
2	P	204/202 (101%)	203 (100%)	1 (0%)	81	72
2	Q	205/202 (102%)	203 (99%)	2 (1%)	68	52
2	R	204/202 (101%)	200 (98%)	4 (2%)	48	26
All	All	2225/2190 (102%)	2198 (99%)	27 (1%)	65	45

5 of 27 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	43	ASP
1	E	180	LYS
2	R	395	THR
1	E	165	GLN
2	Q	395	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
2	O	530	GLN
2	P	502	GLN
2	R	502	GLN
2	P	334	GLN
1	E	59	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 65 ligands modelled in this entry, 15 are monoatomic - leaving 50 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	$\# Z > 2$
4	BME	O	27	-	3,3,3	0.41	0	2,2,2	0.07	0
8	GOL	M	16	-	5,5,5	0.65	0	5,5,5	0.55	0
4	BME	P	23	-	3,3,3	0.31	0	2,2,2	0.75	0
4	BME	O	45	-	3,3,3	0.41	0	2,2,2	0.55	0
4	BME	O	49	-	3,3,3	0.29	0	2,2,2	0.60	0
4	BME	M	36	-	3,3,3	0.50	0	2,2,2	0.45	0
4	BME	O	30	6	3,3,3	0.65	0	2,2,2	1.30	0
4	BME	Q	19	-	3,3,3	0.31	0	2,2,2	0.23	0
3	SO4	D	201	-	4,4,4	0.27	0	6,6,6	0.27	0
4	BME	C	203	-	3,3,3	0.40	0	2,2,2	0.66	0
4	BME	A	202	-	3,3,3	0.43	0	2,2,2	0.43	0
5	TRS	E	202	-	7,7,7	0.35	0	9,9,9	0.58	0
4	BME	N	18	-	3,3,3	0.29	0	2,2,2	0.34	0
4	BME	M	21[C]	-	3,3,3	0.27	0	2,2,2	0.71	0
3	SO4	E	201	-	4,4,4	0.23	0	6,6,6	0.15	0
4	BME	Q	46	-	3,3,3	0.44	0	2,2,2	0.25	0
5	TRS	A	203	-	7,7,7	0.42	0	9,9,9	0.58	0
4	BME	O	33	-	3,3,3	0.24	0	2,2,2	0.54	0
3	SO4	C	201	-	4,4,4	0.21	0	6,6,6	0.16	0
4	BME	N	32[A]	6	3,3,3	0.33	0	2,2,2	1.12	0
4	BME	P	31	6	3,3,3	0.72	0	2,2,2	1.30	0
4	BME	P	25	-	3,3,3	0.28	0	2,2,2	0.70	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	BME	P	48	-	3,3,3	0.34	0	2,2,2	0.51	0
4	BME	M	47	-	3,3,3	0.31	0	2,2,2	0.69	0
5	TRS	B	202	-	7,7,7	0.33	0	9,9,9	0.71	0
4	BME	N	32[B]	6	3,3,3	0.76	0	2,2,2	1.73	1 (50%)
4	BME	P	22[A]	-	3,3,3	0.34	0	2,2,2	0.31	0
8	GOL	C	202	-	5,5,5	0.32	0	5,5,5	0.35	0
4	BME	P	41	-	3,3,3	0.32	0	2,2,2	0.54	0
4	BME	Q	34[A]	6	3,3,3	0.49	0	2,2,2	1.46	0
4	BME	R	26	-	3,3,3	0.42	0	2,2,2	0.07	0
3	SO4	B	201	-	4,4,4	0.24	0	6,6,6	0.15	0
4	BME	N	37	-	3,3,3	0.41	0	2,2,2	0.19	0
4	BME	R	43	-	3,3,3	0.26	0	2,2,2	0.66	0
4	BME	Q	34[B]	6	3,3,3	0.40	0	2,2,2	1.31	0
4	BME	Q	24	-	3,3,3	0.36	0	2,2,2	0.32	0
4	BME	P	22[B]	-	3,3,3	0.51	0	2,2,2	0.23	0
4	BME	R	20	-	3,3,3	0.29	0	2,2,2	0.41	0
4	BME	P	40	-	3,3,3	0.34	0	2,2,2	0.45	0
3	SO4	F	201	-	4,4,4	0.25	0	6,6,6	0.19	0
4	BME	M	21[A]	-	3,3,3	0.34	0	2,2,2	0.14	0
4	BME	O	42	-	3,3,3	0.40	0	2,2,2	0.14	0
3	SO4	A	201	-	4,4,4	0.23	0	6,6,6	0.15	0
4	BME	P	35	-	3,3,3	0.30	0	2,2,2	0.54	0
4	BME	M	29	6	3,3,3	0.69	0	2,2,2	1.45	1 (50%)
5	TRS	F	202	-	7,7,7	0.30	0	9,9,9	0.80	0
4	BME	R	28	6	3,3,3	0.21	0	2,2,2	1.23	0
4	BME	M	21[B]	-	3,3,3	0.66	0	2,2,2	0.68	0
5	TRS	D	202	-	7,7,7	0.43	0	9,9,9	0.44	0
4	BME	N	44	-	3,3,3	0.37	0	2,2,2	0.40	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
4	BME	O	27	-	-	0/1/1/1	-
8	GOL	M	16	-	-	2/4/4/4	-
4	BME	P	23	-	-	0/1/1/1	-
4	BME	O	45	-	-	1/1/1/1	-
4	BME	M	36	-	-	1/1/1/1	-
4	BME	O	30	6	-	1/1/1/1	-
4	BME	Q	19	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	BME	C	203	-	-	1/1/1/1	-
4	BME	A	202	-	-	1/1/1/1	-
5	TRS	E	202	-	-	6/9/9/9	-
4	BME	N	18	-	-	1/1/1/1	-
4	BME	M	21[C]	-	-	0/1/1/1	-
4	BME	Q	46	-	-	0/1/1/1	-
5	TRS	A	203	-	-	6/9/9/9	-
4	BME	O	33	-	-	1/1/1/1	-
4	BME	N	32[A]	6	-	1/1/1/1	-
4	BME	P	31	6	-	1/1/1/1	-
4	BME	P	25	-	-	0/1/1/1	-
4	BME	P	48	-	-	1/1/1/1	-
4	BME	M	47	-	-	0/1/1/1	-
5	TRS	B	202	-	-	8/9/9/9	-
4	BME	N	32[B]	6	-	1/1/1/1	-
4	BME	P	22[A]	-	-	1/1/1/1	-
8	GOL	C	202	-	-	4/4/4/4	-
4	BME	P	41	-	-	1/1/1/1	-
4	BME	Q	34[A]	6	-	1/1/1/1	-
4	BME	R	26	-	-	0/1/1/1	-
4	BME	N	37	-	-	0/1/1/1	-
4	BME	R	43	-	-	1/1/1/1	-
4	BME	Q	34[B]	6	-	1/1/1/1	-
4	BME	Q	24	-	-	0/1/1/1	-
4	BME	P	22[B]	-	-	1/1/1/1	-
4	BME	R	20	-	-	1/1/1/1	-
4	BME	P	40	-	-	1/1/1/1	-
4	BME	M	21[A]	-	-	1/1/1/1	-
4	BME	O	42	-	-	1/1/1/1	-
4	BME	P	35	-	-	1/1/1/1	-
4	BME	M	21[B]	-	-	1/1/1/1	-
4	BME	M	29	6	-	1/1/1/1	-
5	TRS	F	202	-	-	5/9/9/9	-
4	BME	R	28	6	-	0/1/1/1	-
4	BME	O	49	-	-	1/1/1/1	-
5	TRS	D	202	-	-	4/9/9/9	-
4	BME	N	44	-	-	0/1/1/1	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	N	32[B]	BME	C1-C2-S2	-2.43	94.22	111.57
4	M	29	BME	C1-C2-S2	-2.01	97.21	111.57

There are no chirality outliers.

5 of 61 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	M	21[B]	BME	O1-C1-C2-S2
4	M	29	BME	O1-C1-C2-S2
4	M	36	BME	O1-C1-C2-S2
4	N	18	BME	O1-C1-C2-S2
4	N	32[A]	BME	O1-C1-C2-S2

There are no ring outliers.

33 monomers are involved in 87 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	M	16	GOL	1	0
4	P	23	BME	1	0
4	O	45	BME	1	0
4	M	36	BME	1	0
4	O	30	BME	1	0
4	Q	19	BME	8	0
4	C	203	BME	2	0
4	A	202	BME	2	0
4	N	18	BME	8	0
4	M	21[C]	BME	7	0
4	Q	46	BME	1	0
5	A	203	TRS	1	0
4	O	33	BME	7	0
4	N	32[A]	BME	3	0
4	P	31	BME	1	0
5	B	202	TRS	1	0
4	N	32[B]	BME	2	0
4	P	22[A]	BME	4	0
4	Q	34[A]	BME	2	0
4	R	26	BME	1	0
4	R	43	BME	1	0
4	Q	34[B]	BME	2	0
4	P	22[B]	BME	1	0
4	R	20	BME	10	0
4	P	40	BME	3	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	O	42	BME	2	0
4	P	35	BME	1	0
4	M	29	BME	1	0
5	F	202	TRS	1	0
4	R	28	BME	2	0
4	M	21[B]	BME	3	0
5	D	202	TRS	4	0
4	N	44	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	200/200 (100%)	-1.30	0 100 100	13, 18, 28, 37	6 (3%)
1	B	200/200 (100%)	-1.20	0 100 100	11, 21, 34, 40	7 (3%)
1	C	200/200 (100%)	-1.26	0 100 100	10, 18, 27, 37	14 (7%)
1	D	200/200 (100%)	-1.31	0 100 100	11, 18, 30, 42	3 (1%)
1	E	200/200 (100%)	-1.20	0 100 100	13, 21, 33, 45	6 (3%)
1	F	200/200 (100%)	-1.26	0 100 100	10, 18, 26, 38	15 (7%)
2	M	238/238 (100%)	-1.37	0 100 100	11, 16, 25, 34	7 (2%)
2	N	238/238 (100%)	-1.30	0 100 100	10, 17, 26, 38	6 (2%)
2	O	238/238 (100%)	-1.36	0 100 100	9, 16, 25, 34	3 (1%)
2	P	238/238 (100%)	-1.38	0 100 100	9, 16, 25, 34	3 (1%)
2	Q	238/238 (100%)	-1.31	0 100 100	8, 17, 26, 37	6 (2%)
2	R	238/238 (100%)	-1.37	0 100 100	7, 16, 25, 35	2 (0%)
All	All	2628/2628 (100%)	-1.31	0 100 100	7, 18, 29, 45	78 (2%)

There are no RSRZ outliers to report.

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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(Å ²)	Q<0.9
4	BME	O	27	4/4	0.94	0.09	49,49,50,50	4
4	BME	P	48	4/4	0.95	0.08	42,42,42,43	4
4	BME	P	41	4/4	0.96	0.09	44,45,45,45	4
4	BME	M	36	4/4	0.96	0.10	41,41,41,42	4
4	BME	R	26	4/4	0.96	0.09	47,48,49,49	4
7	CL	O	12	1/1	0.96	0.06	70,70,70,70	0
4	BME	P	25	4/4	0.97	0.07	32,34,34,36	4
4	BME	N	18	4/4	0.97	0.06	23,27,30,36	4
4	BME	M	47	4/4	0.97	0.07	34,37,40,44	4
4	BME	Q	24	4/4	0.97	0.08	34,36,38,40	4
4	BME	O	33	4/4	0.97	0.07	20,27,27,33	4
5	TRS	E	202	8/8	0.97	0.06	46,47,47,47	0
7	CL	M	14	1/1	0.97	0.08	61,61,61,61	0
7	CL	N	13	1/1	0.97	0.07	64,64,64,64	0
4	BME	O	49	4/4	0.97	0.08	37,38,38,38	4
7	CL	R	10	1/1	0.97	0.06	68,68,68,68	0
4	BME	P	22[B]	4/4	0.98	0.06	21,29,29,35	4
4	BME	M	21[B]	4/4	0.98	0.05	17,18,19,25	4
4	BME	P	35	4/4	0.98	0.07	37,37,37,37	4
4	BME	P	40	4/4	0.98	0.07	37,38,38,40	4
4	BME	N	37	4/4	0.98	0.06	56,58,59,62	0
4	BME	N	44	4/4	0.98	0.07	35,37,38,40	4
4	BME	Q	19	4/4	0.98	0.07	24,30,33,38	4
4	BME	C	203	4/4	0.98	0.08	32,33,34,35	4
4	BME	Q	46	4/4	0.98	0.06	36,38,39,41	4
4	BME	M	21[C]	4/4	0.98	0.05	18,21,21,22	4
5	TRS	A	203	8/8	0.98	0.06	36,37,39,40	0
5	TRS	B	202	8/8	0.98	0.06	44,45,46,47	0
5	TRS	D	202	8/8	0.98	0.06	34,35,37,38	8
3	SO4	B	201	5/5	0.98	0.05	39,41,42,42	5
5	TRS	F	202	8/8	0.98	0.06	41,41,42,43	8
7	CL	M	8	1/1	0.98	0.07	59,59,59,59	0
4	BME	O	42	4/4	0.98	0.08	28,32,33,36	4
4	BME	O	45	4/4	0.98	0.06	32,33,34,35	4
4	BME	M	21[A]	4/4	0.98	0.05	28,30,30,31	4
7	CL	P	15	1/1	0.98	0.06	60,60,60,60	0
7	CL	Q	11	1/1	0.98	0.10	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	BME	P	22[A]	4/4	0.98	0.06	31,31,32,32	4
8	GOL	M	16	6/6	0.98	0.05	29,35,36,40	0
8	GOL	C	202	6/6	0.98	0.04	36,41,42,43	0
4	BME	R	43	4/4	0.99	0.05	34,36,36,37	4
3	SO4	A	201	5/5	0.99	0.04	36,37,38,38	5
4	BME	P	23	4/4	0.99	0.06	30,31,34,37	4
3	SO4	C	201	5/5	0.99	0.03	42,44,45,45	5
4	BME	P	31	4/4	0.99	0.04	23,24,26,28	0
3	SO4	D	201	5/5	0.99	0.04	35,37,37,38	5
7	CL	M	7	1/1	0.99	0.09	38,38,38,38	0
4	BME	M	29	4/4	0.99	0.04	21,23,25,28	0
7	CL	M	9	1/1	0.99	0.07	45,45,45,45	0
4	BME	O	30	4/4	0.99	0.04	23,24,26,28	0
3	SO4	E	201	5/5	0.99	0.04	38,39,40,41	5
3	SO4	F	201	5/5	0.99	0.04	41,43,44,44	5
4	BME	A	202	4/4	0.99	0.04	28,30,30,34	4
4	BME	N	32[A]	4/4	0.99	0.07	42,43,43,44	4
4	BME	R	20	4/4	0.99	0.04	20,28,29,33	4
4	BME	N	32[B]	4/4	0.99	0.07	17,17,18,23	4
4	BME	R	28	4/4	0.99	0.06	14,14,15,18	0
6	FE	N	600	1/1	1.00	0.02	16,16,16,16	0
6	FE	O	600	1/1	1.00	0.01	15,15,15,15	0
6	FE	P	600	1/1	1.00	0.01	15,15,15,15	0
6	FE	Q	600	1/1	1.00	0.01	16,16,16,16	0
6	FE	R	600	1/1	1.00	0.01	15,15,15,15	0
4	BME	Q	34[A]	4/4	1.00	0.03	11,13,14,16	4
4	BME	Q	34[B]	4/4	1.00	0.03	56,57,57,57	4
6	FE	M	600	1/1	1.00	0.01	15,15,15,15	0

6.5 Other polymers

There are no such residues in this entry.