



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 08:58 PM UTC

PDB ID : 5HPI / pdb_00005hpi
Title : Crystal Structure of the Double Mutant of PobR Transcription Factor Inducer Binding Domain-3-Hydroxy Benzoic Acid complex from Acinetobacter
Authors : Kim, Y.; Tesar, C.; Jedrejszak, R.; Jha, R.; Strauss, C.E.M.; Joachimiak, A.
Deposited on : 2016-01-20
Resolution : 2.96 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 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

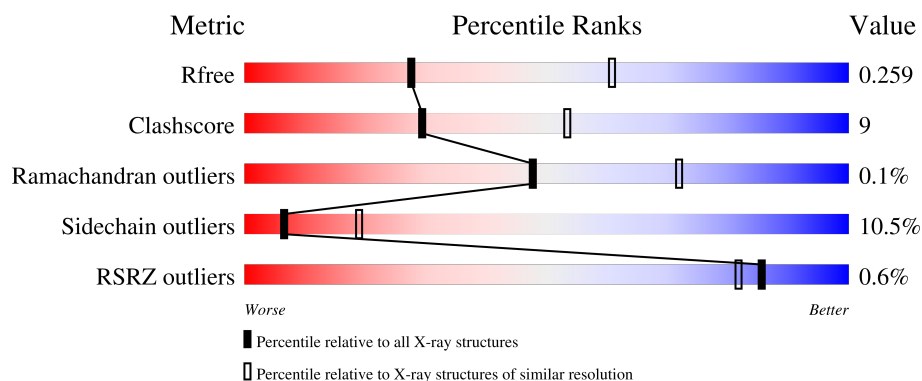
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.96 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	1130 (2.98-2.94)
Clashscore	190562	1157 (2.98-2.94)
Ramachandran outliers	187476	1101 (2.98-2.94)
Sidechain outliers	187428	1101 (2.98-2.94)
RSRZ outliers	180081	1130 (2.98-2.94)

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	178	
1	B	178	
1	C	178	
1	D	178	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5557 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.

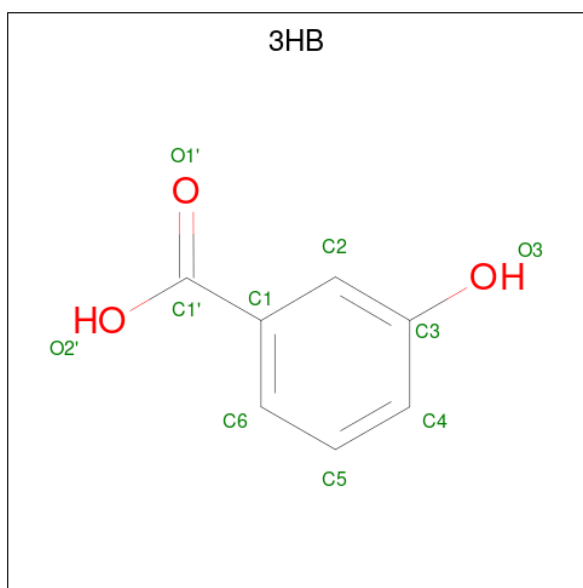
- Molecule 1 is a protein called p-hydroxybenzoate hydroxylase transcriptional activator.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	175	Total	C	N	O	S	Se	0	0	0
			1376	872	239	260	3	2			
1	B	172	Total	C	N	O	S	Se	0	0	0
			1353	857	234	257	3	2			
1	C	174	Total	C	N	O	S	Se	0	1	0
			1381	875	241	260	3	2			
1	D	170	Total	C	N	O	S	Se	0	2	0
			1357	858	238	257	3	1			

There are 20 discrepancies between the modelled and reference sequences:

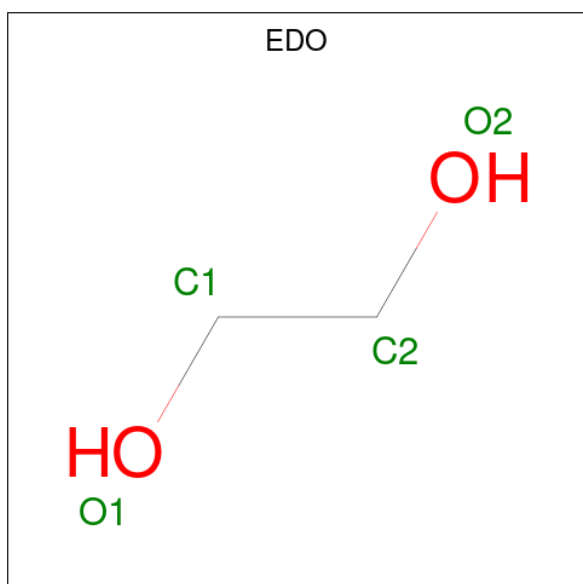
Chain	Residue	Modelled	Actual	Comment	Reference
A	93	SER	-	expression tag	UNP Q43992
A	94	ASN	-	expression tag	UNP Q43992
A	95	ALA	-	expression tag	UNP Q43992
A	?	-	LEU	deletion	UNP Q43992
A	220	VAL	LEU	engineered mutation	UNP Q43992
B	93	SER	-	expression tag	UNP Q43992
B	94	ASN	-	expression tag	UNP Q43992
B	95	ALA	-	expression tag	UNP Q43992
B	?	-	LEU	deletion	UNP Q43992
B	220	VAL	LEU	engineered mutation	UNP Q43992
C	93	SER	-	expression tag	UNP Q43992
C	94	ASN	-	expression tag	UNP Q43992
C	95	ALA	-	expression tag	UNP Q43992
C	?	-	LEU	deletion	UNP Q43992
C	220	VAL	LEU	engineered mutation	UNP Q43992
D	93	SER	-	expression tag	UNP Q43992
D	94	ASN	-	expression tag	UNP Q43992
D	95	ALA	-	expression tag	UNP Q43992
D	?	-	LEU	deletion	UNP Q43992
D	220	VAL	LEU	engineered mutation	UNP Q43992

- Molecule 2 is 3-HYDROXYBENZOIC ACID (CCD ID: 3HB) (formula: $C_7H_6O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			10	7	3		
2	B	1	Total	C	O	0	0
			10	7	3		
2	C	1	Total	C	O	0	0
			10	7	3		
2	D	1	Total	C	O	0	0
			10	7	3		

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



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

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	5	Total O 5 5	0	0
5	B	2	Total O 2 2	0	0

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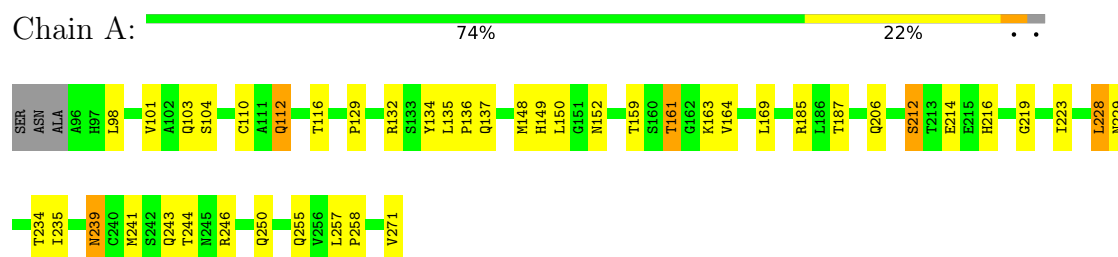
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	3	Total	O	0	0
			3	3		
5	D	3	Total	O	0	0
			3	3		

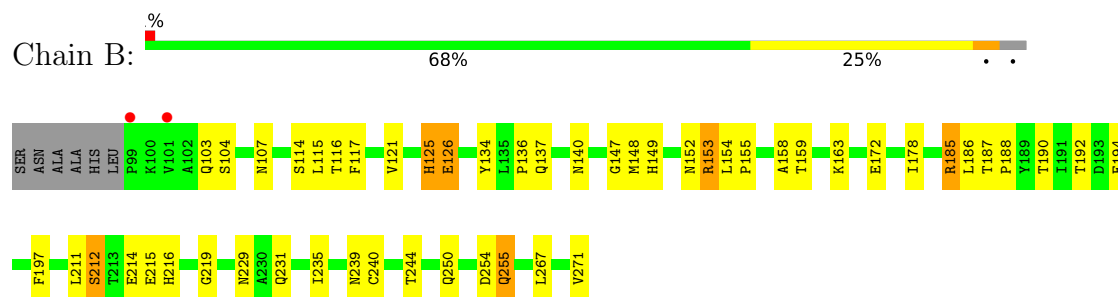
3 Residue-property plots

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.

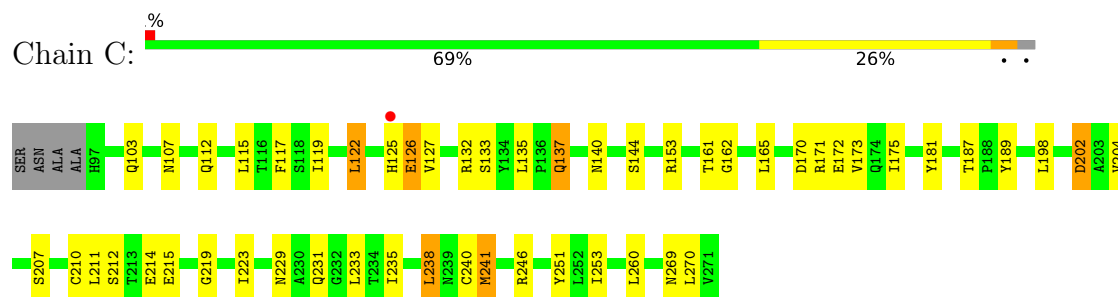
- Molecule 1: p-hydroxybenzoate hydroxylase transcriptional activator



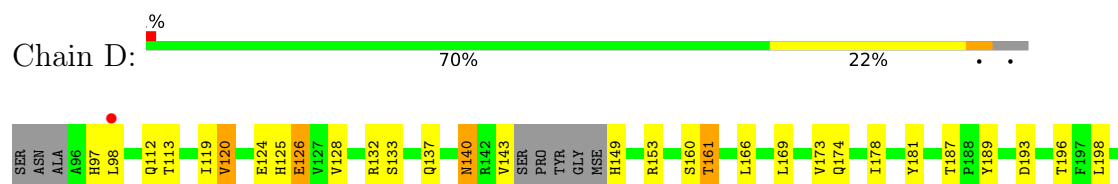
- Molecule 1: p-hydroxybenzoate hydroxylase transcriptional activator



- Molecule 1: p-hydroxybenzoate hydroxylase transcriptional activator



- Molecule 1: p-hydroxybenzoate hydroxylase transcriptional activator





4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	83.49Å 125.66Å 156.67Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.01 – 2.96 49.01 – 2.96	Depositor EDS
% Data completeness (in resolution range)	95.0 (49.01-2.96) 95.1 (49.01-2.96)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.10 (at 2.96Å)	Xtriage
Refinement program	PHENIX (1.10pre_2104: ???)	Depositor
R, R_{free}	0.197 , 0.258 0.200 , 0.259	Depositor DCC
R_{free} test set	818 reflections (4.67%)	wwPDB-VP
Wilson B-factor (Å ²)	65.7	Xtriage
Anisotropy	0.548	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 54.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5557	wwPDB-VP
Average B, all atoms (Å ²)	76.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.35% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, 3HB, SO4

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	0/1399	0.57	0/1908
1	B	0.39	0/1375	0.57	0/1874
1	C	0.42	0/1405	0.58	0/1916
1	D	0.40	1/1378 (0.1%)	0.56	0/1880
All	All	0.40	1/5557 (0.0%)	0.57	0/7578

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	98	LEU	C-N	6.18	1.48	1.33

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	1376	0	1395	21	1
1	B	1353	0	1371	26	1
1	C	1381	0	1396	30	0
1	D	1357	0	1375	27	0
2	A	10	0	5	1	0
2	B	10	0	5	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	10	0	5	1	0
2	D	10	0	5	0	0
3	A	8	0	12	0	0
3	B	4	0	6	1	0
4	B	10	0	0	0	0
4	C	5	0	0	0	0
4	D	10	0	0	1	0
5	A	5	0	0	1	0
5	B	2	0	0	0	0
5	C	3	0	0	0	0
5	D	3	0	0	0	0
All	All	5557	0	5575	96	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

All (96) 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:112:GLN:O	1:D:250[B]:GLN:NE2	2.16	0.79
1:D:250[B]:GLN:NE2	1:D:254:ASP:OD1	2.23	0.72
1:C:132:ARG:NH1	1:C:133:SER:O	2.28	0.67
1:D:219:GLY:O	1:D:244:THR:N	2.30	0.64
1:B:158:ALA:HB1	1:B:216:HIS:HB2	1.84	0.59
1:B:190:THR:HA	1:B:215:GLU:HG3	1.85	0.58
1:C:115:LEU:HD23	1:C:240:CYS:SG	2.43	0.58
1:D:140:ASN:HB3	1:D:143:VAL:HG23	1.86	0.57
1:B:147:GLY:HA2	1:B:154:LEU:HD11	1.85	0.57
1:C:171:ARG:NH1	1:C:202:ASP:OD2	2.34	0.57
1:A:134:TYR:CE2	1:A:136:PRO:HG3	2.40	0.56
1:C:122:LEU:HB2	1:C:165:LEU:HD13	1.88	0.56
1:D:149:HIS:N	4:D:302:SO4:O4	2.39	0.56
1:D:169:LEU:HD23	1:D:173:VAL:HG12	1.88	0.56
1:D:193:ASP:HB3	1:D:196:THR:HB	1.89	0.55
1:A:159:THR:O	1:A:163:LYS:HG3	2.08	0.54
1:B:134:TYR:CE2	1:B:136:PRO:HG3	2.42	0.54
1:C:103:GLN:O	1:C:107:ASN:ND2	2.41	0.54
1:D:126:GLU:HG3	1:D:153:ARG:HB3	1.90	0.54
1:B:214:GLU:HG2	1:B:219:GLY:H	1.73	0.54
1:C:246:ARG:O	1:D:248[B]:GLN:NE2	2.38	0.53
1:D:125:HIS:HB2	1:D:181:TYR:CE1	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:155:PRO:HG2	1:B:186:LEU:HD11	1.89	0.52
1:C:170:ASP:OD2	1:C:171:ARG:N	2.42	0.52
1:C:229:ASN:HB3	1:C:235:ILE:HD13	1.92	0.51
1:A:129:PRO:HD2	1:A:152:ASN:O	2.09	0.51
1:C:214:GLU:OE2	1:C:219:GLY:N	2.42	0.51
1:C:238:LEU:HG	1:C:260:LEU:HD22	1.93	0.50
1:B:178:ILE:HD11	1:B:197:PHE:HD2	1.77	0.50
1:B:159:THR:O	1:B:163:LYS:HG3	2.12	0.49
1:D:119:ILE:HD13	1:D:238:LEU:HD13	1.94	0.49
1:A:239:ASN:HD21	1:A:241:MSE:CG	2.25	0.49
1:D:128:VAL:HG22	1:D:153:ARG:HG2	1.95	0.49
1:D:267:LEU:O	1:D:271:VAL:HG12	2.13	0.48
1:C:175:ILE:HD11	1:C:198:LEU:HD11	1.96	0.48
1:D:126:GLU:CG	1:D:153:ARG:HB3	2.43	0.48
1:A:110:CYS:SG	1:A:135:LEU:HD12	2.55	0.47
1:B:158:ALA:HA	1:B:215:GLU:HG2	1.96	0.47
1:A:101:VAL:HG22	5:A:402:HOH:O	2.14	0.47
1:C:210:CYS:O	1:C:223:ILE:HA	2.13	0.47
1:A:216:HIS:ND1	2:A:301:3HB:O3	2.31	0.47
1:C:122:LEU:HD12	1:C:127:VAL:HG12	1.96	0.47
1:C:125[B]:HIS:HB2	1:C:181:TYR:CE1	2.50	0.47
1:C:140:ASN:ND2	1:D:215:GLU:OE2	2.44	0.46
1:A:161:THR:HG23	1:A:239:ASN:HB3	1.97	0.46
1:A:185:ARG:NH2	1:A:187:THR:O	2.49	0.46
1:A:243:GLN:HG3	1:A:246:ARG:NH2	2.30	0.46
1:D:174:GLN:O	1:D:178:ILE:HG13	2.14	0.46
1:A:163:LYS:NZ	1:A:212:SER:HB2	2.30	0.46
1:B:185:ARG:HG3	1:B:192:THR:HG21	1.98	0.46
1:B:158:ALA:CB	1:B:216:HIS:HB2	2.45	0.46
1:B:187:THR:HB	1:B:188:PRO:HD2	1.98	0.46
1:A:229:ASN:HB3	1:A:235:ILE:HG21	1.98	0.46
1:B:250:GLN:NE2	1:B:254:ASP:OD1	2.49	0.46
1:A:103:GLN:NE2	1:A:132:ARG:O	2.36	0.45
1:B:255:GLN:NE2	1:B:255:GLN:HA	2.31	0.45
1:C:135:LEU:HD23	1:C:135:LEU:HA	1.78	0.45
1:A:228:LEU:HD12	1:A:234:THR:HA	1.97	0.45
1:A:239:ASN:HD21	1:A:241:MSE:HG2	1.82	0.45
1:B:149:HIS:HB3	1:B:152:ASN:ND2	2.31	0.45
1:B:103:GLN:NE2	1:B:107:ASN:OD1	2.48	0.45
1:B:163:LYS:NZ	1:B:212:SER:OG	2.50	0.45
1:C:127:VAL:HG11	1:C:162:GLY:HA2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:214:GLU:HG2	1:A:219:GLY:H	1.83	0.44
1:B:126:GLU:OE1	1:B:153:ARG:HD3	2.17	0.44
1:C:125[A]:HIS:HB3	1:C:181:TYR:CD1	2.53	0.44
1:C:251:TYR:OH	1:D:250[B]:GLN:HG2	2.17	0.44
1:D:120:VAL:HB	1:D:161:THR:HG21	1.99	0.44
1:D:198:LEU:HD23	1:D:198:LEU:HA	1.83	0.44
1:C:214:GLU:HG2	1:C:219:GLY:H	1.82	0.44
1:D:112:GLN:HG3	1:D:113:THR:HG23	2.00	0.44
1:B:155:PRO:HD2	1:B:216:HIS:CD2	2.54	0.43
1:D:160:SER:HB3	1:D:212:SER:HB2	2.00	0.43
1:A:250:GLN:NE2	1:B:114:SER:OG	2.52	0.43
1:A:257:LEU:HB3	1:A:258:PRO:HD3	2.00	0.43
1:B:125:HIS:ND1	1:B:126:GLU:HG3	2.33	0.43
1:B:229:ASN:HB3	1:B:235:ILE:HD13	2.01	0.42
1:C:119:ILE:HD13	1:C:238:LEU:HB2	2.02	0.42
1:D:132:ARG:HG2	1:D:133:SER:O	2.19	0.42
1:C:117:PHE:CE1	1:C:240:CYS:HB2	2.55	0.42
1:A:132:ARG:NH1	1:A:148:MSE:O	2.53	0.41
1:B:114:SER:O	1:B:115:LEU:HD23	2.20	0.41
1:C:211:LEU:HD12	1:C:211:LEU:HA	1.90	0.41
1:D:166:LEU:HD23	1:D:166:LEU:HA	1.92	0.41
1:B:267:LEU:O	1:B:271:VAL:HG22	2.19	0.41
1:C:241:MSE:HG2	2:C:301:3HB:C6	2.51	0.41
1:D:126:GLU:CD	1:D:153:ARG:HB3	2.46	0.41
1:A:206:GLN:HE22	1:C:269:ASN:HD21	1.67	0.41
1:C:125[A]:HIS:CD2	1:C:126:GLU:HG2	2.56	0.41
1:C:137:GLN:HG3	1:D:203:ALA:HB1	2.02	0.41
1:B:125:HIS:HB2	3:B:304:EDO:H22	2.02	0.41
1:D:187:THR:C	1:D:189:TYR:H	2.28	0.41
1:B:117:PHE:CE1	1:B:240:CYS:HB2	2.57	0.40
1:C:189:TYR:O	1:C:215:GLU:HG2	2.21	0.40
1:C:251:TYR:OH	1:D:250[A]:GLN:HG3	2.21	0.40
1:A:98:LEU:HD12	1:A:271:VAL:HG23	2.02	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:112:GLN:O	1:B:250:GLN:NE2[3_454]	2.16	0.04

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	173/178 (97%)	164 (95%)	9 (5%)	0	100	100
1	B	170/178 (96%)	164 (96%)	6 (4%)	0	100	100
1	C	173/178 (97%)	165 (95%)	8 (5%)	0	100	100
1	D	168/178 (94%)	155 (92%)	12 (7%)	1 (1%)	21	45
All	All	684/712 (96%)	648 (95%)	35 (5%)	1 (0%)	48	72

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	124	GLU

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	156/156 (100%)	141 (90%)	15 (10%)	8	22
1	B	154/156 (99%)	136 (88%)	18 (12%)	5	16
1	C	157/156 (101%)	138 (88%)	19 (12%)	5	14
1	D	154/156 (99%)	140 (91%)	14 (9%)	9	23
All	All	621/624 (100%)	555 (89%)	66 (11%)	6	19

All (66) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	104	SER
1	A	112	GLN
1	A	116	THR
1	A	137	GLN
1	A	149	HIS
1	A	150	LEU
1	A	161	THR
1	A	164	VAL
1	A	169	LEU
1	A	212	SER
1	A	223	ILE
1	A	228	LEU
1	A	239	ASN
1	A	244	THR
1	A	255	GLN
1	B	104	SER
1	B	116	THR
1	B	121	VAL
1	B	125	HIS
1	B	126	GLU
1	B	137	GLN
1	B	140	ASN
1	B	148	MSE
1	B	153	ARG
1	B	172	GLU
1	B	185	ARG
1	B	194	GLU
1	B	211	LEU
1	B	212	SER
1	B	231	GLN
1	B	239	ASN
1	B	244	THR
1	B	255	GLN
1	C	122	LEU
1	C	126	GLU
1	C	137	GLN
1	C	144	SER
1	C	153	ARG
1	C	161	THR
1	C	172	GLU
1	C	173	VAL
1	C	187	THR
1	C	202	ASP

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Mol	Chain	Res	Type
1	C	204	VAL
1	C	207	SER
1	C	212	SER
1	C	231	GLN
1	C	233	LEU
1	C	238	LEU
1	C	241	MSE
1	C	253	ILE
1	C	270	LEU
1	D	97	HIS
1	D	120	VAL
1	D	126	GLU
1	D	137	GLN
1	D	140	ASN
1	D	161	THR
1	D	212	SER
1	D	223	ILE
1	D	228	LEU
1	D	241	MSE
1	D	245	ASN
1	D	250[A]	GLN
1	D	250[B]	GLN
1	D	270	LEU

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

Mol	Chain	Res	Type
1	A	112	GLN
1	A	149	HIS
1	A	152	ASN
1	A	250	GLN
1	A	255	GLN
1	A	265	ASN
1	B	152	ASN
1	B	229	ASN
1	B	255	GLN
1	C	107	ASN
1	C	174	GLN
1	C	195	HIS
1	C	229	ASN
1	C	231	GLN
1	C	269	ASN

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Mol	Chain	Res	Type
1	D	112	GLN
1	D	137	GLN
1	D	149	HIS
1	D	152	ASN
1	D	239	ASN
1	D	269	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

12 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	$\# Z > 2$
4	SO4	B	303	-	4,4,4	0.24	0	6,6,6	0.07	0
3	EDO	B	304	-	3,3,3	0.57	0	2,2,2	0.02	0
3	EDO	A	303	-	3,3,3	0.42	0	2,2,2	0.32	0
4	SO4	B	302	-	4,4,4	0.37	0	6,6,6	0.30	0
2	3HB	A	301	-	10,10,10	0.64	0	13,13,13	1.12	0
2	3HB	B	301	-	10,10,10	0.69	0	13,13,13	0.90	0
3	EDO	A	302	-	3,3,3	0.41	0	2,2,2	0.50	0
4	SO4	D	302	-	4,4,4	0.36	0	6,6,6	0.26	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	SO4	D	303	-	4,4,4	0.27	0	6,6,6	0.17	0
2	3HB	C	301	-	10,10,10	0.81	0	13,13,13	0.96	0
2	3HB	D	301	-	10,10,10	0.69	0	13,13,13	0.92	0
4	SO4	C	302	-	4,4,4	0.27	0	6,6,6	0.13	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	EDO	B	304	-	-	0/1/1/1	-
3	EDO	A	303	-	-	0/1/1/1	-
2	3HB	A	301	-	-	4/4/4/4	0/1/1/1
2	3HB	B	301	-	-	4/4/4/4	0/1/1/1
3	EDO	A	302	-	-	1/1/1/1	-
2	3HB	C	301	-	-	0/4/4/4	0/1/1/1
2	3HB	D	301	-	-	4/4/4/4	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	302	EDO	O1-C1-C2-O2
2	A	301	3HB	C2-C1-C1'-O2'
2	B	301	3HB	C2-C1-C1'-O1'
2	A	301	3HB	C2-C1-C1'-O1'
2	B	301	3HB	C2-C1-C1'-O2'
2	B	301	3HB	C6-C1-C1'-O1'
2	A	301	3HB	C6-C1-C1'-O2'
2	B	301	3HB	C6-C1-C1'-O2'
2	D	301	3HB	C2-C1-C1'-O1'
2	D	301	3HB	C2-C1-C1'-O2'
2	D	301	3HB	C6-C1-C1'-O1'
2	A	301	3HB	C6-C1-C1'-O1'
2	D	301	3HB	C6-C1-C1'-O2'

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	304	EDO	1	0
2	A	301	3HB	1	0
4	D	302	SO4	1	0
2	C	301	3HB	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 [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	173/178 (97%)	-0.12	0 100 100	38, 71, 136, 174	0
1	B	170/178 (95%)	-0.20	2 (1%) 76 71	44, 71, 109, 156	0
1	C	172/178 (96%)	-0.27	1 (0%) 85 82	40, 65, 107, 128	1 (0%)
1	D	169/178 (94%)	-0.15	1 (0%) 85 82	42, 73, 126, 157	2 (1%)
All	All	684/712 (96%)	-0.18	4 (0%) 85 82	38, 70, 121, 174	3 (0%)

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	99	PRO	4.2
1	C	125[A]	HIS	2.7
1	B	101	VAL	2.6
1	D	98	LEU	2.5

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 oligosaccharides 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($\text{\AA}^2$)	Q<0.9
4	SO4	D	303	5/5	0.72	0.16	118,118,118,119	0
4	SO4	B	303	5/5	0.74	0.09	141,141,141,141	0
4	SO4	C	302	5/5	0.75	0.09	143,143,144,144	0
3	EDO	A	302	4/4	0.75	0.16	62,62,62,62	0
4	SO4	D	302	5/5	0.86	0.17	78,85,85,90	0
2	3HB	D	301	10/10	0.88	0.13	83,84,84,84	0
3	EDO	B	304	4/4	0.89	0.13	58,58,58,58	0
2	3HB	A	301	10/10	0.91	0.08	71,71,71,71	0
2	3HB	C	301	10/10	0.92	0.10	59,61,61,61	0
2	3HB	B	301	10/10	0.93	0.14	56,56,57,57	0
3	EDO	A	303	4/4	0.94	0.12	72,72,73,73	0
4	SO4	B	302	5/5	0.94	0.07	36,39,39,39	5

6.5 Other polymers ⓘ

There are no such residues in this entry.