



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 27, 2025 – 09:04 am GMT

PDB ID : 9H6R / pdb_00009h6r
Title : X-ray structure of Hydrogenosomal processing peptidase (HPP), E56Q inactive mutant, from Trichomonas vaginalis co-crystallized with presequence peptide from ferredoxin oxidoreductase (PFO) - not visible in the structure model
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Deposited on : 2024-10-25
Resolution : 2.65 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	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
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)	:	2.46

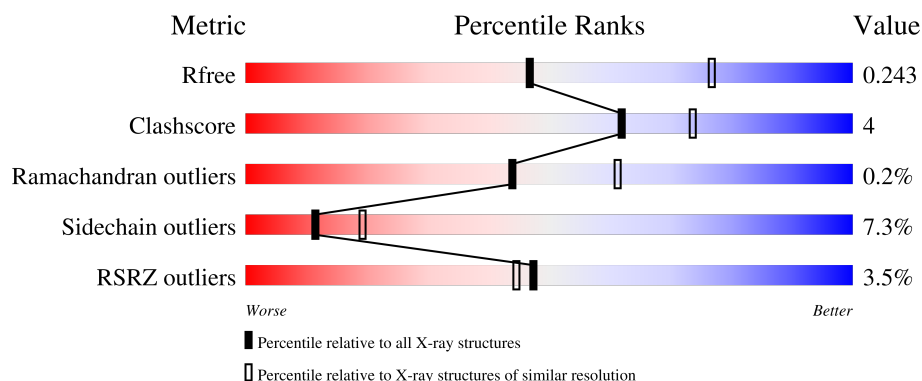
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.65 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}	164625	1003 (2.66-2.66)
Clashscore	180529	1063 (2.66-2.66)
Ramachandran outliers	177936	1052 (2.66-2.66)
Sidechain outliers	177891	1052 (2.66-2.66)
RSRZ outliers	164620	1003 (2.66-2.66)

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	431	<div> <div>5%</div> <div> <div></div> <div>76%</div> <div>15%</div> <div>9%</div> </div> </div>
2	B	419	<div> <div>%</div> <div> <div></div> <div>82%</div> <div>15%</div> <div>...</div> </div> </div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6510 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 Alpha-MPP.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	393	Total	C	N	O	S	0	3	0
			3063	1958	515	576	14			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	240	GLY	GLU	conflict	UNP A2D7B7
A	419	GLY	-	expression tag	UNP A2D7B7
A	420	SER	-	expression tag	UNP A2D7B7
A	421	ALA	-	expression tag	UNP A2D7B7
A	422	LEU	-	expression tag	UNP A2D7B7
A	423	GLU	-	expression tag	UNP A2D7B7
A	424	HIS	-	expression tag	UNP A2D7B7
A	425	HIS	-	expression tag	UNP A2D7B7
A	426	HIS	-	expression tag	UNP A2D7B7
A	427	HIS	-	expression tag	UNP A2D7B7
A	428	HIS	-	expression tag	UNP A2D7B7
A	429	HIS	-	expression tag	UNP A2D7B7
A	430	HIS	-	expression tag	UNP A2D7B7
A	431	HIS	-	expression tag	UNP A2D7B7

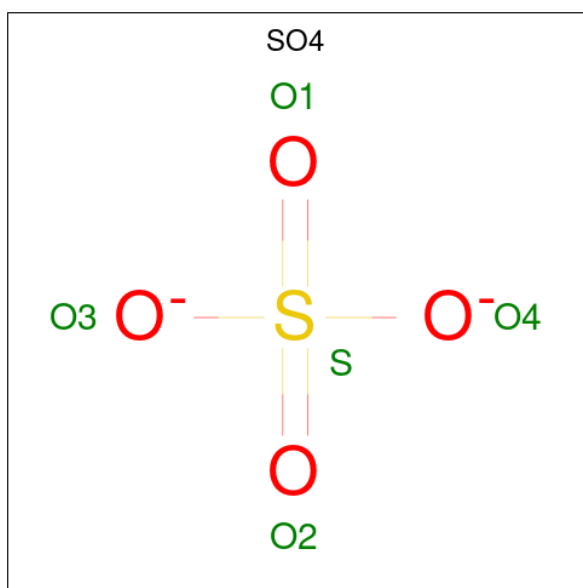
- Molecule 2 is a protein called Clan ME, family M16, insulinase-like metallopeptidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	416	Total	C	N	O	S	0	0	0
			3277	2079	553	639	6			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	56	GLN	GLU	engineered mutation	UNP A2ES04
B	260	SER	PRO	conflict	UNP A2ES04

- 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	A	1	Total	O	S	0	0
			5	4	1		
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	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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

- Molecule 5 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Zn	0	0
			1	1		

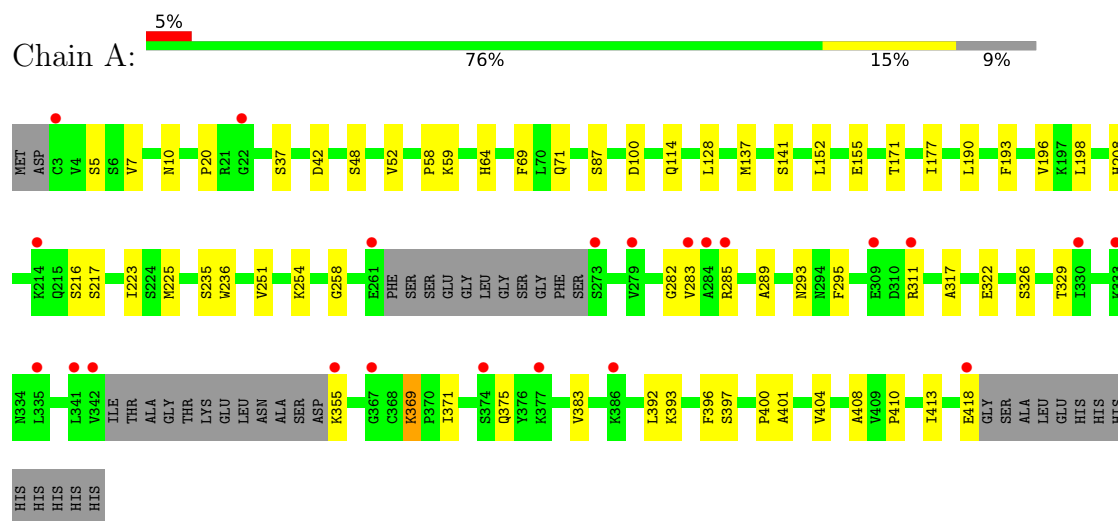
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	58	Total	O	0	0
			58	58		
6	B	70	Total	O	0	0
			70	70		

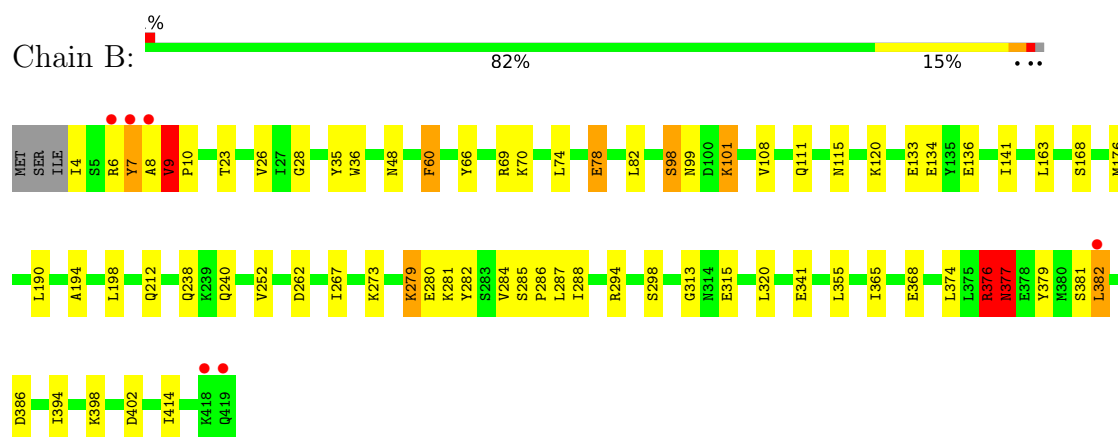
3 Residue-property plots [i](#)

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: Alpha-MPP



• Molecule 2: Clan ME, family M16, insulinase-like metallopeptidase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	88.24Å 115.03Å 124.01Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	84.00 – 2.65 84.00 – 2.65	Depositor EDS
% Data completeness (in resolution range)	100.0 (84.00-2.65) 100.0 (84.00-2.65)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.65 (at 2.65Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.186 , 0.240 0.189 , 0.243	Depositor DCC
R_{free} test set	1830 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å ²)	44.8	Xtriage
Anisotropy	0.076	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 39.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6510	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.68% 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: SO4, ZN, 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	0.88	0/3131	1.17	3/4231 (0.1%)
2	B	0.93	0/3340	1.19	8/4532 (0.2%)
All	All	0.91	0/6471	1.18	11/8763 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	2

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	9	VAL	N-CA-C	8.66	127.59	108.88
1	A	282	GLY	N-CA-C	7.48	121.18	112.50
2	B	198	LEU	CA-C-N	-6.63	113.47	120.03
2	B	198	LEU	C-N-CA	-6.63	113.47	120.03
2	B	287	LEU	N-CA-C	6.26	118.91	111.71
2	B	267	ILE	O-C-N	5.77	124.11	120.42
2	B	7	TYR	N-CA-C	5.68	122.90	110.80
2	B	28	GLY	N-CA-C	5.57	117.75	111.85
2	B	99	ASN	N-CA-C	5.35	117.87	111.71
1	A	193	PHE	CA-C-N	-5.01	114.42	119.83
1	A	193	PHE	C-N-CA	-5.01	114.42	119.83

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	376	ARG	Peptide
2	B	8	ALA	Peptide

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	3063	0	3108	26	0
2	B	3277	0	3257	32	0
3	A	20	0	0	0	0
3	B	15	0	0	0	0
4	A	6	0	8	0	0
5	B	1	0	0	0	0
6	A	58	0	0	0	0
6	B	70	0	0	1	0
All	All	6510	0	6373	51	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.

All (51) 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)
2:B:341:GLU:HG3	2:B:394:ILE:HD11	1.51	0.93
2:B:23:THR:HG22	2:B:194:ALA:HB3	1.54	0.87
1:A:59:LYS:HG2	2:B:286:PRO:HA	1.68	0.75
2:B:376:ARG:HH11	2:B:376:ARG:HG2	1.52	0.74
1:A:369:LYS:HE2	1:A:375:GLN:HB3	1.77	0.66
1:A:251:VAL:HG21	1:A:383:VAL:HG21	1.83	0.60
1:A:208:HIS:HB3	1:A:410:PRO:HB2	1.82	0.60
1:A:225:MET:HE1	2:B:136:GLU:HA	1.83	0.59
2:B:376:ARG:HG2	2:B:376:ARG:NH1	2.19	0.57
1:A:392:LEU:HD12	1:A:396:PHE:CD2	2.41	0.55
2:B:252:VAL:HB	2:B:320:LEU:HD11	1.91	0.53
2:B:240:GLN:HG2	2:B:414:ILE:HB	1.90	0.53
2:B:279:LYS:HB2	2:B:284:VAL:HG23	1.91	0.53
2:B:10:PRO:HD3	2:B:379:TYR:CE2	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:225:MET:CE	2:B:136:GLU:HA	2.43	0.48
2:B:98:SER:OG	2:B:101:LYS:HE2	2.14	0.48
1:A:37:SER:HB3	1:A:42:ASP:CB	2.45	0.47
1:A:293:ASN:ND2	1:A:295:PHE:CZ	2.82	0.46
2:B:262:ASP:HB3	2:B:377:ASN:ND2	2.31	0.46
2:B:74:LEU:HD23	2:B:78:GLU:HG3	1.99	0.45
1:A:37:SER:HB3	1:A:42:ASP:HB3	1.97	0.45
1:A:152:LEU:HB2	1:A:155:GLU:HG3	1.98	0.45
1:A:223:ILE:HD12	2:B:141:ILE:HD11	1.99	0.45
1:A:20:PRO:HG2	2:B:4:ILE:HG22	1.99	0.45
2:B:48:ASN:HA	2:B:176:MET:HE3	1.98	0.45
1:A:69:PHE:CE2	1:A:71:GLN:HB2	2.52	0.44
2:B:285:SER:HB3	2:B:288:ILE:HG12	2.00	0.44
1:A:235:SER:HB2	1:A:401:ALA:HB3	2.00	0.43
2:B:313:GLY:HA2	6:B:633:HOH:O	2.18	0.43
2:B:60:PHE:CZ	2:B:82:LEU:HB3	2.53	0.43
2:B:273:LYS:HG2	2:B:298:SER:HB3	2.00	0.43
1:A:393:LYS:O	1:A:397:SER:OG	2.35	0.43
2:B:35:TYR:HD1	2:B:190:LEU:HD13	1.83	0.43
2:B:262:ASP:HB3	2:B:377:ASN:HD21	1.84	0.42
2:B:382:LEU:H	2:B:382:LEU:HG	1.67	0.42
1:A:317:ALA:HB2	1:A:413:ILE:HG23	2.00	0.42
1:A:404:VAL:HG11	1:A:408:ALA:HB3	2.01	0.42
1:A:258:GLY:HA3	1:A:289:ALA:O	2.20	0.42
1:A:10:ASN:ND2	1:A:190:LEU:O	2.51	0.42
2:B:111:GLN:O	2:B:115:ASN:HB3	2.20	0.42
2:B:36:TRP:HB3	2:B:374:LEU:HD11	2.02	0.42
1:A:64:HIS:HB3	1:A:87:SER:OG	2.20	0.42
1:A:236:TRP:CE2	1:A:400:PRO:HB3	2.55	0.42
2:B:294:ARG:N	2:B:315:GLU:OE2	2.48	0.42
1:A:58:PRO:HA	2:B:282:TYR:O	2.21	0.41
1:A:58:PRO:HB2	2:B:284:VAL:HG12	2.03	0.41
1:A:48:SER:O	1:A:52:VAL:HG13	2.20	0.41
2:B:66:TYR:CZ	2:B:108:VAL:HG22	2.55	0.41
2:B:9:VAL:HA	2:B:10:PRO:HD3	2.01	0.41
1:A:254:LYS:HD3	1:A:254:LYS:HA	1.87	0.41
2:B:273:LYS:HE3	2:B:273:LYS:HB3	1.80	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	390/431 (90%)	364 (93%)	26 (7%)	0	100	100
2	B	414/419 (99%)	391 (94%)	21 (5%)	2 (0%)	25	40
All	All	804/850 (95%)	755 (94%)	47 (6%)	2 (0%)	44	61

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	9	VAL
2	B	377	ASN

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	344/371 (93%)	320 (93%)	24 (7%)	12	21
2	B	371/375 (99%)	342 (92%)	29 (8%)	10	17
All	All	715/746 (96%)	662 (93%)	53 (7%)	11	19

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	SER
1	A	7	VAL
1	A	100	ASP
1	A	114	GLN

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Mol	Chain	Res	Type
1	A	128	LEU
1	A	137	MET
1	A	141	SER
1	A	171	THR
1	A	177	ILE
1	A	196	VAL
1	A	198	LEU
1	A	216	SER
1	A	217[A]	SER
1	A	217[B]	SER
1	A	283	VAL
1	A	285	ARG
1	A	311	ARG
1	A	322	GLU
1	A	326	SER
1	A	329	THR
1	A	355	LYS
1	A	369	LYS
1	A	371	ILE
1	A	418	GLU
2	B	6	ARG
2	B	7	TYR
2	B	26	VAL
2	B	60	PHE
2	B	69	ARG
2	B	70	LYS
2	B	78	GLU
2	B	98	SER
2	B	101	LYS
2	B	120	LYS
2	B	133	GLU
2	B	134	GLU
2	B	163	LEU
2	B	168	SER
2	B	212	GLN
2	B	238	GLN
2	B	279	LYS
2	B	280	GLU
2	B	281	LYS
2	B	355	LEU
2	B	365	ILE
2	B	368	GLU

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Mol	Chain	Res	Type
2	B	376	ARG
2	B	377	ASN
2	B	381	SER
2	B	382	LEU
2	B	386	ASP
2	B	398	LYS
2	B	402	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	44	GLN
1	A	106	ASN
1	A	114	GLN
1	A	149	ASN
1	A	199	HIS
1	A	203	ASN
1	A	287	HIS
1	A	358	ASN
1	A	411	ASN
2	B	56	GLN
2	B	73	GLN
2	B	94	ASN
2	B	142	ASN
2	B	167	GLN
2	B	238	GLN
2	B	329	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 9 ligands modelled in this entry, 1 is monoatomic - leaving 8 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	503	-	4,4,4	0.40	0	6,6,6	0.26	0
3	SO4	B	504	-	4,4,4	0.39	0	6,6,6	0.26	0
3	SO4	A	504	-	4,4,4	0.45	0	6,6,6	0.32	0
3	SO4	A	501	-	4,4,4	0.41	0	6,6,6	0.34	0
3	SO4	B	503	-	4,4,4	0.39	0	6,6,6	0.56	0
3	SO4	A	502	-	4,4,4	0.35	0	6,6,6	0.24	0
4	GOL	A	505	-	5,5,5	0.24	0	5,5,5	0.47	0
3	SO4	B	502	-	4,4,4	0.51	0	6,6,6	0.52	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	GOL	A	505	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	393/431 (91%)	-0.06	22 (5%) 31 29	26, 55, 102, 119	3 (0%)
2	B	416/419 (99%)	-0.54	6 (1%) 73 71	27, 44, 74, 113	0
All	All	809/850 (95%)	-0.31	28 (3%) 47 44	26, 49, 95, 119	3 (0%)

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	341	LEU	4.4
2	B	419	GLN	4.1
1	A	284	ALA	4.0
1	A	355	LYS	3.8
2	B	7	TYR	3.3
1	A	330	ILE	3.3
2	B	382	LEU	3.3
1	A	367	GLY	3.1
2	B	8	ALA	3.0
1	A	377	LYS	2.8
1	A	333	LYS	2.8
1	A	374	SER	2.7
1	A	386	LYS	2.7
2	B	6	ARG	2.7
1	A	418	GLU	2.6
1	A	342	VAL	2.6
1	A	283	VAL	2.4
1	A	3	CYS	2.4
1	A	309	GLU	2.4
1	A	214	LYS	2.3
1	A	285	ARG	2.3
1	A	22	GLY	2.2
2	B	418	LYS	2.2
1	A	335	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	311	ARG	2.1
1	A	261	GLU	2.1
1	A	273	SER	2.0
1	A	279	VAL	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 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(\AA^2)	Q<0.9
3	SO4	A	502	5/5	0.80	0.15	116,119,132,138	0
3	SO4	B	502	5/5	0.80	0.16	77,82,103,110	0
3	SO4	A	504	5/5	0.85	0.21	56,58,64,65	5
3	SO4	B	503	5/5	0.88	0.19	85,94,100,102	0
4	GOL	A	505	6/6	0.89	0.17	65,67,69,80	0
3	SO4	A	501	5/5	0.90	0.08	94,97,102,107	0
3	SO4	A	503	5/5	0.93	0.11	76,82,93,95	0
3	SO4	B	504	5/5	0.95	0.11	80,88,99,101	0
5	ZN	B	501	1/1	0.99	0.02	44,44,44,44	0

6.5 Other polymers [i](#)

There are no such residues in this entry.