



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:47 AM UTC

PDB ID : 7QNO / pdb_00007qno
Title : Crystal structure of ligand-free Danio rerio HDAC6 CD1 CD2
Authors : Kempf, G.; Langousis, G.; Sanchez, J.; Matthias, P.
Deposited on : 2021-12-21
Resolution : 2.38 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

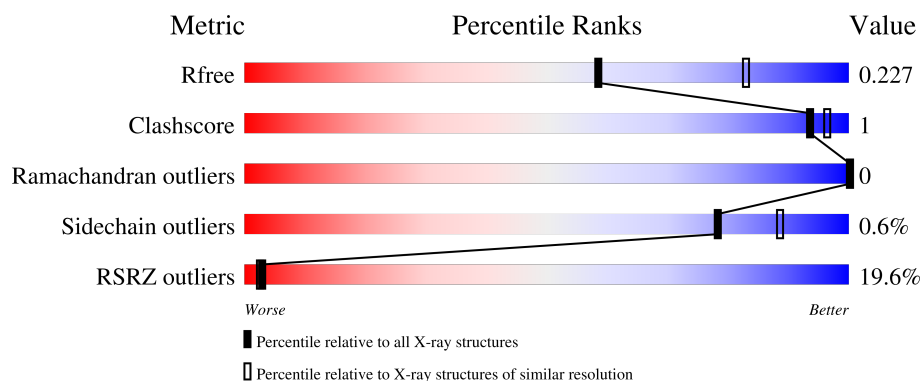
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.38 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	7164 (2.40-2.36)
Clashscore	190562	7722 (2.40-2.36)
Ramachandran outliers	187476	7626 (2.40-2.36)
Sidechain outliers	187428	7627 (2.40-2.36)
RSRZ outliers	180081	7170 (2.40-2.36)

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	837	18% 87% 10%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 11771 atoms, of which 5818 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 Histone deacetylase 6.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	755	Total	C	H	N	O	S	5851	8	0
			11651	3718	5763	1029	1102	39			

There are 45 discrepancies between the modelled and reference sequences:

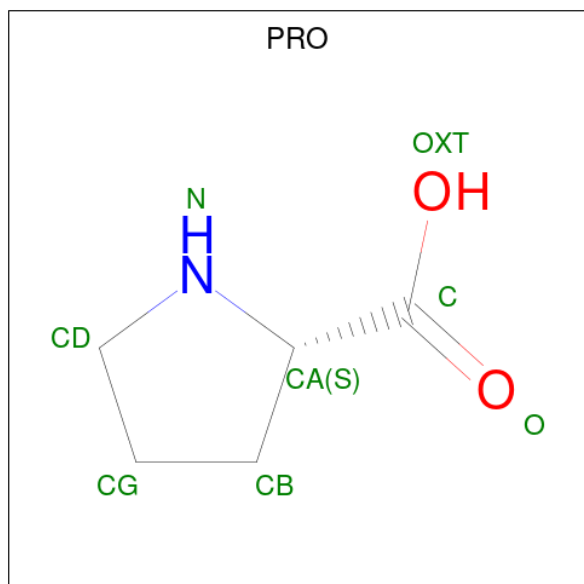
Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	MET	-	initiating methionine	UNP F8W4B7
A	-4	ASP	-	expression tag	UNP F8W4B7
A	-3	SER	-	expression tag	UNP F8W4B7
A	-2	ALA	-	expression tag	UNP F8W4B7
A	-1	TRP	-	expression tag	UNP F8W4B7
A	0	SER	-	expression tag	UNP F8W4B7
A	1	HIS	-	expression tag	UNP F8W4B7
A	2	PRO	-	expression tag	UNP F8W4B7
A	3	GLN	-	expression tag	UNP F8W4B7
A	4	PHE	-	expression tag	UNP F8W4B7
A	5	GLU	-	expression tag	UNP F8W4B7
A	6	LYS	-	expression tag	UNP F8W4B7
A	7	GLY	-	expression tag	UNP F8W4B7
A	8	GLY	-	expression tag	UNP F8W4B7
A	9	GLY	-	expression tag	UNP F8W4B7
A	10	SER	-	expression tag	UNP F8W4B7
A	11	GLY	-	expression tag	UNP F8W4B7
A	12	GLY	-	expression tag	UNP F8W4B7
A	13	GLY	-	expression tag	UNP F8W4B7
A	14	SER	-	expression tag	UNP F8W4B7
A	15	GLY	-	expression tag	UNP F8W4B7
A	16	GLY	-	expression tag	UNP F8W4B7
A	17	SER	-	expression tag	UNP F8W4B7
A	18	ALA	-	expression tag	UNP F8W4B7
A	19	TRP	-	expression tag	UNP F8W4B7
A	20	SER	-	expression tag	UNP F8W4B7
A	21	HIS	-	expression tag	UNP F8W4B7

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Chain	Residue	Modelled	Actual	Comment	Reference
A	22	PRO	-	expression tag	UNP F8W4B7
A	23	GLN	-	expression tag	UNP F8W4B7
A	24	PHE	-	expression tag	UNP F8W4B7
A	25	GLU	-	expression tag	UNP F8W4B7
A	26	LYS	-	expression tag	UNP F8W4B7
A	27	SER	-	expression tag	UNP F8W4B7
A	28	ALA	-	expression tag	UNP F8W4B7
A	29	VAL	-	expression tag	UNP F8W4B7
A	30	ASP	-	expression tag	UNP F8W4B7
A	31	LEU	-	expression tag	UNP F8W4B7
A	32	GLU	-	expression tag	UNP F8W4B7
A	33	VAL	-	expression tag	UNP F8W4B7
A	34	LEU	-	expression tag	UNP F8W4B7
A	35	PHE	-	expression tag	UNP F8W4B7
A	36	GLN	-	expression tag	UNP F8W4B7
A	37	GLY	-	expression tag	UNP F8W4B7
A	38	PRO	-	expression tag	UNP F8W4B7
A	39	GLY	-	expression tag	UNP F8W4B7

- Molecule 2 is PROLINE (CCD ID: PRO) (formula: $C_5H_9NO_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	H	N	O	7	0
			14	5	7	1	1		

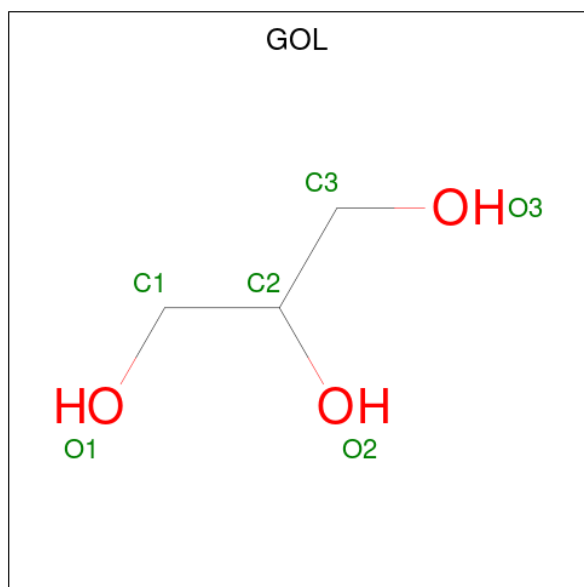
- Molecule 3 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	4	Total K 4 4	0	0

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Zn 1 1	0	0

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C H O 14 3 8 3	8	0
5	A	1	Total C H O 14 3 8 3	8	0
5	A	1	Total C H O 14 3 8 3	8	0
5	A	1	Total C H O 14 3 8 3	8	0
5	A	1	Total C H O 14 3 8 3	8	0
5	A	1	Total C H O 14 3 8 3	8	0

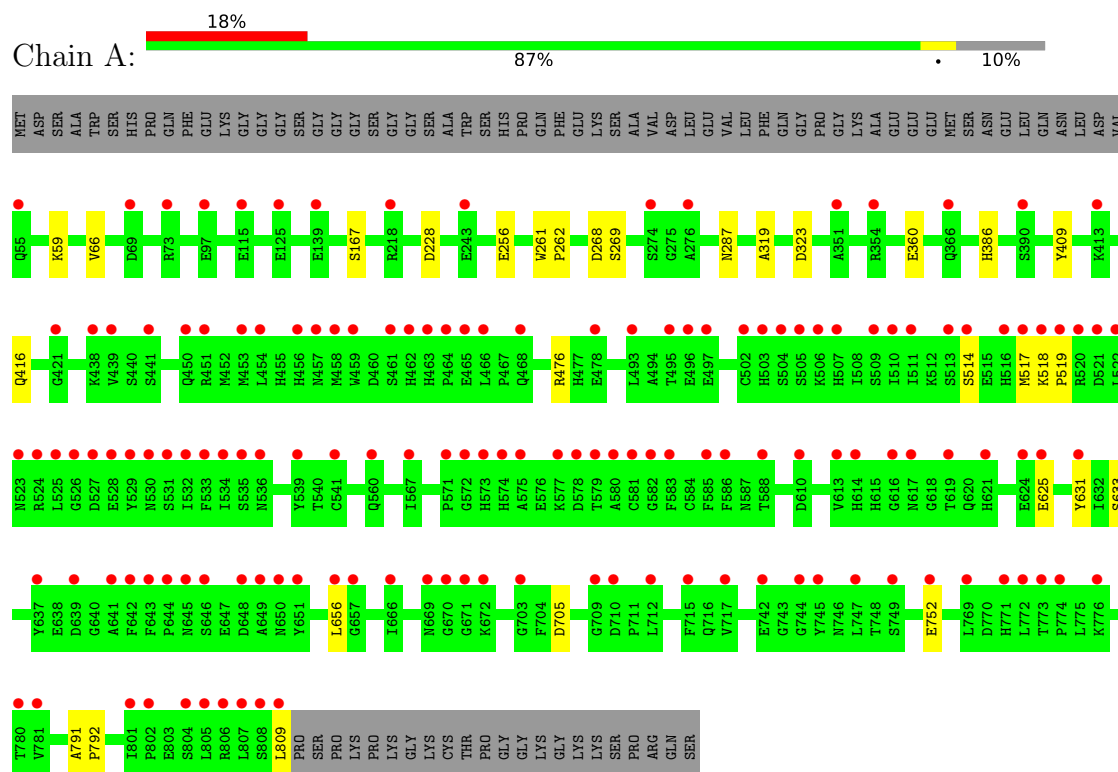
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	17	Total	O	0	0
			17	17		

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: Histone deacetylase 6



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	186.13Å 186.13Å 102.44Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	63.34 – 2.38 63.34 – 2.38	Depositor EDS
% Data completeness (in resolution range)	53.6 (63.34-2.38) 53.8 (63.34-2.38)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.38 (at 2.37Å)	Xtriage
Refinement program	PHENIX (1.19.1_4122: ???), ISOLDE	Depositor
R, R_{free}	0.212 , 0.228 0.212 , 0.227	Depositor DCC
R_{free} test set	2217 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	56.6	Xtriage
Anisotropy	0.100	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 53.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.032 for -h,-k,l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	11771	wwPDB-VP
Average B, all atoms (Å ²)	82.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.18% 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: K, 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	0.18	0/6059	0.39	0/8222

There are no bond length outliers.

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	5888	5763	5734	16	0
2	A	7	7	7	2	0
3	A	4	0	0	0	0
4	A	1	0	0	0	0
5	A	36	48	48	0	0
6	A	17	0	0	0	0
All	All	5953	5818	5789	16	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 1.

All (16) 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:A:476:ARG:NE	1:A:752:GLU:OE2	2.43	0.52
1:A:268:ASP:OD1	1:A:269:SER:N	2.44	0.51
1:A:791:ALA:N	1:A:792:PRO:HD2	2.26	0.51
1:A:809:LEU:C	2:A:901:PRO:N	2.69	0.50
1:A:809:LEU:C	1:A:809:LEU:HD12	2.37	0.49
1:A:319:ALA:HB1	1:A:360:GLU:HG3	1.94	0.49
1:A:66:VAL:HG11	1:A:167:SER:HB2	1.94	0.48
1:A:625:GLU:HA	1:A:656:LEU:O	2.14	0.47
1:A:409:TYR:CE1	1:A:416:GLN:HA	2.51	0.45
1:A:631:TYR:CZ	1:A:633:SER:HB2	2.53	0.44
1:A:809:LEU:HA	2:A:901:PRO:HD2	1.98	0.44
1:A:228:ASP:HA	1:A:319:ALA:HB3	1.99	0.44
1:A:514:SER:HA	1:A:517:MET:HB2	2.00	0.44
1:A:256:GLU:HA	1:A:287:ASN:HA	2.00	0.42
1:A:518:LYS:HB3	1:A:519:PRO:HD2	2.01	0.42
1:A:261:TRP:CG	1:A:262:PRO:HA	2.56	0.41

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	761/837 (91%)	733 (96%)	28 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	645/703 (92%)	641 (99%)	4 (1%)	78 88

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	59	LYS
1	A	323	ASP
1	A	386	HIS
1	A	705	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	170	GLN
1	A	216	GLN
1	A	312	GLN
1	A	386	HIS
1	A	573	HIS
1	A	771	HIS

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 12 ligands modelled in this entry, 5 are monoatomic - leaving 7 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	$\# Z > 2$
5	GOL	A	907	-	5,5,5	0.73	0	5,5,5	0.91	0
5	GOL	A	908	-	5,5,5	0.92	0	5,5,5	1.02	0
5	GOL	A	911	-	5,5,5	0.83	0	5,5,5	1.06	0
2	PRO	A	901	-	6,7,8	0.49	0	7,8,10	1.37	1 (14%)
5	GOL	A	909	-	5,5,5	0.82	0	5,5,5	0.91	0
5	GOL	A	912	-	5,5,5	0.93	0	5,5,5	1.09	0
5	GOL	A	910	-	5,5,5	0.84	0	5,5,5	1.03	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
5	GOL	A	907	-	-	0/4/4/4	-
5	GOL	A	908	-	-	2/4/4/4	-
5	GOL	A	911	-	-	0/4/4/4	-
2	PRO	A	901	-	-	0/0/9/11	0/1/1/1
5	GOL	A	909	-	-	0/4/4/4	-
5	GOL	A	912	-	-	2/4/4/4	-
5	GOL	A	910	-	-	2/4/4/4	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	A	901	PRO	O-C-CA	-2.46	118.45	124.77

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	908	GOL	C1-C2-C3-O3
5	A	912	GOL	C1-C2-C3-O3

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Mol	Chain	Res	Type	Atoms
5	A	910	GOL	O1-C1-C2-C3
5	A	908	GOL	O2-C2-C3-O3
5	A	912	GOL	O2-C2-C3-O3
5	A	910	GOL	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	901	PRO	2	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	755/837 (90%)	1.13	148 (19%) 3 2	13, 35, 60, 85	25 (3%)

All (148) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	459	TRP	6.8
1	A	809	LEU	6.5
1	A	518	LYS	5.8
1	A	807	LEU	5.8
1	A	585	PHE	5.6
1	A	458	MET	5.6
1	A	656	LEU	5.5
1	A	505[A]	SER	5.1
1	A	520	ARG	5.0
1	A	519	PRO	5.0
1	A	581	CYS	4.9
1	A	802	PRO	4.8
1	A	218[A]	ARG	4.7
1	A	805	LEU	4.5
1	A	801	ILE	4.5
1	A	536	ASN	4.3
1	A	577	LYS	4.2
1	A	781	VAL	4.2
1	A	530	ASN	4.2
1	A	666	ILE	4.1
1	A	463	HIS	4.0
1	A	527	ASP	4.0
1	A	461	SER	4.0
1	A	617	ASN	4.0
1	A	513	SER	4.0
1	A	579	THR	3.9
1	A	583	PHE	3.9

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Mol	Chain	Res	Type	RSRZ
1	A	588	THR	3.8
1	A	528	GLU	3.8
1	A	539	TYR	3.8
1	A	524	ARG	3.8
1	A	450	GLN	3.8
1	A	642	PHE	3.8
1	A	646	SER	3.7
1	A	366[A]	GLN	3.7
1	A	517	MET	3.7
1	A	525	LEU	3.6
1	A	578	ASP	3.6
1	A	531	SER	3.5
1	A	516	HIS	3.4
1	A	532	ILE	3.4
1	A	580	ALA	3.4
1	A	497	GLU	3.4
1	A	534	ILE	3.3
1	A	456	HIS	3.3
1	A	616	GLY	3.3
1	A	457	ASN	3.2
1	A	745	TYR	3.2
1	A	771	HIS	3.2
1	A	806	ARG	3.2
1	A	510	ILE	3.2
1	A	643	PHE	3.1
1	A	533	PHE	3.1
1	A	526	GLY	3.1
1	A	468	GLN	3.1
1	A	644	PRO	3.1
1	A	506[A]	LYS	3.1
1	A	649	ALA	3.1
1	A	462	HIS	3.0
1	A	529	TYR	3.0
1	A	582	GLY	3.0
1	A	521	ASP	2.9
1	A	614	HIS	2.9
1	A	639	ASP	2.9
1	A	55	GLN	2.9
1	A	522	LEU	2.8
1	A	575	ALA	2.8
1	A	637	TYR	2.8
1	A	441	SER	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	541	CYS	2.8
1	A	613	VAL	2.8
1	A	560	GLN	2.7
1	A	495	THR	2.7
1	A	631	TYR	2.7
1	A	523	ASN	2.7
1	A	703	GLY	2.7
1	A	69	ASP	2.6
1	A	650	ASN	2.6
1	A	535	SER	2.6
1	A	717	VAL	2.6
1	A	709	GLY	2.6
1	A	744	GLY	2.6
1	A	502	CYS	2.6
1	A	808	SER	2.6
1	A	438	LYS	2.6
1	A	97	GLU	2.6
1	A	276	ALA	2.6
1	A	572	GLY	2.6
1	A	573	HIS	2.6
1	A	465	GLU	2.5
1	A	451	ARG	2.5
1	A	669	ASN	2.5
1	A	672	LYS	2.5
1	A	493	LEU	2.5
1	A	73	ARG	2.5
1	A	454	LEU	2.5
1	A	772	LEU	2.5
1	A	351	ALA	2.5
1	A	747	LEU	2.5
1	A	511	ILE	2.4
1	A	645	ASN	2.4
1	A	641	ALA	2.4
1	A	139	GLU	2.4
1	A	742	GLU	2.4
1	A	619	THR	2.4
1	A	774	PRO	2.4
1	A	651	TYR	2.3
1	A	671	GLY	2.3
1	A	507	HIS	2.3
1	A	574	HIS	2.3
1	A	712	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	780	THR	2.3
1	A	514	SER	2.3
1	A	625	GLU	2.3
1	A	413	LYS	2.3
1	A	421	GLY	2.3
1	A	115	GLU	2.3
1	A	354	ARG	2.3
1	A	509	SER	2.3
1	A	567	ILE	2.3
1	A	496	GLU	2.2
1	A	657	GLY	2.2
1	A	769	LEU	2.2
1	A	503	HIS	2.2
1	A	773	THR	2.2
1	A	586	PHE	2.2
1	A	710	ASP	2.2
1	A	571	PRO	2.2
1	A	749	SER	2.2
1	A	804	SER	2.2
1	A	439	VAL	2.1
1	A	752	GLU	2.1
1	A	624	GLU	2.1
1	A	648	ASP	2.1
1	A	464	PRO	2.1
1	A	670	GLY	2.1
1	A	478	GLU	2.1
1	A	715	PHE	2.1
1	A	243	GLU	2.0
1	A	466	LEU	2.0
1	A	125	GLU	2.0
1	A	453	MET	2.0
1	A	274	SER	2.0
1	A	390	SER	2.0
1	A	504	SER	2.0
1	A	621	HIS	2.0
1	A	610	ASP	2.0
1	A	776	LYS	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($\text{\AA}^2$)	Q<0.9
5	GOL	A	910	6/6	0.68	0.28	73,89,96,101	8
5	GOL	A	907	6/6	0.76	0.29	70,86,97,98	8
2	PRO	A	901	7/8	0.77	0.35	116,130,142,158	7
5	GOL	A	909	6/6	0.82	0.26	54,67,87,87	8
5	GOL	A	912	6/6	0.86	0.20	67,82,91,92	8
5	GOL	A	908	6/6	0.88	0.18	74,90,105,105	8
3	K	A	905	1/1	0.88	0.16	95,95,95,95	0
4	ZN	A	904	1/1	0.90	0.09	99,99,99,99	0
3	K	A	902	1/1	0.90	0.10	60,60,60,60	0
3	K	A	903	1/1	0.91	0.20	72,72,72,72	0
3	K	A	906	1/1	0.92	0.16	81,81,81,81	0
5	GOL	A	911	6/6	0.93	0.15	58,71,78,80	14

6.5 Other polymers [i](#)

There are no such residues in this entry.