



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 05:19 PM UTC

PDB ID : 4HTZ / pdb_00004htz
Title : Crystal structure of PDE2 catalytic domain in space group P1
Authors : Zhu, J.; Huang, Q.
Deposited on : 2012-11-02
Resolution : 2.00 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
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

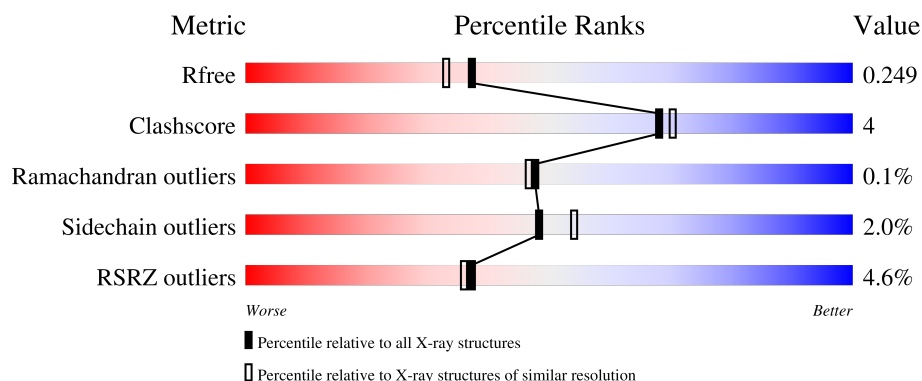
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	342	4% 90% 8% ..
1	B	342	4% 88% 10% .
1	C	342	4% 85% 10% 5%
1	D	342	6% 87% 8% 5%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 11502 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 cGMP-dependent 3',5'-cyclic phosphodiesterase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	338	Total	C	N	O	S	0	2	0
			2712	1738	456	492	26			
1	B	337	Total	C	N	O	S	0	2	0
			2712	1736	460	491	25			
1	C	325	Total	C	N	O	S	0	1	0
			2571	1656	434	456	25			
1	D	326	Total	C	N	O	S	0	1	0
			2610	1672	444	469	25			

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		
2	B	1	Total	Zn	0	0
			1	1		
2	C	1	Total	Zn	0	0
			1	1		
2	D	1	Total	Zn	0	0
			1	1		

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		
3	B	1	Total	Mg	0	0
			1	1		
3	C	1	Total	Mg	0	0
			1	1		
3	D	1	Total	Mg	0	0
			1	1		

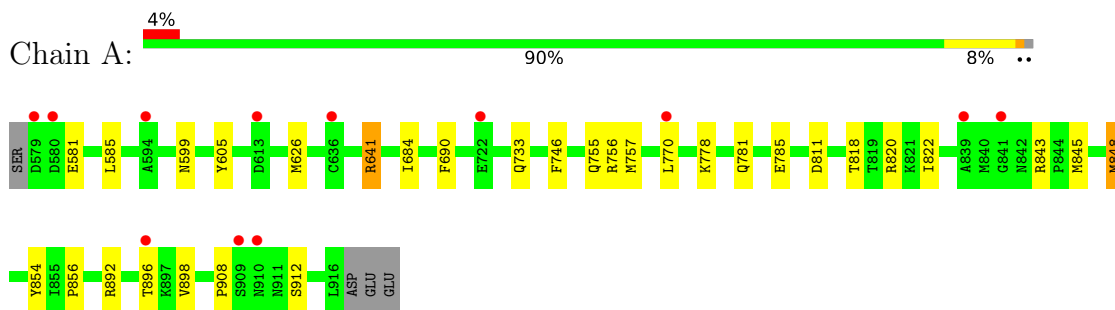
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	268	Total 268	O 268	0	0
4	B	241	Total 241	O 241	0	0
4	C	190	Total 190	O 190	0	0
4	D	190	Total 190	O 190	0	0

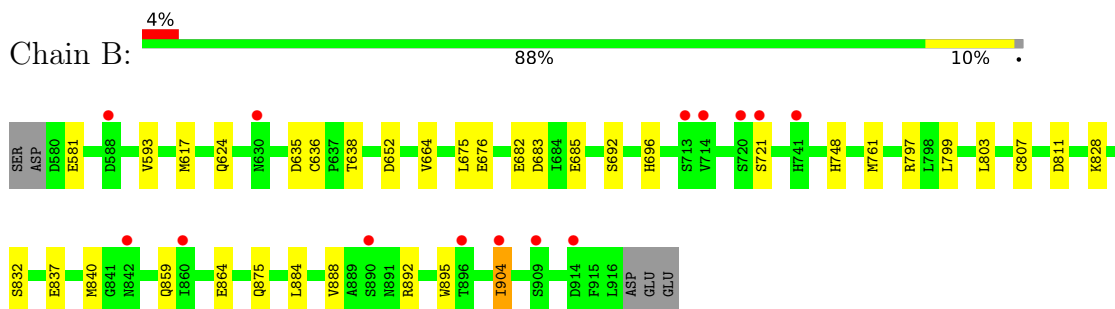
3 Residue-property plots [i](#)

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.

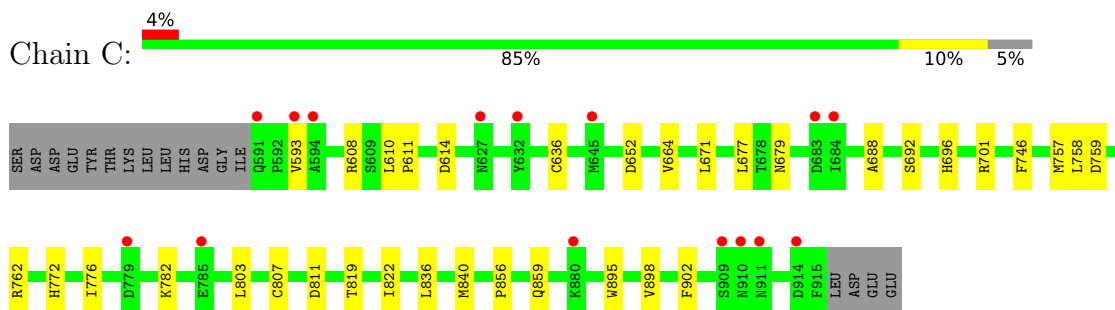
- Molecule 1: cGMP-dependent 3',5'-cyclic phosphodiesterase



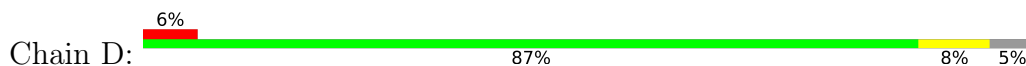
- Molecule 1: cGMP-dependent 3',5'-cyclic phosphodiesterase

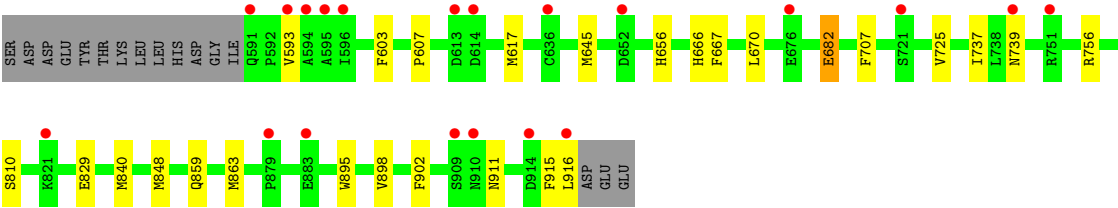


- Molecule 1: cGMP-dependent 3',5'-cyclic phosphodiesterase



- Molecule 1: cGMP-dependent 3',5'-cyclic phosphodiesterase





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	56.19Å 73.87Å 92.61Å 109.68° 91.71° 90.91°	Depositor
Resolution (Å)	33.81 – 2.00 33.81 – 2.00	Depositor EDS
% Data completeness (in resolution range)	92.6 (33.81-2.00) 87.9 (33.81-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.18 (at 2.00Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.1_743)	Depositor
R, R_{free}	0.188 , 0.249 0.190 , 0.249	Depositor DCC
R_{free} test set	4441 reflections (4.69%)	wwPDB-VP
Wilson B-factor (Å ²)	14.3	Xtriage
Anisotropy	0.337	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 58.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.028 for h,-k,-l	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	11502	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.20% 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: ZN, MG

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	0.54	0/2779	0.80	2/3759 (0.1%)
1	B	0.50	0/2779	0.79	4/3760 (0.1%)
1	C	0.48	0/2636	0.78	2/3566 (0.1%)
1	D	0.49	0/2675	0.76	1/3620 (0.0%)
All	All	0.50	0/10869	0.78	9/14705 (0.1%)

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	652	ASP	CA-C-N	-6.37	113.82	120.38
1	B	652	ASP	C-N-CA	-6.37	113.82	120.38
1	C	652	ASP	CA-C-N	-5.65	114.56	120.38
1	C	652	ASP	C-N-CA	-5.65	114.56	120.38
1	A	843	ARG	CA-C-N	5.35	125.25	119.85
1	A	843	ARG	C-N-CA	5.35	125.25	119.85
1	B	636	CYS	CA-C-N	-5.28	113.19	119.05
1	B	636	CYS	C-N-CA	-5.28	113.19	119.05
1	D	725	VAL	N-CA-C	5.04	115.47	110.23

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	2712	0	2598	20	0
1	B	2712	0	2594	20	0
1	C	2571	0	2461	20	0
1	D	2610	0	2509	17	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	268	0	0	9	0
4	B	241	0	0	6	0
4	C	190	0	0	4	0
4	D	190	0	0	3	0
All	All	11502	0	10162	75	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 (75) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:685:GLU:OE2	4:B:1226:HOH:O	2.11	0.69
1:D:682:GLU:OE2	1:D:756:ARG:NH2	2.29	0.66
1:A:756:ARG:NH1	4:A:1261:HOH:O	2.26	0.59
1:A:845:MET:HB2	1:A:848:MET:HG3	1.84	0.59
1:C:811:ASP:OD2	4:C:1137:HOH:O	2.18	0.57
1:D:859:GLN:HG2	1:D:895:TRP:CE2	2.40	0.56
1:B:864:GLU:OE2	1:B:892:ARG:NH2	2.38	0.56
1:A:733:GLN:NE2	4:A:1179:HOH:O	2.36	0.56
1:C:688:ALA:HA	1:C:757:MET:HE1	1.88	0.56
1:A:811:ASP:HB3	1:A:822:ILE:HG13	1.87	0.55
1:B:837:GLU:HA	1:B:840:MET:HE2	1.88	0.55
1:A:755:GLN:NE2	4:A:1292:HOH:O	2.36	0.55
1:C:819:THR:CG2	1:C:895:TRP:HE1	2.19	0.54
1:B:859:GLN:HG2	1:B:895:TRP:CE2	2.42	0.54
1:C:671:LEU:HD13	1:C:803:LEU:HD22	1.89	0.54
1:D:656:HIS:ND1	1:D:829:GLU:OE1	2.35	0.53
1:B:828[A]:LYS:HE2	1:D:911:ASN:HB3	1.91	0.53
1:A:892:ARG:NH1	1:A:896:THR:OG1	2.42	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:915:PHE:O	1:D:916:LEU:HB2	2.09	0.51
1:D:911:ASN:ND2	4:D:1159:HOH:O	2.41	0.51
1:A:746:PHE:CE2	1:A:757:MET:HG2	2.46	0.51
1:C:762:ARG:NH1	4:C:1278:HOH:O	2.43	0.51
1:A:599:ASN:O	1:A:605:TYR:HB2	2.11	0.51
1:B:811:ASP:OD2	4:B:1341:HOH:O	2.18	0.50
1:B:617:MET:HG3	4:B:1290:HOH:O	2.11	0.50
1:D:607:PRO:HG3	1:D:666:HIS:ND1	2.26	0.50
1:C:610:LEU:HD12	1:C:611:PRO:HD2	1.95	0.49
1:C:759:ASP:OD1	1:C:762:ARG:NH2	2.46	0.49
1:C:701:ARG:NH1	4:C:1259:HOH:O	2.44	0.48
1:D:859:GLN:O	1:D:863:MET:HG3	2.13	0.48
1:A:811:ASP:OD2	4:A:1252:HOH:O	2.20	0.48
1:A:641:ARG:HG2	4:A:1343:HOH:O	2.13	0.48
1:C:819:THR:HG21	1:C:895:TRP:HE1	1.79	0.47
1:B:675:LEU:O	1:B:676:GLU:HG2	2.14	0.47
1:C:611:PRO:HG2	1:C:614:ASP:OD2	2.13	0.47
1:B:664:VAL:HG13	1:B:807:CYS:HB3	1.97	0.46
1:A:684:ILE:HD12	1:A:684:ILE:HA	1.82	0.46
1:C:859:GLN:HG2	1:C:895:TRP:CE2	2.51	0.46
1:A:785:GLU:OE2	4:A:1324:HOH:O	2.21	0.45
1:A:818:THR:O	1:A:822:ILE:HG12	2.15	0.45
1:A:781:GLN:HG2	4:A:1328:HOH:O	2.16	0.45
1:A:854:TYR:CZ	1:A:856:PRO:HG2	2.51	0.45
1:A:778:LYS:HD2	1:A:781:GLN:OE1	2.17	0.45
1:B:624:GLN:HG3	4:B:1166:HOH:O	2.16	0.45
1:B:799:LEU:O	1:B:803:LEU:HG	2.17	0.45
1:B:859:GLN:HG2	1:B:895:TRP:CD2	2.53	0.44
1:A:581:GLU:OE2	4:A:1277:HOH:O	2.21	0.44
1:C:772:HIS:CE1	1:C:776:ILE:HD13	2.52	0.44
1:D:617:MET:HE3	1:D:617:MET:HB3	1.93	0.44
1:C:746:PHE:CZ	1:C:757:MET:HE2	2.52	0.44
1:D:756:ARG:NH1	4:D:1228:HOH:O	2.30	0.44
1:D:603:PHE:HA	1:D:670:LEU:HD13	2.00	0.43
1:B:635:ASP:OD2	1:B:638:THR:OG1	2.36	0.43
1:B:682:GLU:HG2	4:B:1185:HOH:O	2.19	0.43
1:D:607:PRO:HD2	4:D:1133:HOH:O	2.19	0.43
1:B:581:GLU:H	1:B:581:GLU:CD	2.27	0.43
1:D:848:MET:HB3	1:D:848:MET:HE3	1.69	0.43
1:B:904:ILE:HG22	1:D:902:PHE:O	2.19	0.42
1:C:819:THR:HG22	1:C:895:TRP:HE1	1.83	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:884:LEU:O	1:B:888:VAL:HG23	2.19	0.42
1:C:608:ARG:NH1	4:C:1107:HOH:O	2.52	0.42
1:D:667:PHE:CD1	1:D:810:SER:HB2	2.55	0.42
1:A:585:LEU:HA	4:A:1299:HOH:O	2.20	0.42
1:A:908:PRO:HG2	1:A:912:SER:O	2.20	0.41
1:B:748:HIS:HB3	4:B:1325:HOH:O	2.20	0.41
1:C:856:PRO:HG3	1:C:902:PHE:CD1	2.55	0.41
1:C:677:LEU:HD23	1:C:677:LEU:HA	1.88	0.41
1:D:707:PHE:CE1	1:D:840:MET:HE1	2.55	0.41
1:C:664:VAL:HG13	1:C:807:CYS:HB3	2.02	0.41
1:A:626:MET:HE1	1:A:690:PHE:CD1	2.56	0.41
1:D:645:MET:HG2	1:D:737:ILE:HG12	2.03	0.41
1:C:692:SER:O	1:C:696:HIS:HB3	2.20	0.41
1:B:761:MET:HE2	1:B:761:MET:HB3	1.99	0.40
1:C:836:LEU:O	1:C:840:MET:HG3	2.21	0.40
1:B:692:SER:O	1:B:696:HIS:HB3	2.21	0.40

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	338/342 (99%)	337 (100%)	1 (0%)	0	100	100
1	B	337/342 (98%)	327 (97%)	9 (3%)	1 (0%)	36	35
1	C	324/342 (95%)	322 (99%)	2 (1%)	0	100	100
1	D	325/342 (95%)	321 (99%)	4 (1%)	0	100	100
All	All	1324/1368 (97%)	1307 (99%)	16 (1%)	1 (0%)	48	46

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	721	SER

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	288/309 (93%)	283 (98%)	5 (2%)	53	60
1	B	286/309 (93%)	280 (98%)	6 (2%)	47	52
1	C	267/309 (86%)	260 (97%)	7 (3%)	40	44
1	D	277/309 (90%)	273 (99%)	4 (1%)	59	66
All	All	1118/1236 (90%)	1096 (98%)	22 (2%)	48	54

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	641	ARG
1	A	770	LEU
1	A	820	ARG
1	A	848	MET
1	A	898	VAL
1	B	593	VAL
1	B	683	ASP
1	B	797	ARG
1	B	832	SER
1	B	875	GLN
1	B	904	ILE
1	C	593	VAL
1	C	636	CYS
1	C	679	ASN
1	C	758	LEU
1	C	782	LYS
1	C	822	ILE
1	C	898	VAL
1	D	593	VAL
1	D	682	GLU
1	D	739	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	898	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	859	GLN
1	B	875	GLN
1	B	900	HIS
1	C	599	ASN
1	C	781	GLN
1	C	865	HIS
1	D	911	ASN

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 8 ligands modelled in this entry, 8 are monoatomic - leaving 0 for Mogul analysis.

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 [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	338/342 (98%)	0.40	12 (3%)	46 45	7, 23, 39, 50	2 (0%)
1	B	337/342 (98%)	0.62	14 (4%)	40 39	8, 26, 41, 61	2 (0%)
1	C	325/342 (95%)	0.53	15 (4%)	37 36	9, 26, 44, 58	1 (0%)
1	D	326/342 (95%)	0.60	20 (6%)	27 26	8, 27, 46, 65	1 (0%)
All	All	1326/1368 (96%)	0.54	61 (4%)	37 36	7, 25, 43, 65	6 (0%)

All (61) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	910	ASN	4.4
1	B	914	ASP	4.1
1	A	839	ALA	4.0
1	D	613	ASP	3.9
1	B	720	SER	3.9
1	C	909	SER	3.7
1	D	595	ALA	3.6
1	A	909	SER	3.2
1	D	821	LYS	3.2
1	D	909	SER	3.1
1	B	721	SER	3.0
1	C	632	TYR	3.0
1	D	914	ASP	3.0
1	B	714	VAL	3.0
1	B	630	ASN	2.9
1	B	909	SER	2.8
1	B	860	ILE	2.8
1	C	627	ASN	2.7
1	B	896	THR	2.7
1	B	842	ASN	2.7
1	D	910	ASN	2.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	594	ALA	2.6
1	D	916	LEU	2.6
1	C	911	ASN	2.6
1	A	896	THR	2.6
1	B	890	SER	2.6
1	D	593	VAL	2.5
1	A	910	ASN	2.5
1	D	751	ARG	2.5
1	C	785	GLU	2.5
1	B	904	ILE	2.5
1	D	652	ASP	2.5
1	D	879	PRO	2.5
1	A	594	ALA	2.5
1	B	741	HIS	2.4
1	C	684	ILE	2.4
1	D	636	CYS	2.4
1	D	594	ALA	2.4
1	A	580	ASP	2.4
1	A	636	CYS	2.4
1	D	883	GLU	2.3
1	A	770	LEU	2.3
1	C	645	MET	2.3
1	D	721	SER	2.3
1	D	614	ASP	2.3
1	A	613	ASP	2.3
1	C	593	VAL	2.2
1	A	841	GLY	2.2
1	C	779	ASP	2.2
1	B	588	ASP	2.2
1	C	914	ASP	2.2
1	D	596	ILE	2.1
1	C	880	LYS	2.1
1	D	739	ASN	2.1
1	A	579	ASP	2.1
1	D	591	GLN	2.1
1	B	713	SER	2.1
1	D	676	GLU	2.1
1	C	683	ASP	2.1
1	A	722	GLU	2.0
1	C	591	GLN	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
3	MG	A	1002	1/1	0.90	0.06	11,11,11,11	0
3	MG	B	1002	1/1	0.90	0.09	15,15,15,15	0
3	MG	D	1002	1/1	0.97	0.03	11,11,11,11	0
3	MG	C	1002	1/1	0.98	0.03	12,12,12,12	0
2	ZN	B	1001	1/1	0.99	0.03	16,16,16,16	0
2	ZN	C	1001	1/1	0.99	0.02	16,16,16,16	0
2	ZN	A	1001	1/1	1.00	0.01	15,15,15,15	0
2	ZN	D	1001	1/1	1.00	0.03	18,18,18,18	0

6.5 Other polymers [i](#)

There are no such residues in this entry.