



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 12:39 PM UTC

PDB ID : 4Q92 / pdb_00004q92
Title : 1.90 Angstrom resolution crystal structure of apo betaine aldehyde dehydrogenase (betB) G234S mutant from *Staphylococcus aureus* (IDP00699) with BME-modified Cys289
Authors : Halavaty, A.S.; Minasov, G.; Chen, C.; Joo, J.C.; Yakunin, A.F.; Anderson, W.F.; Center for Structural Genomics of Infectious Diseases (CSGID)
Deposited on : 2014-04-28
Resolution : 1.90 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

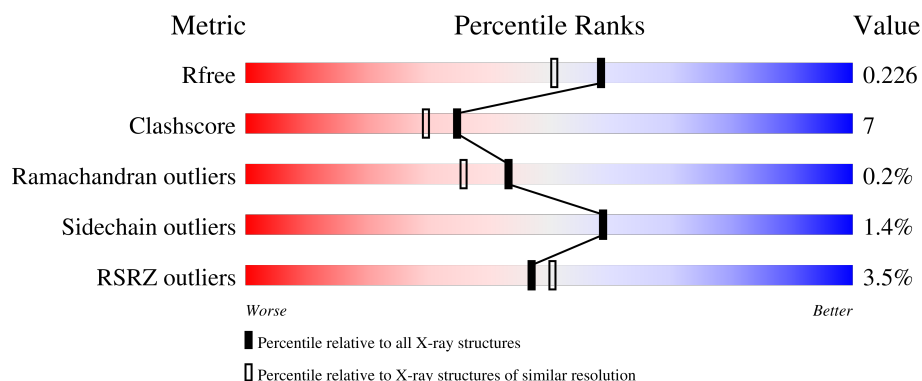
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	517	2% 85% 11% .
1	B	517	5% 85% 10% ..
1	C	517	3% 86% 9% ..
1	D	517	4% 86% 9% ..

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 17730 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 Betaine aldehyde dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	497	Total	C	N	O	S	0	20	0
			4042	2546	681	799	16			
1	B	497	Total	C	N	O	S	0	16	0
			3995	2518	677	784	16			
1	C	496	Total	C	N	O	S	0	17	0
			3990	2510	675	790	15			
1	D	501	Total	C	N	O	S	0	20	0
			4069	2563	686	804	16			

There are 88 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-20	MET	-	expression tag	UNP Q5HCU0
A	-19	GLY	-	expression tag	UNP Q5HCU0
A	-18	SER	-	expression tag	UNP Q5HCU0
A	-17	SER	-	expression tag	UNP Q5HCU0
A	-16	HIS	-	expression tag	UNP Q5HCU0
A	-15	HIS	-	expression tag	UNP Q5HCU0
A	-14	HIS	-	expression tag	UNP Q5HCU0
A	-13	HIS	-	expression tag	UNP Q5HCU0
A	-12	HIS	-	expression tag	UNP Q5HCU0
A	-11	HIS	-	expression tag	UNP Q5HCU0
A	-10	SER	-	expression tag	UNP Q5HCU0
A	-9	SER	-	expression tag	UNP Q5HCU0
A	-8	GLY	-	expression tag	UNP Q5HCU0
A	-7	ARG	-	expression tag	UNP Q5HCU0
A	-6	GLU	-	expression tag	UNP Q5HCU0
A	-5	ASN	-	expression tag	UNP Q5HCU0
A	-4	LEU	-	expression tag	UNP Q5HCU0
A	-3	TYR	-	expression tag	UNP Q5HCU0
A	-2	PHE	-	expression tag	UNP Q5HCU0
A	-1	GLN	-	expression tag	UNP Q5HCU0
A	0	GLY	-	expression tag	UNP Q5HCU0

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Chain	Residue	Modelled	Actual	Comment	Reference
A	234	SER	GLY	engineered mutation	UNP Q5HCU0
B	-20	MET	-	expression tag	UNP Q5HCU0
B	-19	GLY	-	expression tag	UNP Q5HCU0
B	-18	SER	-	expression tag	UNP Q5HCU0
B	-17	SER	-	expression tag	UNP Q5HCU0
B	-16	HIS	-	expression tag	UNP Q5HCU0
B	-15	HIS	-	expression tag	UNP Q5HCU0
B	-14	HIS	-	expression tag	UNP Q5HCU0
B	-13	HIS	-	expression tag	UNP Q5HCU0
B	-12	HIS	-	expression tag	UNP Q5HCU0
B	-11	HIS	-	expression tag	UNP Q5HCU0
B	-10	SER	-	expression tag	UNP Q5HCU0
B	-9	SER	-	expression tag	UNP Q5HCU0
B	-8	GLY	-	expression tag	UNP Q5HCU0
B	-7	ARG	-	expression tag	UNP Q5HCU0
B	-6	GLU	-	expression tag	UNP Q5HCU0
B	-5	ASN	-	expression tag	UNP Q5HCU0
B	-4	LEU	-	expression tag	UNP Q5HCU0
B	-3	TYR	-	expression tag	UNP Q5HCU0
B	-2	PHE	-	expression tag	UNP Q5HCU0
B	-1	GLN	-	expression tag	UNP Q5HCU0
B	0	GLY	-	expression tag	UNP Q5HCU0
B	234	SER	GLY	engineered mutation	UNP Q5HCU0
C	-20	MET	-	expression tag	UNP Q5HCU0
C	-19	GLY	-	expression tag	UNP Q5HCU0
C	-18	SER	-	expression tag	UNP Q5HCU0
C	-17	SER	-	expression tag	UNP Q5HCU0
C	-16	HIS	-	expression tag	UNP Q5HCU0
C	-15	HIS	-	expression tag	UNP Q5HCU0
C	-14	HIS	-	expression tag	UNP Q5HCU0
C	-13	HIS	-	expression tag	UNP Q5HCU0
C	-12	HIS	-	expression tag	UNP Q5HCU0
C	-11	HIS	-	expression tag	UNP Q5HCU0
C	-10	SER	-	expression tag	UNP Q5HCU0
C	-9	SER	-	expression tag	UNP Q5HCU0
C	-8	GLY	-	expression tag	UNP Q5HCU0
C	-7	ARG	-	expression tag	UNP Q5HCU0
C	-6	GLU	-	expression tag	UNP Q5HCU0
C	-5	ASN	-	expression tag	UNP Q5HCU0
C	-4	LEU	-	expression tag	UNP Q5HCU0
C	-3	TYR	-	expression tag	UNP Q5HCU0
C	-2	PHE	-	expression tag	UNP Q5HCU0

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-1	GLN	-	expression tag	UNP Q5HCU0
C	0	GLY	-	expression tag	UNP Q5HCU0
C	234	SER	GLY	engineered mutation	UNP Q5HCU0
D	-20	MET	-	expression tag	UNP Q5HCU0
D	-19	GLY	-	expression tag	UNP Q5HCU0
D	-18	SER	-	expression tag	UNP Q5HCU0
D	-17	SER	-	expression tag	UNP Q5HCU0
D	-16	HIS	-	expression tag	UNP Q5HCU0
D	-15	HIS	-	expression tag	UNP Q5HCU0
D	-14	HIS	-	expression tag	UNP Q5HCU0
D	-13	HIS	-	expression tag	UNP Q5HCU0
D	-12	HIS	-	expression tag	UNP Q5HCU0
D	-11	HIS	-	expression tag	UNP Q5HCU0
D	-10	SER	-	expression tag	UNP Q5HCU0
D	-9	SER	-	expression tag	UNP Q5HCU0
D	-8	GLY	-	expression tag	UNP Q5HCU0
D	-7	ARG	-	expression tag	UNP Q5HCU0
D	-6	GLU	-	expression tag	UNP Q5HCU0
D	-5	ASN	-	expression tag	UNP Q5HCU0
D	-4	LEU	-	expression tag	UNP Q5HCU0
D	-3	TYR	-	expression tag	UNP Q5HCU0
D	-2	PHE	-	expression tag	UNP Q5HCU0
D	-1	GLN	-	expression tag	UNP Q5HCU0
D	0	GLY	-	expression tag	UNP Q5HCU0
D	234	SER	GLY	engineered mutation	UNP Q5HCU0

- Molecule 2 is SODIUM ION (CCD ID: NA) (formula: Na).

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

- Molecule 3 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			7	4	3		
3	C	1	Total	C	O	0	0
			7	4	3		

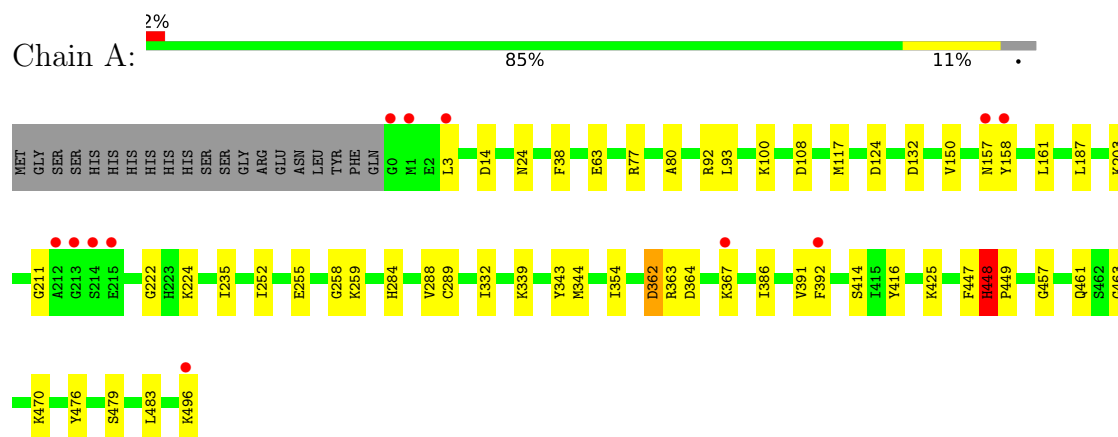
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	408	Total	O	0	8
			410	410		
4	B	330	Total	O	0	11
			336	336		
4	C	439	Total	O	0	17
			447	447		
4	D	414	Total	O	0	18
			421	421		

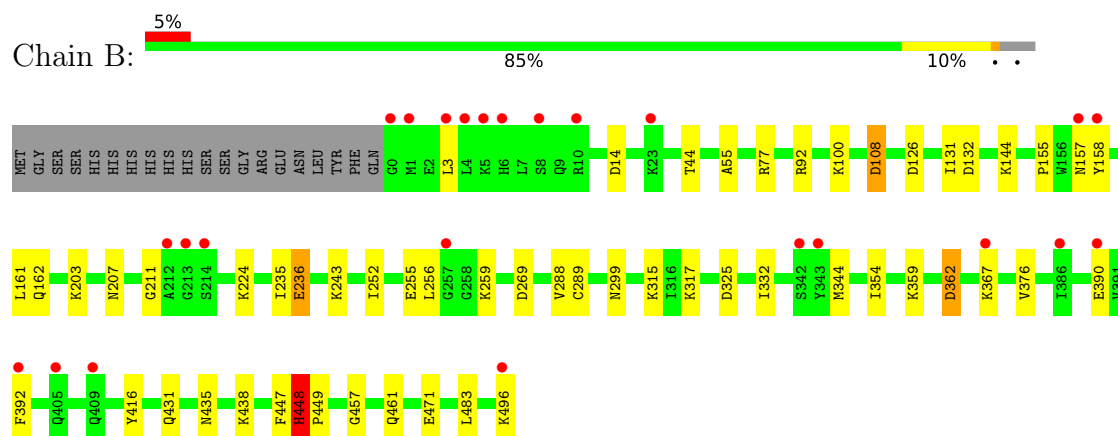
3 Residue-property plots [i](#)

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.

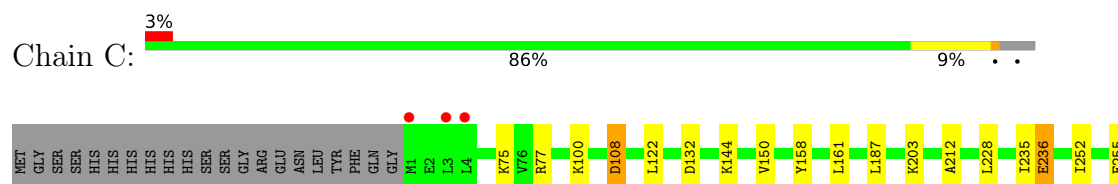
- Molecule 1: Betaine aldehyde dehydrogenase

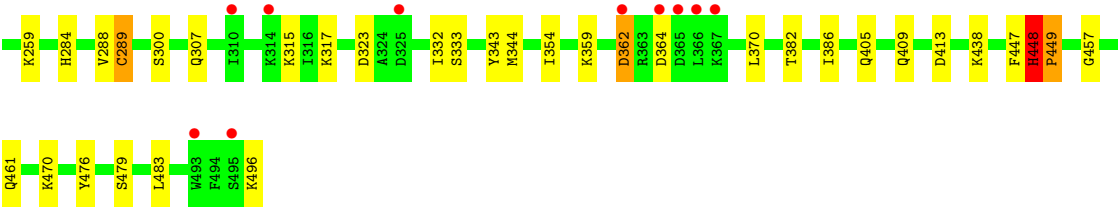


- Molecule 1: Betaine aldehyde dehydrogenase

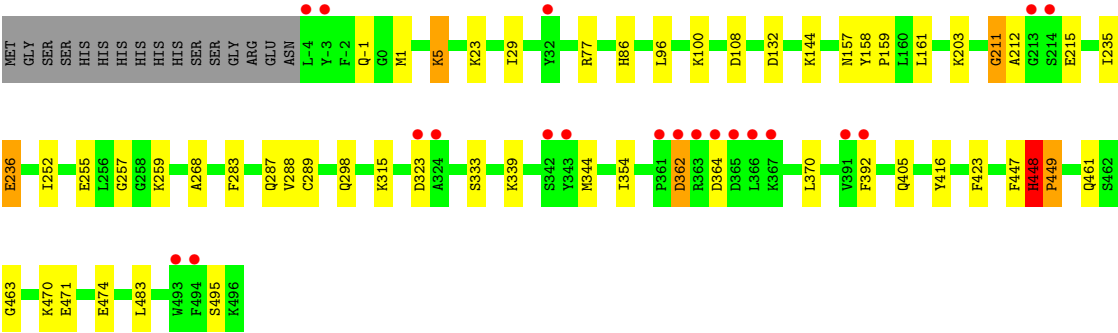
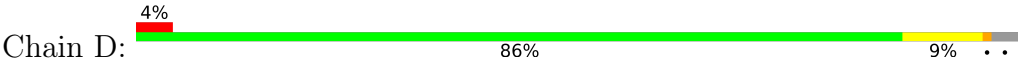


- Molecule 1: Betaine aldehyde dehydrogenase





● Molecule 1: Betaine aldehyde dehydrogenase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	157.36Å 156.44Å 88.42Å 90.00° 110.01° 90.00°	Depositor
Resolution (Å)	29.50 – 1.90 29.50 – 1.90	Depositor EDS
% Data completeness (in resolution range)	98.7 (29.50-1.90) 98.7 (29.50-1.90)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.60 (at 1.91Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.194 , 0.223 0.198 , 0.226	Depositor DCC
R_{free} test set	7795 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	20.2	Xtriage
Anisotropy	0.523	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 48.6	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	17730	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.64% 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: PEG, NA, CME

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	0.80	0/4105	0.90	9/5548 (0.2%)
1	B	0.74	0/4057	0.92	10/5481 (0.2%)
1	C	0.81	0/4051	0.91	9/5478 (0.2%)
1	D	0.82	0/4134	0.91	7/5588 (0.1%)
All	All	0.79	0/16347	0.91	35/22095 (0.2%)

There are no bond length outliers.

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	448	HIS	CA-C-N	-8.36	110.80	119.83
1	A	448	HIS	C-N-CA	-8.36	110.80	119.83
1	B	448	HIS	CA-C-N	-7.85	111.35	119.83
1	B	448	HIS	C-N-CA	-7.85	111.35	119.83
1	B	256	LEU	N-CA-C	-7.47	97.09	109.80
1	C	448	HIS	CA-C-N	-7.40	111.83	119.83
1	C	448	HIS	C-N-CA	-7.40	111.83	119.83
1	C	332	ILE	N-CA-C	6.90	117.69	110.72
1	C	457	GLY	CA-C-N	-6.58	117.64	122.18
1	C	457	GLY	C-N-CA	-6.58	117.64	122.18
1	D	448	HIS	CA-C-N	-6.48	112.83	119.83
1	D	448	HIS	C-N-CA	-6.48	112.83	119.83
1	B	457	GLY	CA-C-N	-6.23	117.88	122.18
1	B	457	GLY	C-N-CA	-6.23	117.88	122.18
1	C	259	LYS	N-CA-C	-6.22	98.39	108.41
1	C	187	LEU	N-CA-C	5.98	117.47	111.07
1	D	449	PRO	N-CA-C	5.79	119.95	111.03
1	A	332	ILE	N-CA-C	5.74	118.26	111.09
1	A	457	GLY	CA-C-N	-5.54	118.36	122.18
1	A	457	GLY	C-N-CA	-5.54	118.36	122.18

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	211	GLY	N-CA-C	5.52	117.98	111.63
1	C	449	PRO	N-CA-C	5.40	119.35	111.03
1	B	269	ASP	N-CA-C	-5.38	101.40	109.15
1	B	211	GLY	N-CA-C	5.34	118.51	111.52
1	D	463	GLY	N-CA-C	5.23	118.61	110.88
1	B	299	ASN	N-CA-C	5.21	117.71	111.71
1	D	211	GLY	N-CA-C	5.17	118.30	111.52
1	A	448	HIS	N-CA-C	5.16	121.22	109.81
1	A	463	GLY	N-CA-C	5.12	117.95	110.63
1	A	187	LEU	N-CA-C	5.11	116.54	111.07
1	C	212	ALA	N-CA-C	-5.08	104.25	110.61
1	B	332	ILE	N-CA-C	5.06	117.42	111.09
1	B	448	HIS	N-CA-C	5.05	120.97	109.81
1	D	212	ALA	N-CA-C	-5.04	104.30	110.61
1	D	203	LYS	CB-CG-CD	-5.02	99.76	111.30

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	4042	0	3956	77	0
1	B	3995	0	3934	71	0
1	C	3990	0	3918	53	0
1	D	4069	0	3972	53	0
2	A	2	0	0	0	0
2	B	1	0	0	0	0
2	C	2	0	0	0	0
2	D	1	0	0	0	0
3	A	7	0	10	0	0
3	C	7	0	10	0	0
4	A	410	0	0	21	0
4	B	336	0	0	24	0
4	C	447	0	0	24	0
4	D	421	0	0	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	17730	0	15800	240	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 7.

All (240) 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:157[B]:ASN:ND2	1:B:158[B]:TYR:H	1.47	1.13
1:B:100[A]:LYS:NZ	1:B:158[A]:TYR:CZ	2.25	1.04
1:D:96:LEU:HD22	4:D:975:HOH:O	1.61	0.97
1:A:343[B]:TYR:CD2	1:A:391:VAL:HG22	2.00	0.96
1:A:117[B]:MET:CE	1:A:117[B]:MET:HA	1.97	0.93
1:B:100[A]:LYS:NZ	1:B:158[A]:TYR:CE1	2.40	0.90
1:A:343[B]:TYR:CE2	1:A:391:VAL:HG22	2.06	0.89
1:A:343[B]:TYR:CE2	1:A:391:VAL:CG2	2.56	0.88
1:D:323:ASP:HB3	4:D:921:HOH:O	1.75	0.87
1:C:108:ASP:OD1	1:C:158[A]:TYR:CE2	2.28	0.86
1:C:108:ASP:OD1	1:C:158[B]:TYR:CE2	2.28	0.86
1:A:77[B]:ARG:HG3	1:A:117[B]:MET:HE1	1.55	0.85
1:D:268:ALA:HB1	4:D:877:HOH:O	1.78	0.82
4:C:760:HOH:O	1:D:470:LYS:HE2	1.79	0.82
1:A:470:LYS:HE2	4:B:799:HOH:O	1.79	0.82
1:A:157[B]:ASN:OD1	1:A:157[B]:ASN:O	1.99	0.81
1:B:157[B]:ASN:ND2	1:B:158[B]:TYR:N	2.27	0.80
1:B:376:VAL:HG11	4:B:888:HOH:O	1.82	0.79
1:B:157[B]:ASN:HD22	1:B:158[B]:TYR:H	1.27	0.79
1:C:284:HIS:HB3	1:C:288:VAL:HG23	1.64	0.79
1:A:117[B]:MET:HA	1:A:117[B]:MET:HE2	1.64	0.78
1:A:158[A]:TYR:OH	1:A:288:VAL:HB	1.85	0.77
1:C:323:ASP:HB3	4:C:972:HOH:O	1.85	0.76
1:B:157[A]:ASN:O	1:B:157[A]:ASN:OD1	2.03	0.75
1:C:108:ASP:OD1	1:C:158[A]:TYR:HE2	1.70	0.74
1:B:317[A]:LYS:NZ	1:B:325:ASP:HB3	2.02	0.74
1:A:496:LYS:HA	4:A:794:HOH:O	1.88	0.73
1:A:117[B]:MET:HA	1:A:117[B]:MET:HE3	1.71	0.73
1:B:496:LYS:HA	4:B:857:HOH:O	1.88	0.73
1:A:414:SER:HB3	4:A:901[A]:HOH:O	1.87	0.72
1:A:100[B]:LYS:NZ	1:A:108:ASP:OD2	2.22	0.72
1:A:158[A]:TYR:CZ	1:A:288:VAL:HG23	2.26	0.71
1:A:100[A]:LYS:NZ	1:A:158[A]:TYR:CE2	2.57	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:392[A]:PHE:HB2	4:B:856[A]:HOH:O	1.90	0.71
1:A:124:ASP:HB2	4:C:876:HOH:O	1.91	0.70
1:B:100[A]:LYS:HD2	4:B:726:HOH:O	1.91	0.70
4:A:716:HOH:O	1:B:438:LYS:HE2	1.91	0.70
1:D:86[B]:HIS:HD2	4:D:688:HOH:O	1.75	0.69
1:C:405[A]:GLN:HG2	4:C:1028:HOH:O	1.91	0.69
1:C:108:ASP:OD1	1:C:158[B]:TYR:HE2	1.70	0.69
1:A:343[B]:TYR:CZ	1:A:391:VAL:CG2	2.76	0.69
1:D:158[B]:TYR:CE1	1:D:288:VAL:HG12	2.30	0.67
1:B:431[A]:GLN:NE2	4:B:866:HOH:O	2.28	0.67
1:B:108:ASP:OD1	1:B:158[B]:TYR:CE2	2.49	0.66
1:C:284:HIS:CB	1:C:288:VAL:HG23	2.26	0.66
1:B:157[A]:ASN:CG	4:B:800:HOH:O	2.39	0.65
1:A:343[B]:TYR:CZ	1:A:391:VAL:HG21	2.32	0.65
1:C:255[B]:GLU:HG2	4:C:926:HOH:O	1.97	0.65
1:A:100[A]:LYS:NZ	1:A:158[A]:TYR:CD2	2.65	0.64
1:C:496:LYS:NZ	4:C:989:HOH:O	2.30	0.64
1:B:100[A]:LYS:NZ	1:B:158[A]:TYR:CE2	2.64	0.63
1:A:77[A]:ARG:HD3	1:D:77:ARG:HD3	1.80	0.63
1:D:100:LYS:NZ	1:D:108:ASP:OD2	2.31	0.63
1:A:224:LYS:HE2	4:A:897:HOH:O	1.98	0.63
1:B:108:ASP:OD1	1:B:158[A]:TYR:CE2	2.52	0.63
1:A:117[B]:MET:HE2	1:A:117[B]:MET:CA	2.29	0.62
1:B:158[A]:TYR:CE1	1:B:288:VAL:HG12	2.35	0.62
1:C:255[B]:GLU:CG	4:C:926:HOH:O	2.48	0.62
1:A:496:LYS:O	1:B:315[A]:LYS:NZ	2.27	0.61
1:C:317:LYS:HG3	4:C:861:HOH:O	2.00	0.61
1:B:157[B]:ASN:HD22	1:B:157[B]:ASN:N	1.96	0.61
1:C:470:LYS:HE2	4:C:961:HOH:O	2.01	0.61
1:A:343[A]:TYR:CD1	4:A:949:HOH:O	2.51	0.61
1:B:158[B]:TYR:CE1	1:B:288:VAL:HG12	2.37	0.60
1:A:108:ASP:OD2	1:A:158[B]:TYR:CE2	2.55	0.60
1:A:343[B]:TYR:CE1	1:A:391:VAL:HG21	2.37	0.59
1:C:359:LYS:HB2	4:C:1033:HOH:O	2.00	0.59
1:C:158[B]:TYR:CE1	1:C:288:VAL:HG22	2.38	0.59
1:C:158[A]:TYR:CE1	1:C:288:VAL:HG22	2.38	0.59
1:A:158[A]:TYR:CE1	1:A:288:VAL:HG23	2.37	0.59
1:A:391:VAL:HG23	4:A:712:HOH:O	2.02	0.59
1:B:317[A]:LYS:HZ2	1:B:325:ASP:HB3	1.68	0.59
1:A:343[B]:TYR:CD2	1:A:391:VAL:CG2	2.79	0.58
1:D:1:MET:HE2	4:D:977:HOH:O	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:339:LYS:NZ	4:A:869:HOH:O	2.32	0.58
1:B:100[B]:LYS:NZ	1:B:108:ASP:OD2	2.33	0.58
1:B:203:LYS:HE2	4:B:730:HOH:O	2.04	0.58
1:A:343[A]:TYR:CE1	4:A:949:HOH:O	2.56	0.57
1:C:307:GLN:HB2	4:C:832:HOH:O	2.03	0.57
1:C:382[B]:THR:CG2	1:C:413:ASP:OD2	2.53	0.57
1:A:158[A]:TYR:HE1	1:A:288:VAL:HA	1.68	0.57
1:B:162:GLN:CG	4:B:914:HOH:O	2.53	0.56
1:C:100:LYS:NZ	1:C:108:ASP:OD2	2.33	0.56
4:C:861:HOH:O	1:D:495:SER:CB	2.54	0.56
1:C:483[A]:LEU:CD2	1:D:449:PRO:HB2	2.36	0.56
1:A:93[A]:LEU:HD12	4:A:814:HOH:O	2.06	0.55
1:D:236[A]:GLU:CD	4:D:961:HOH:O	2.49	0.55
1:A:483:LEU:CD2	1:B:449:PRO:HB2	2.37	0.55
1:B:359:LYS:HE3	4:B:894:HOH:O	2.07	0.55
1:A:108:ASP:OD2	1:A:158[B]:TYR:CD2	2.60	0.54
1:B:155:PRO:HG2	1:B:157[B]:ASN:ND2	2.23	0.54
1:B:243:LYS:NZ	4:B:774:HOH:O	2.40	0.54
1:C:288:VAL:HG13	1:C:289:CME:HZ3	1.89	0.54
1:A:367:LYS:HD2	4:A:955:HOH:O	2.07	0.54
1:A:449:PRO:HB2	1:B:483[A]:LEU:CD2	2.38	0.53
1:B:317[A]:LYS:HZ3	1:B:325:ASP:HB3	1.70	0.53
1:C:150[A]:VAL:HG11	1:C:476:TYR:HE2	1.72	0.53
1:A:343[A]:TYR:HE2	4:A:860:HOH:O	1.91	0.53
1:D:423:PHE:HB3	4:D:877:HOH:O	2.08	0.52
1:A:158[A]:TYR:CE1	1:A:288:VAL:HA	2.45	0.52
1:B:157[B]:ASN:HD22	1:B:158[B]:TYR:N	1.97	0.52
1:D:287:GLN:O	1:D:392[A]:PHE:HE1	1.93	0.52
1:D:283:PHE:HE2	4:D:915:HOH:O	1.90	0.52
1:A:344:MET:CE	1:A:354:ILE:HD12	2.39	0.52
1:B:55:ALA:N	4:B:890:HOH:O	2.43	0.51
1:B:108:ASP:OD1	1:B:158[B]:TYR:HE2	1.90	0.51
1:D:23:LYS:HE3	4:D:896:HOH:O	2.10	0.51
1:A:14:ASP:OD2	1:A:203:LYS:NZ	2.38	0.51
1:A:157[B]:ASN:O	1:A:157[B]:ASN:CG	2.54	0.51
1:B:344:MET:CE	1:B:354:ILE:HD12	2.40	0.51
1:C:382[B]:THR:HG22	1:C:413:ASP:OD2	2.11	0.51
1:D:29:ILE:HD11	4:D:981:HOH:O	2.09	0.51
1:C:483[A]:LEU:HD23	1:D:449:PRO:HB2	1.93	0.51
4:C:861:HOH:O	1:D:495:SER:HB2	2.10	0.51
1:D:344:MET:CE	1:D:354:ILE:HD12	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:449:PRO:HB2	1:D:483[A]:LEU:CD2	2.42	0.50
1:C:75:LYS:NZ	4:C:987:HOH:O	2.42	0.50
1:B:144:LYS:HD2	4:B:765:HOH:O	2.11	0.50
1:D:132[B]:ASP:OD1	1:D:132[B]:ASP:N	2.44	0.50
1:B:155:PRO:HG2	1:B:157[B]:ASN:HD21	1.76	0.50
1:B:157[A]:ASN:O	1:B:157[A]:ASN:CG	2.55	0.49
1:D:257:GLY:N	4:D:881:HOH:O	2.44	0.49
1:C:344:MET:CE	1:C:354:ILE:HD12	2.42	0.49
1:C:409:GLN:HG2	4:C:894:HOH:O	2.12	0.49
1:D:405[A]:GLN:HG3	4:D:962:HOH:O	2.12	0.49
1:B:157[B]:ASN:CG	1:B:158[B]:TYR:N	2.70	0.49
1:B:77[A]:ARG:HD3	1:C:77:ARG:HD3	1.94	0.49
1:D:5:LYS:HZ2	1:D:5:LYS:HB2	1.77	0.49
1:B:157[A]:ASN:ND2	4:B:800:HOH:O	2.45	0.49
1:D:-1[B]:GLN:HA	1:D:-1[B]:GLN:OE1	2.11	0.48
1:D:144:LYS:HD2	4:D:725:HOH:O	2.13	0.48
1:D:215:GLU:HA	4:D:891:HOH:O	2.12	0.48
1:C:122:LEU:HD11	4:C:884:HOH:O	2.13	0.48
1:C:315:LYS:HE3	4:C:807:HOH:O	2.13	0.48
1:B:471:GLU:OE2	4:B:920:HOH:O	2.20	0.48
1:C:382[B]:THR:HG21	1:C:413:ASP:OD2	2.14	0.48
1:D:298:GLN:HG2	4:D:743:HOH:O	2.14	0.48
1:B:157[B]:ASN:ND2	1:B:157[B]:ASN:N	2.61	0.48
1:A:362:ASP:OD1	1:A:362:ASP:N	2.46	0.48
1:C:203:LYS:NZ	4:C:946:HOH:O	2.47	0.48
1:D:5:LYS:HB2	1:D:5:LYS:NZ	2.28	0.47
1:B:14:ASP:OD2	1:B:203:LYS:NZ	2.40	0.47
1:B:367:LYS:HG2	4:B:887:HOH:O	2.14	0.47
4:C:861:HOH:O	1:D:495:SER:HB3	2.13	0.47
1:B:126:ASP:HA	4:D:940:HOH:O	2.13	0.47
1:D:235:ILE:HD11	1:D:461:GLN:OE1	2.14	0.47
1:D:470:LYS:HB3	4:D:990:HOH:O	2.14	0.47
1:A:14:ASP:OD1	1:A:203:LYS:HE3	2.14	0.47
1:A:235:ILE:HD11	1:A:461:GLN:OE1	2.14	0.47
1:A:447:PHE:O	1:A:448:HIS:HB2	2.14	0.47
1:B:390[A]:GLU:HG3	4:B:658[A]:HOH:O	2.14	0.47
1:D:255[B]:GLU:OE1	4:D:979:HOH:O	2.21	0.47
1:A:63:GLU:CD	4:A:960:HOH:O	2.56	0.47
1:A:80:ALA:HB1	1:A:117[B]:MET:HG2	1.96	0.47
1:A:157[A]:ASN:ND2	1:A:392[A]:PHE:HZ	2.13	0.47
1:B:158[B]:TYR:HB3	1:B:161:LEU:HB3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:235:ILE:HD11	1:B:461:GLN:OE1	2.15	0.47
1:C:158[A]:TYR:HB3	1:C:161:LEU:HB3	1.96	0.47
1:A:222:GLY:HA2	4:A:777:HOH:O	2.15	0.46
1:D:157[B]:ASN:O	1:D:158[B]:TYR:HB2	2.15	0.46
1:D:447:PHE:O	1:D:448:HIS:HB2	2.15	0.46
1:B:14:ASP:OD1	1:B:203:LYS:HE3	2.15	0.46
1:B:108:ASP:OD1	1:B:158[A]:TYR:HE2	1.94	0.46
1:A:77[B]:ARG:HG3	1:A:117[B]:MET:CE	2.38	0.46
1:A:343[B]:TYR:OH	4:A:877:HOH:O	2.21	0.46
1:C:447:PHE:O	1:C:448:HIS:HB2	2.16	0.46
1:D:86[B]:HIS:HE1	4:D:780:HOH:O	1.99	0.46
1:C:144:LYS:HD2	4:C:722:HOH:O	2.16	0.46
1:A:496:LYS:HG2	4:A:794:HOH:O	2.16	0.45
1:B:435:ASN:HB3	4:B:831:HOH:O	2.15	0.45
1:B:158[A]:TYR:HB3	1:B:161:LEU:HB3	1.97	0.45
1:D:5:LYS:O	1:D:5:LYS:HG2	2.16	0.45
1:C:362:ASP:N	1:C:362:ASP:OD1	2.49	0.45
1:A:363:ARG:HD3	4:A:885:HOH:O	2.15	0.45
1:A:158[B]:TYR:HB3	1:A:161:LEU:HB3	1.97	0.45
1:D:158[A]:TYR:HB3	1:D:161:LEU:HB3	1.98	0.45
1:A:158[A]:TYR:CZ	1:A:288:VAL:CG2	2.96	0.45
1:D:323:ASP:CB	4:D:921:HOH:O	2.47	0.45
1:D:474:GLU:HG2	4:D:799:HOH:O	2.15	0.45
1:A:158[A]:TYR:OH	1:A:288:VAL:CB	2.60	0.44
1:A:38:PHE:HA	4:A:945:HOH:O	2.18	0.44
1:A:483:LEU:HD23	1:B:449:PRO:HB2	2.00	0.44
1:C:449:PRO:HB2	1:D:483[A]:LEU:HD23	1.99	0.44
1:A:117[B]:MET:CE	1:A:117[B]:MET:CA	2.77	0.44
1:B:131:ILE:HD13	4:B:844:HOH:O	2.17	0.44
1:B:157[A]:ASN:ND2	1:B:392[A]:PHE:HZ	2.15	0.44
1:A:449:PRO:HB2	1:B:483[A]:LEU:HD23	1.98	0.44
1:C:235:ILE:HD11	1:C:461:GLN:OE1	2.17	0.44
1:A:158[A]:TYR:OH	1:A:288:VAL:CG2	2.66	0.44
1:B:362:ASP:N	1:B:362:ASP:OD1	2.50	0.44
1:B:44:THR:HB	4:B:839[A]:HOH:O	2.16	0.44
1:C:158[B]:TYR:HB3	1:C:161:LEU:HB3	1.99	0.44
1:D:362:ASP:N	1:D:362:ASP:OD1	2.49	0.43
1:A:3:LEU:HD11	1:A:92:ARG:HB3	2.01	0.43
1:B:224:LYS:NZ	4:B:789:HOH:O	2.50	0.43
1:C:405[A]:GLN:HG3	4:C:689:HOH:O	2.19	0.43
1:A:496:LYS:CA	4:A:794:HOH:O	2.59	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:447:PHE:C	1:B:449:PRO:HD3	2.44	0.43
1:D:283:PHE:CE2	4:D:915:HOH:O	2.56	0.43
1:C:300:SER:HB2	4:C:742:HOH:O	2.18	0.43
1:A:14:ASP:CG	1:A:203:LYS:NZ	2.77	0.43
1:A:447:PHE:C	1:A:449:PRO:HD3	2.44	0.43
1:D:259:LYS:HB3	1:D:416:TYR:CD2	2.54	0.43
1:A:3:LEU:HD11	1:A:92:ARG:CB	2.49	0.42
1:B:438:LYS:HD2	4:B:832:HOH:O	2.19	0.42
1:C:150[B]:VAL:HG12	1:C:228:LEU:HB3	2.00	0.42
1:A:259:LYS:HB3	1:A:416:TYR:CD2	2.54	0.42
1:B:236:GLU:CD	1:B:236:GLU:H	2.28	0.42
1:B:447:PHE:O	1:B:448:HIS:HB2	2.18	0.42
1:C:438:LYS:HE3	4:D:802:HOH:O	2.19	0.42
1:C:300:SER:CB	4:C:742:HOH:O	2.67	0.42
1:A:93[A]:LEU:CD1	4:A:814:HOH:O	2.65	0.42
1:A:150[A]:VAL:HG11	1:A:476:TYR:HE1	1.84	0.42
1:D:483[B]:LEU:C	1:D:483[B]:LEU:HD23	2.44	0.42
1:A:479:SER:OG	1:B:471:GLU:OE2	2.21	0.42
1:C:333:SER:HA	1:C:370:LEU:HD13	2.02	0.42
1:D:344:MET:HE1	1:D:354:ILE:HD12	2.02	0.42
1:A:258:GLY:HA2	1:A:416:TYR:CD1	2.55	0.41
1:D:236[A]:GLU:CD	1:D:236[A]:GLU:H	2.28	0.41
1:C:447:PHE:C	1:C:449:PRO:HD3	2.46	0.41
1:C:496:LYS:OXT	1:D:315:LYS:HD3	2.21	0.41
1:A:24:ASN:HB3	4:A:815:HOH:O	2.20	0.41
1:D:333:SER:HA	1:D:370:LEU:HD13	2.02	0.41
1:A:343[B]:TYR:OH	1:A:386:ILE:O	2.28	0.41
1:B:207:ASN:ND2	4:B:890:HOH:O	2.44	0.41
1:A:425:LYS:NZ	4:A:831:HOH:O	2.51	0.41
1:B:390[A]:GLU:HG2	4:B:856[A]:HOH:O	2.20	0.41
1:D:211:GLY:HA3	4:D:716:HOH:O	2.21	0.41
1:B:344:MET:HE1	1:B:354:ILE:HD12	2.02	0.41
1:B:3:LEU:HD11	1:B:92:ARG:CB	2.51	0.40
1:B:259:LYS:HB3	1:B:416:TYR:CD2	2.56	0.40
1:D:158[B]:TYR:N	1:D:159:PRO:HD3	2.36	0.40
1:C:77:ARG:NH1	4:C:739:HOH:O	2.53	0.40
1:C:343:TYR:OH	1:C:386:ILE:O	2.27	0.40
1:B:14:ASP:CG	1:B:203:LYS:NZ	2.79	0.40
1:C:479:SER:OG	1:D:471:GLU:OE2	2.22	0.40
1:A:158[A]:TYR:CE1	1:A:284:HIS:HD2	2.38	0.40
1:A:158[A]:TYR:HB3	1:A:161:LEU:HB3	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:150[A]:VAL:HG11	1:C:476:TYR:CE2	2.55	0.40
1:C:236[A]:GLU:CD	1:C:236[A]:GLU:H	2.29	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	515/517 (100%)	505 (98%)	9 (2%)	1 (0%)	43	36
1	B	510/517 (99%)	498 (98%)	11 (2%)	1 (0%)	43	36
1	C	510/517 (99%)	498 (98%)	11 (2%)	1 (0%)	43	36
1	D	518/517 (100%)	505 (98%)	12 (2%)	1 (0%)	43	36
All	All	2053/2068 (99%)	2006 (98%)	43 (2%)	4 (0%)	43	36

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	448	HIS
1	B	448	HIS
1	C	448	HIS
1	D	448	HIS

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	432/429 (101%)	426 (99%)	6 (1%)	59	59
1	B	427/429 (100%)	421 (99%)	6 (1%)	59	59
1	C	428/429 (100%)	421 (98%)	7 (2%)	55	54
1	D	435/429 (101%)	428 (98%)	7 (2%)	55	54
All	All	1722/1716 (100%)	1696 (98%)	26 (2%)	59	56

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	132	ASP
1	A	252	ILE
1	A	255[A]	GLU
1	A	255[B]	GLU
1	A	362	ASP
1	A	364	ASP
1	B	108	ASP
1	B	132	ASP
1	B	236	GLU
1	B	252	ILE
1	B	255	GLU
1	B	362	ASP
1	C	108	ASP
1	C	132	ASP
1	C	236[A]	GLU
1	C	236[B]	GLU
1	C	252	ILE
1	C	362	ASP
1	C	364	ASP
1	D	5	LYS
1	D	236[A]	GLU
1	D	236[B]	GLU
1	D	252	ILE
1	D	339	LYS
1	D	362	ASP
1	D	364	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	34	GLN

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Mol	Chain	Res	Type
1	A	248	ASN
1	A	279	ASN
1	A	409	GLN
1	A	435	ASN
1	B	279	ASN
1	C	6	HIS
1	C	66	GLN
1	C	279	ASN
1	D	9	GLN
1	D	248	ASN
1	D	279	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	CME	C	289	1	8,9,10	0.80	0	6,9,11	1.43	1 (16%)
1	CME	A	289	1	8,9,10	0.87	0	6,9,11	1.37	1 (16%)
1	CME	D	289	1	8,9,10	0.87	0	6,9,11	1.51	1 (16%)
1	CME	B	289	1	8,9,10	0.63	0	6,9,11	1.42	1 (16%)

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
1	CME	C	289	1	-	2/5/8/10	-
1	CME	A	289	1	-	1/5/8/10	-
1	CME	D	289	1	-	2/5/8/10	-
1	CME	B	289	1	-	1/5/8/10	-

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	289	CME	CB-SG-SD	3.18	112.08	103.86
1	C	289	CME	CB-SG-SD	2.94	111.48	103.86
1	B	289	CME	CB-SG-SD	2.76	111.00	103.86
1	A	289	CME	CB-SG-SD	2.68	110.81	103.86

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	289	CME	CZ-CE-SD-SG
1	B	289	CME	CZ-CE-SD-SG
1	C	289	CME	CZ-CE-SD-SG
1	D	289	CME	CZ-CE-SD-SG
1	C	289	CME	N-CA-CB-SG
1	D	289	CME	N-CA-CB-SG

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	C	289	CME	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 6 are monoatomic - leaving 2 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	PEG	C	503	-	6,6,6	0.46	0	5,5,5	0.25	0
3	PEG	A	503	-	6,6,6	0.59	0	5,5,5	0.31	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	PEG	C	503	-	-	3/4/4/4	-
3	PEG	A	503	-	-	3/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	503	PEG	O1-C1-C2-O2
3	C	503	PEG	C1-C2-O2-C3
3	A	503	PEG	C4-C3-O2-C2
3	A	503	PEG	O2-C3-C4-O4
3	A	503	PEG	O1-C1-C2-O2
3	C	503	PEG	C4-C3-O2-C2

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

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	496/517 (95%)	0.11	12 (2%) 59 63	7, 20, 34, 62	20 (4%)
1	B	496/517 (95%)	0.47	24 (4%) 35 38	6, 27, 48, 76	16 (3%)
1	C	495/517 (95%)	0.27	13 (2%) 57 61	7, 22, 40, 72	17 (3%)
1	D	500/517 (96%)	0.26	20 (4%) 42 45	6, 20, 44, 76	20 (4%)
All	All	1987/2068 (96%)	0.28	69 (3%) 47 50	6, 22, 44, 76	73 (3%)

All (69) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	392[A]	PHE	5.5
1	B	392[A]	PHE	4.6
1	D	323	ASP	4.0
1	A	212	ALA	4.0
1	A	158[A]	TYR	4.0
1	B	343	TYR	3.7
1	D	493	TRP	3.7
1	D	365	ASP	3.6
1	B	0	GLY	3.6
1	A	0	GLY	3.5
1	C	3	LEU	3.3
1	D	343	TYR	3.3
1	B	367	LYS	3.2
1	C	1	MET	3.1
1	D	362	ASP	3.1
1	D	367	LYS	3.1
1	B	158[A]	TYR	3.1
1	C	365	ASP	3.1
1	D	363	ARG	3.0
1	D	324	ALA	2.9
1	A	214	SER	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	1	MET	2.9
1	C	362	ASP	2.8
1	B	405	GLN	2.8
1	A	1	MET	2.8
1	B	212	ALA	2.7
1	B	213	GLY	2.7
1	B	214	SER	2.7
1	D	364	ASP	2.7
1	A	367	LYS	2.6
1	D	213	GLY	2.6
1	B	409	GLN	2.6
1	B	3	LEU	2.6
1	C	367	LYS	2.6
1	A	157[A]	ASN	2.6
1	B	257	GLY	2.5
1	D	342	SER	2.5
1	B	390[A]	GLU	2.5
1	B	342	SER	2.5
1	C	495	SER	2.5
1	B	5	LYS	2.4
1	C	325	ASP	2.4
1	B	8[A]	SER	2.4
1	B	23	LYS	2.4
1	C	364	ASP	2.4
1	A	213	GLY	2.4
1	B	4	LEU	2.4
1	B	496	LYS	2.4
1	D	-4	LEU	2.3
1	B	6	HIS	2.3
1	C	366	LEU	2.3
1	A	496	LYS	2.3
1	B	10	ARG	2.2
1	C	493	TRP	2.2
1	B	157[A]	ASN	2.2
1	C	314	LYS	2.2
1	D	214	SER	2.2
1	D	366	LEU	2.2
1	D	-3	TYR	2.1
1	D	391	VAL	2.1
1	A	215	GLU	2.1
1	C	4	LEU	2.1
1	D	494	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	310	ILE	2.1
1	A	3	LEU	2.1
1	B	386	ILE	2.0
1	D	32	TYR	2.0
1	D	361	PRO	2.0
1	A	392[A]	PHE	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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(Å ²)	Q<0.9
1	CME	B	289	10/11	0.85	0.16	25,33,37,38	0
1	CME	A	289	10/11	0.91	0.12	19,28,33,35	0
1	CME	D	289	10/11	0.94	0.10	22,27,28,29	0
1	CME	C	289	10/11	0.96	0.10	22,24,26,26	0

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(Å ²)	Q<0.9
3	PEG	A	503	7/7	0.78	0.14	34,36,47,48	0
3	PEG	C	503	7/7	0.88	0.12	39,42,46,49	0
2	NA	A	501	1/1	0.94	0.09	23,23,23,23	0
2	NA	B	501	1/1	0.94	0.07	24,24,24,24	0
2	NA	D	501	1/1	0.97	0.04	14,14,14,14	0
2	NA	A	502	1/1	0.97	0.03	17,17,17,17	0
2	NA	C	501	1/1	0.97	0.03	14,14,14,14	0
2	NA	C	502	1/1	0.98	0.04	23,23,23,23	0

6.5 Other polymers [i](#)

There are no such residues in this entry.