



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 02:57 PM UTC

PDB ID : 3PRY / pdb_00003pry
Title : Crystal structure of the middle domain of human HSP90-beta refined at 2.3 Å resolution
Authors : Chaikuad, A.; Pilka, E.; Sharpe, T.D.; Cooper, C.D.O.; Phillips, C.; Berridge, G.; Ayinampudi, V.; Fedorov, O.; Keates, T.; Thangaratnarajah, C.; Zimmermann, T.; Vollmar, M.; Yue, W.W.; Che, K.H.; Krojer, T.; Muniz, J.R.C.; von Delft, F.; Bountra, C.; Arrowsmith, C.H.; Weigelt, J.; Edwards, A.; Bullock, A.; Structural Genomics Consortium (SGC)
Deposited on : 2010-11-30
Resolution : 2.28 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)

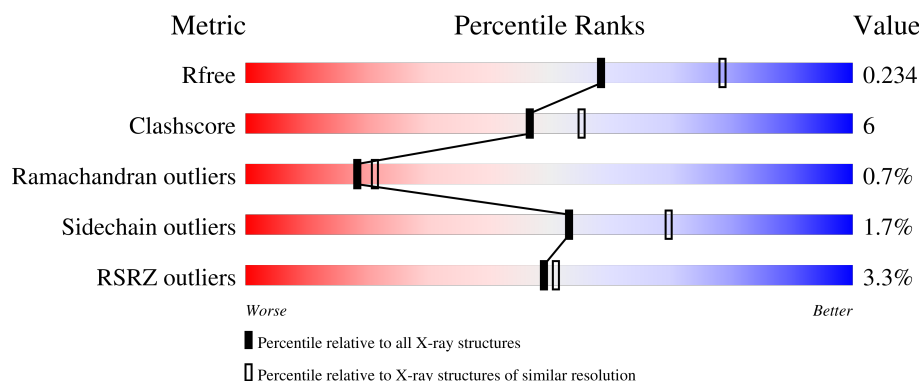
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.28 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	9078 (2.30-2.26)
Clashscore	190562	9802 (2.30-2.26)
Ramachandran outliers	187476	9690 (2.30-2.26)
Sidechain outliers	187428	9691 (2.30-2.26)
RSRZ outliers	180081	9085 (2.30-2.26)

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	268	
1	B	268	
1	C	268	

Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	B	3	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6396 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 Heat shock protein HSP 90-beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	255	Total	C	N	O	S	0	1	0
			2074	1319	349	398	8			
1	B	251	Total	C	N	O	S	0	2	0
			2028	1292	345	383	8			
1	C	250	Total	C	N	O	S	0	0	0
			2038	1295	345	390	8			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	283	MET	-	initiating methionine	UNP P08238
A	544	ALA	-	expression tag	UNP P08238
A	545	GLU	-	expression tag	UNP P08238
A	546	ASN	-	expression tag	UNP P08238
A	547	LEU	-	expression tag	UNP P08238
A	548	TYR	-	expression tag	UNP P08238
A	549	PHE	-	expression tag	UNP P08238
A	550	GLN	-	expression tag	UNP P08238
B	283	MET	-	initiating methionine	UNP P08238
B	544	ALA	-	expression tag	UNP P08238
B	545	GLU	-	expression tag	UNP P08238
B	546	ASN	-	expression tag	UNP P08238
B	547	LEU	-	expression tag	UNP P08238
B	548	TYR	-	expression tag	UNP P08238
B	549	PHE	-	expression tag	UNP P08238
B	550	GLN	-	expression tag	UNP P08238
C	283	MET	-	initiating methionine	UNP P08238
C	544	ALA	-	expression tag	UNP P08238
C	545	GLU	-	expression tag	UNP P08238
C	546	ASN	-	expression tag	UNP P08238
C	547	LEU	-	expression tag	UNP P08238
C	548	TYR	-	expression tag	UNP P08238
C	549	PHE	-	expression tag	UNP P08238

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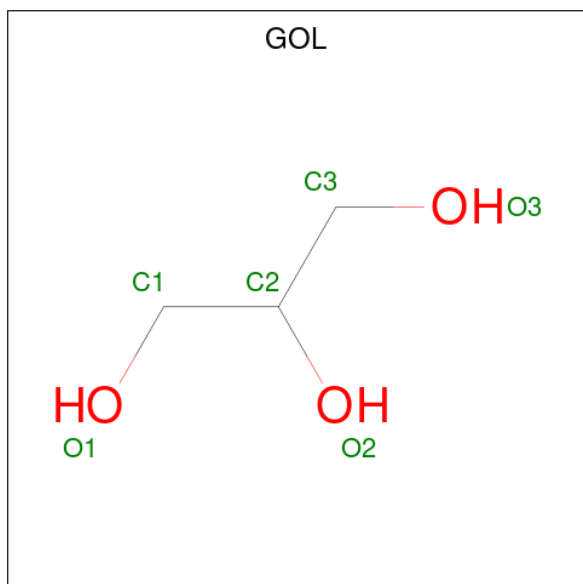
Chain	Residue	Modelled	Actual	Comment	Reference
C	550	GLN	-	expression tag	UNP P08238

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



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

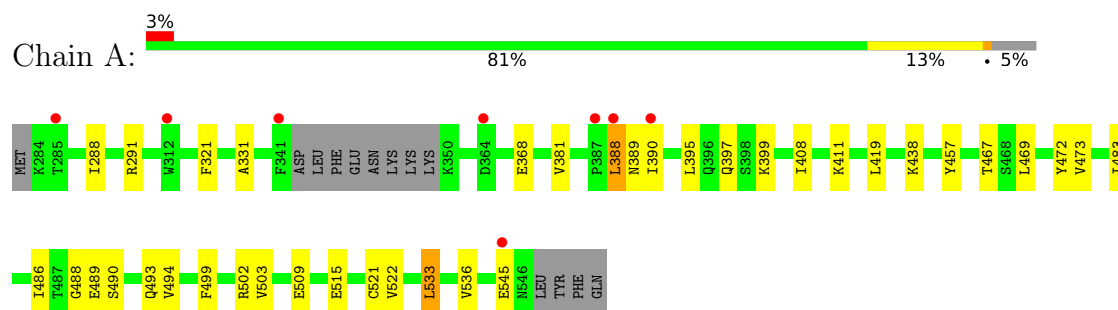
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	88	Total	O	0	0
			88	88		
5	B	67	Total	O	0	0
			67	67		
5	C	65	Total	O	0	0
			65	65		

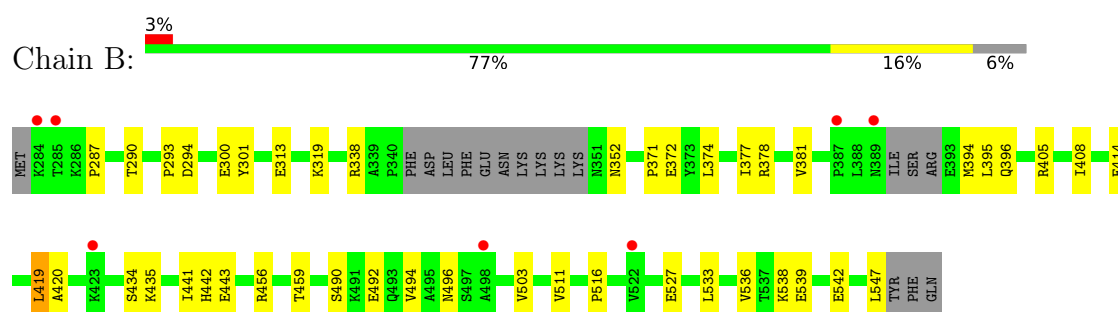
3 Residue-property plots [i](#)

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.

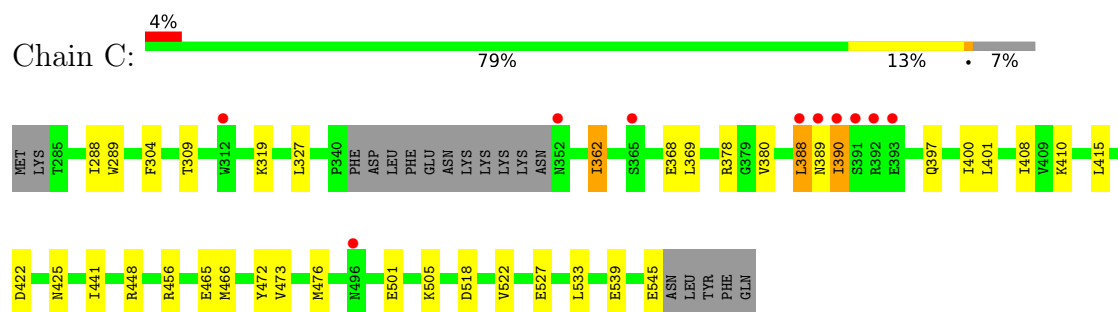
- Molecule 1: Heat shock protein HSP 90-beta



- Molecule 1: Heat shock protein HSP 90-beta



- Molecule 1: Heat shock protein HSP 90-beta



4 Data and refinement statistics

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	73.71Å 73.71Å 149.05Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	39.19 – 2.28 39.19 – 2.28	Depositor EDS
% Data completeness (in resolution range)	99.6 (39.19-2.28) 99.9 (39.19-2.28)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.64 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.5.0110	Depositor
R, R_{free}	0.172 , 0.217 0.191 , 0.234	Depositor DCC
R_{free} test set	2027 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å ²)	46.6	Xtriage
Anisotropy	0.129	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 58.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.005 for -h,-k,l 0.049 for h,-h-k,-l 0.004 for -k,-h,-l	Xtriage
Reported twinning fraction	0.675 for H, K, L 0.325 for -H, H+K, -L	Depositor
Outliers	0 of 41275 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6396	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.23% 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: GOL, EDO, SO4

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.85	0/2115	0.94	1/2850 (0.0%)
1	B	0.82	0/2069	0.88	0/2784
1	C	0.78	0/2075	0.91	1/2794 (0.0%)
All	All	0.82	0/6259	0.91	2/8428 (0.0%)

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
1	A	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	362	ILE	CB-CA-C	-6.22	106.42	111.71
1	A	388	LEU	N-CA-C	5.78	120.01	111.87

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	545	GLU	Peptide

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	2074	0	2012	22	0
1	B	2028	0	1984	27	0
1	C	2038	0	1996	21	0
2	A	5	0	0	0	0
2	B	5	0	0	2	0
3	B	6	0	8	2	0
4	B	16	0	24	2	0
4	C	4	0	6	0	0
5	A	88	0	0	1	0
5	B	67	0	0	2	0
5	C	65	0	0	1	0
All	All	6396	0	6030	69	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 6.

All (69) 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:388:LEU:N	1:A:389:ASN:HA	2.04	0.72
1:C:441:ILE:HG23	1:C:448:ARG:HG3	1.77	0.66
1:C:362:ILE:HD12	1:C:388:LEU:HD13	1.81	0.61
1:C:397:GLN:O	1:C:401:LEU:HG	2.02	0.59
1:B:319:LYS:NZ	3:B:4:GOL:H32	2.17	0.59
1:A:288:ILE:HA	1:A:291:ARG:HD3	1.86	0.58
1:B:372:GLU:HG2	4:B:6:EDO:H12	1.84	0.58
1:B:319:LYS:HZ2	3:B:4:GOL:H32	1.69	0.57
1:B:527:GLU:HA	1:B:533:LEU:HD23	1.86	0.57
1:C:518:ASP:O	1:C:522:VAL:HG12	2.05	0.56
1:C:539:GLU:H	1:C:539:GLU:CD	2.13	0.56
1:A:503:VAL:HG21	1:A:536:VAL:HG12	1.88	0.55
1:A:489:GLU:OE1	1:A:493:GLN:HG3	2.08	0.54
1:C:289:TRP:CE3	1:C:380:VAL:HG21	2.44	0.53
1:B:405:ARG:NH1	4:B:6:EDO:O2	2.42	0.53
1:C:309:THR:HG22	1:C:378:ARG:NH1	2.24	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:313:GLU:OE1	1:B:338:ARG:NH1	2.41	0.52
1:B:496:ASN:HB2	5:B:125:HOH:O	2.07	0.52
1:C:319:LYS:HB2	1:C:415:LEU:HD22	1.91	0.52
1:A:397:GLN:HE22	1:B:516:PRO:HB3	1.74	0.52
1:B:503:VAL:HG21	1:B:536:VAL:HG12	1.91	0.52
1:B:492:GLU:N	1:B:492:GLU:OE1	2.42	0.51
1:A:490:SER:O	1:A:494:VAL:HG12	2.10	0.51
1:C:473:VAL:O	1:C:476:MET:HG2	2.11	0.51
1:B:538:LYS:NZ	2:B:3:SO4:O3	2.38	0.51
1:B:459:THR:HG22	1:B:511:VAL:HA	1.93	0.51
1:C:288:ILE:HG21	1:C:304:PHE:CD1	2.46	0.50
1:A:381:VAL:HG21	1:A:408:ILE:HD11	1.92	0.50
1:B:442:HIS:O	1:B:442:HIS:ND1	2.45	0.50
1:B:539:GLU:HB3	2:B:3:SO4:O4	2.12	0.49
1:A:483:ILE:HB	1:A:533:LEU:HD13	1.95	0.48
1:B:381:VAL:HG21	1:B:408:ILE:HD11	1.96	0.48
1:A:457:TYR:O	1:A:467:THR:HG22	2.14	0.48
1:C:501:GLU:HG3	1:C:505:LYS:HE3	1.95	0.48
1:A:321:PHE:CD2	1:A:411:LYS:HG2	2.48	0.47
1:B:371:PRO:HD2	1:B:374:LEU:HD12	1.96	0.47
1:A:395:LEU:HD11	1:A:399:LYS:HE3	1.97	0.47
1:A:389:ASN:OD1	1:A:389:ASN:C	2.58	0.47
1:A:321:PHE:CE2	1:A:331:ALA:HB3	2.49	0.47
1:B:456:ARG:O	5:B:80:HOH:O	2.21	0.47
1:B:394:MET:C	1:B:396:GLN:H	2.22	0.46
1:A:486:ILE:HD11	1:A:489:GLU:CD	2.41	0.46
1:C:327:LEU:HD21	1:C:400:ILE:HG23	1.98	0.45
1:A:469:LEU:O	1:A:473:VAL:HG23	2.17	0.45
1:A:488:GLY:C	1:A:489:GLU:HG2	2.40	0.45
1:B:542:GLU:OE2	1:B:547:LEU:HD11	2.17	0.45
1:A:472:TYR:CE1	1:A:509:GLU:HB3	2.52	0.44
1:C:472:TYR:C	1:C:472:TYR:CD1	2.96	0.44
1:A:515:GLU:OE2	5:A:97:HOH:O	2.21	0.44
1:B:434:SER:O	1:B:435:LYS:C	2.58	0.44
1:C:456:ARG:HB3	1:C:466:MET:HB3	2.00	0.43
1:C:369:LEU:HD23	1:C:369:LEU:HA	1.83	0.43
1:C:422:ASP:OD1	1:C:425:ASN:HB2	2.18	0.43
1:B:419:LEU:HD12	1:B:419:LEU:HA	1.77	0.43
1:A:438:LYS:HG2	1:A:521:CYS:SG	2.59	0.43
1:C:527:GLU:HA	1:C:533:LEU:HD23	2.01	0.42
1:A:522:VAL:HG23	1:A:533:LEU:HG	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:293:PRO:O	1:B:294:ASP:C	2.63	0.42
1:A:419:LEU:HD12	1:A:419:LEU:HA	1.93	0.42
1:B:319:LYS:NZ	1:B:414:GLU:OE2	2.52	0.42
1:B:300:GLU:O	1:B:301:TYR:C	2.63	0.42
1:C:539:GLU:N	1:C:539:GLU:OE1	2.53	0.41
1:B:352:ASN:HB2	1:B:377:ILE:O	2.20	0.41
1:B:287:PRO:O	1:B:290:THR:OG1	2.37	0.41
1:B:490:SER:O	1:B:494:VAL:HG22	2.21	0.41
1:A:499:PHE:O	1:A:502:ARG:HG2	2.21	0.40
1:C:388:LEU:O	1:C:390:ILE:N	2.51	0.40
1:C:410:LYS:HE3	5:C:168:HOH:O	2.22	0.40
1:C:533:LEU:HD22	1:C:533:LEU:N	2.36	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	252/268 (94%)	245 (97%)	6 (2%)	1 (0%)	30	36
1	B	247/268 (92%)	236 (96%)	9 (4%)	2 (1%)	16	18
1	C	246/268 (92%)	230 (94%)	14 (6%)	2 (1%)	16	18
All	All	745/804 (93%)	711 (95%)	29 (4%)	5 (1%)	18	21

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	420	ALA
1	C	390	ILE
1	C	389	ASN
1	B	395	LEU
1	A	390	ILE

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	225/251 (90%)	223 (99%)	2 (1%)	70	82
1	B	218/251 (87%)	214 (98%)	4 (2%)	51	68
1	C	223/251 (89%)	218 (98%)	5 (2%)	45	62
All	All	666/753 (88%)	655 (98%)	11 (2%)	53	70

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	368	GLU
1	A	533	LEU
1	B	378	ARG
1	B	419	LEU
1	B	441	ILE
1	B	443	GLU
1	C	368	GLU
1	C	388	LEU
1	C	408	ILE
1	C	465	GLU
1	C	545	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	436	ASN
1	A	442	HIS
1	B	523	GLN
1	C	298	GLN
1	C	524	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

8 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	EDO	B	6	-	3,3,3	0.46	0	2,2,2	0.70	0
2	SO4	A	1	-	4,4,4	0.31	0	6,6,6	0.16	0
4	EDO	B	7	-	3,3,3	0.31	0	2,2,2	1.23	0
4	EDO	B	8	-	3,3,3	0.55	0	2,2,2	0.45	0
2	SO4	B	3	-	4,4,4	0.25	0	6,6,6	0.27	0
4	EDO	C	9	-	3,3,3	0.74	0	2,2,2	0.27	0
4	EDO	B	5	-	3,3,3	0.45	0	2,2,2	0.47	0
3	GOL	B	4	-	5,5,5	0.38	0	5,5,5	0.73	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	EDO	B	6	-	-	1/1/1/1	-
4	EDO	B	7	-	-	1/1/1/1	-
4	EDO	B	8	-	-	1/1/1/1	-
4	EDO	C	9	-	-	1/1/1/1	-
4	EDO	B	5	-	-	1/1/1/1	-
3	GOL	B	4	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	4	GOL	C1-C2-C3-O3
3	B	4	GOL	O2-C2-C3-O3
4	B	8	EDO	O1-C1-C2-O2
4	C	9	EDO	O1-C1-C2-O2
4	B	5	EDO	O1-C1-C2-O2
4	B	7	EDO	O1-C1-C2-O2
4	B	6	EDO	O1-C1-C2-O2

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	6	EDO	2	0
2	B	3	SO4	2	0
3	B	4	GOL	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	255/268 (95%)	0.13	8 (3%) 51 53	23, 41, 67, 87	1 (0%)
1	B	251/268 (93%)	0.28	7 (2%) 55 56	25, 44, 67, 86	2 (0%)
1	C	250/268 (93%)	0.32	10 (4%) 42 44	28, 46, 74, 111	0
All	All	756/804 (94%)	0.24	25 (3%) 49 51	23, 44, 70, 111	3 (0%)

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	388	LEU	4.8
1	A	341	PHE	3.8
1	A	312	TRP	3.6
1	A	387	PRO	3.4
1	C	390	ILE	3.3
1	A	545	GLU	3.3
1	C	393	GLU	3.2
1	B	284	LYS	2.7
1	B	389	ASN	2.7
1	C	352	ASN	2.7
1	B	387	PRO	2.7
1	A	390	ILE	2.6
1	C	388	LEU	2.6
1	C	312	TRP	2.6
1	B	498	ALA	2.6
1	C	392	ARG	2.5
1	C	391	SER	2.4
1	B	285	THR	2.3
1	C	365	SER	2.3
1	B	522	VAL	2.3
1	A	364	ASP	2.2
1	C	496	ASN	2.2
1	C	389	ASN	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	285	THR	2.1
1	B	423	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(Å ²)	Q<0.9
4	EDO	B	6	4/4	0.83	0.11	29,33,34,35	0
3	GOL	B	4	6/6	0.85	0.11	37,40,61,61	0
4	EDO	B	7	4/4	0.88	0.09	27,29,34,34	0
4	EDO	B	5	4/4	0.89	0.10	40,40,44,46	0
4	EDO	B	8	4/4	0.90	0.09	36,40,41,44	0
4	EDO	C	9	4/4	0.90	0.10	29,31,39,43	0
2	SO4	A	1	5/5	0.92	0.09	37,47,54,59	0
2	SO4	B	3	5/5	0.95	0.09	35,48,53,55	0

6.5 Other polymers [i](#)

There are no such residues in this entry.