



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:16 PM UTC

PDB ID : 5WVU / pdb_00005wvu
Title : Crystal structure of carboxypeptidase from *Thermus thermophilus*
Authors : Okai, M.; Nagata, K.; Tanokura, M.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)
Deposited on : 2016-12-29
Resolution : 2.60 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

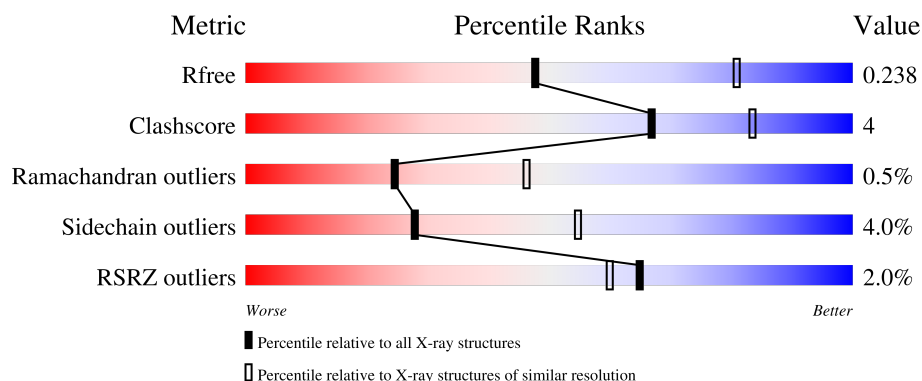
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	510	0% 91% 9%
1	B	510	3% 89% 10% .
1	C	510	2% 88% 11% .

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	GOL	A	802	-	-	X	-

2 Entry composition [i](#)

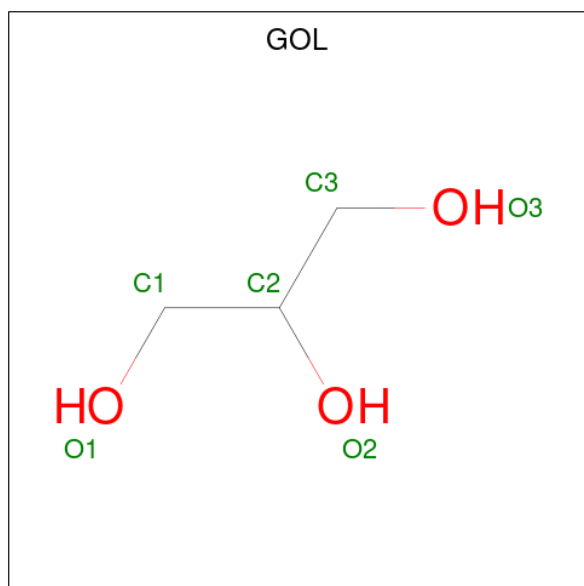
There are 4 unique types of molecules in this entry. The entry contains 12587 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Thermostable carboxypeptidase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	510	Total	C	N	O	S	0	0	0
			4112	2636	722	746	8			
1	B	510	Total	C	N	O	S	0	0	0
			4112	2636	722	746	8			
1	C	510	Total	C	N	O	S	0	0	0
			4112	2636	722	746	8			

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

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

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

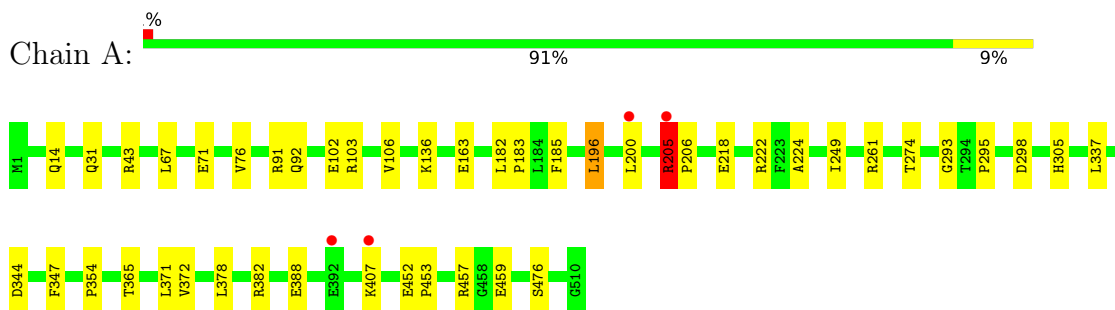
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	151	Total	O	0	0
			151	151		
4	B	21	Total	O	0	0
			21	21		
4	C	52	Total	O	0	0
			52	52		

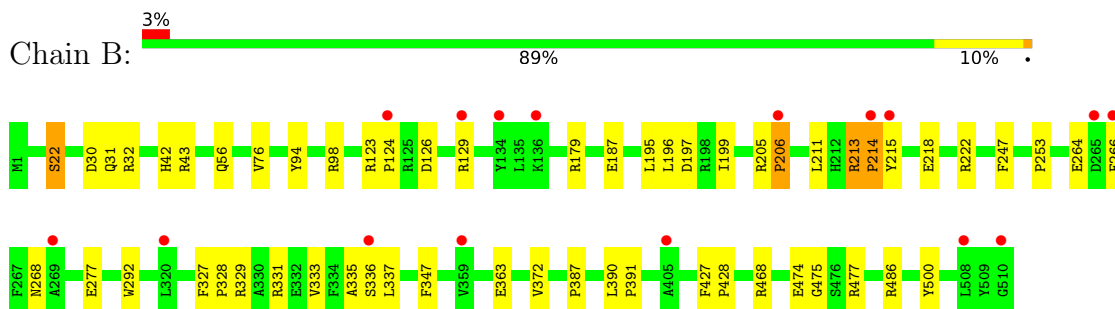
3 Residue-property plots [i](#)

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.

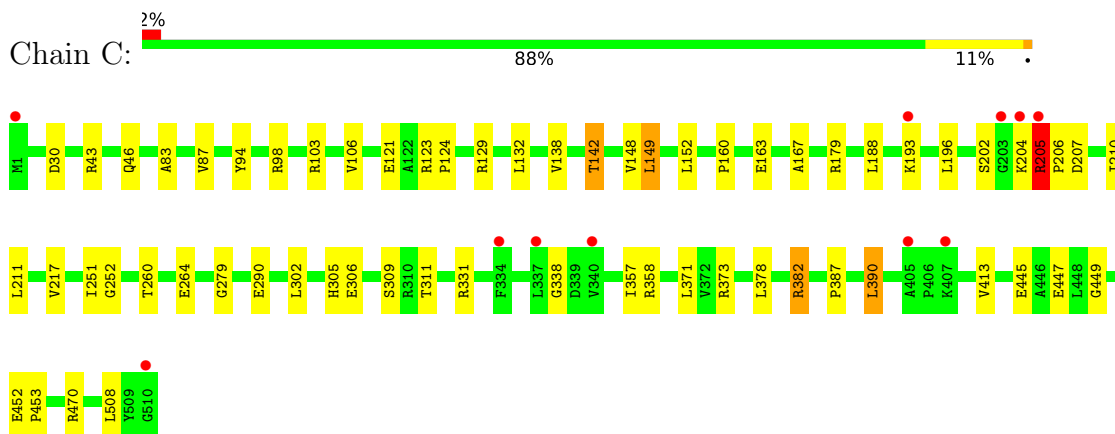
- Molecule 1: Thermostable carboxypeptidase 1



- Molecule 1: Thermostable carboxypeptidase 1



- Molecule 1: Thermostable carboxypeptidase 1



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	170.10Å 233.70Å 124.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.24 – 2.60 41.24 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.3 (41.24-2.60) 99.3 (41.24-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.58 (at 2.61Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.190 , 0.234 0.199 , 0.238	Depositor DCC
R_{free} test set	3798 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	43.6	Xtriage
Anisotropy	0.017	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 39.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	12587	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.65% 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: 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	0.73	1/4230 (0.0%)	0.77	2/5741 (0.0%)
1	B	0.56	0/4230	0.66	0/5741
1	C	0.62	0/4230	0.70	2/5741 (0.0%)
All	All	0.64	1/12690 (0.0%)	0.71	4/17223 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	205	ARG	CA-C	-5.87	1.45	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	205	ARG	CA-C-N	6.10	141.64	127.00
1	A	205	ARG	C-N-CA	6.10	141.64	127.00
1	C	205	ARG	CA-C-N	5.76	140.83	127.00
1	C	205	ARG	C-N-CA	5.76	140.83	127.00

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	4112	0	3999	38	0
1	B	4112	0	3999	28	0
1	C	4112	0	3999	26	0
2	A	18	0	24	7	0
2	C	6	0	8	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
4	A	151	0	0	2	2
4	B	21	0	0	1	0
4	C	52	0	0	0	0
All	All	12587	0	12029	90	2

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 (90) 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:205:ARG:HB3	1:A:206:PRO:HA	1.59	0.82
1:A:43:ARG:HG3	2:A:802:GOL:H2	1.67	0.76
1:A:205:ARG:HB3	1:A:206:PRO:CA	2.20	0.70
1:A:205:ARG:NH2	1:A:344:ASP:OD1	2.24	0.69
1:C:160:PRO:O	1:C:179:ARG:NH2	2.26	0.68
1:B:22:SER:OG	1:C:46:GLN:NE2	2.31	0.64
1:C:138:VAL:O	1:C:142:THR:HG23	1.97	0.63
1:A:205:ARG:CB	1:A:206:PRO:HA	2.29	0.63
1:C:94:TYR:CZ	1:C:98:ARG:HD2	2.34	0.62
1:B:30:ASP:OD2	1:B:43:ARG:NH2	2.34	0.61
1:A:457:ARG:NH1	1:A:459:GLU:OE2	2.34	0.61
1:A:31:GLN:CD	2:A:802:GOL:H32	2.25	0.60
1:C:30:ASP:OD1	1:C:43:ARG:NH2	2.35	0.60
1:C:205:ARG:CB	1:C:206:PRO:HA	2.34	0.58
1:A:295:PRO:O	1:A:476:SER:HB2	2.05	0.56
1:A:31:GLN:OE1	2:A:802:GOL:H32	2.06	0.55
1:A:136:LYS:HE2	1:A:388:GLU:OE2	2.07	0.55
1:A:185:PHE:CD2	1:A:371:LEU:HD22	2.42	0.55
1:A:378:LEU:O	1:A:382:ARG:HG3	2.06	0.55
1:B:195:LEU:O	1:B:199:ILE:HG12	2.07	0.55
1:C:123:ARG:HB3	1:C:124:PRO:HD3	1.89	0.55
1:B:123:ARG:HB3	1:B:124:PRO:HD3	1.88	0.54
1:C:205:ARG:HB3	1:C:206:PRO:HA	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:205:ARG:CB	1:A:206:PRO:CA	2.86	0.53
1:C:331:ARG:NH2	1:C:338:GLY:O	2.35	0.52
1:A:76:VAL:CG1	1:A:76:VAL:O	2.57	0.52
1:B:331:ARG:NH2	1:B:337:LEU:O	2.43	0.52
1:A:102:GLU:O	1:A:106:VAL:HG23	2.10	0.52
1:A:67:LEU:O	1:A:71:GLU:HG3	2.10	0.52
1:B:76:VAL:CG1	1:B:76:VAL:O	2.58	0.51
1:C:358:ARG:HB2	1:C:373:ARG:HH22	1.76	0.50
1:B:474:GLU:OE1	1:B:477:ARG:NH2	2.44	0.50
1:B:31:GLN:HG2	1:B:31:GLN:O	2.12	0.49
1:B:206:PRO:HA	1:B:347:PHE:CE1	2.46	0.49
1:B:213:ARG:HB3	1:B:214:PRO:HD2	1.92	0.49
1:C:279:GLY:HA3	1:C:309:SER:HA	1.94	0.49
1:A:205:ARG:HG2	1:A:206:PRO:C	2.38	0.49
1:B:94:TYR:O	1:B:98:ARG:HG2	2.13	0.49
1:A:205:ARG:HH22	1:A:344:ASP:CG	2.18	0.48
1:C:149:LEU:HB3	1:C:167:ALA:HB1	1.95	0.48
1:B:179:ARG:HG3	4:B:710:HOH:O	2.13	0.48
1:B:206:PRO:HA	1:B:347:PHE:CD1	2.48	0.48
1:C:83:ALA:O	1:C:87:VAL:HG13	2.12	0.48
1:A:92:GLN:HG3	4:A:1026:HOH:O	2.14	0.47
1:B:214:PRO:O	1:B:264:GLU:O	2.32	0.47
1:C:445:GLU:O	1:C:449:GLY:N	2.44	0.47
1:A:182:LEU:HB3	1:A:183:PRO:HD3	1.96	0.47
1:A:293:GLY:O	2:A:803:GOL:H2	2.15	0.47
1:B:218:GLU:O	1:B:222:ARG:HG3	2.14	0.47
1:B:390:LEU:N	1:B:391:PRO:HD2	2.30	0.46
1:A:71:GLU:OE2	1:A:91:ARG:NH1	2.40	0.46
1:A:205:ARG:CG	1:A:206:PRO:HA	2.46	0.46
1:B:329:ARG:O	1:B:333:VAL:HG23	2.15	0.46
1:A:205:ARG:HB3	1:A:347:PHE:CE2	2.51	0.46
1:B:363:GLU:OE2	1:B:500:TYR:OH	2.19	0.46
1:A:218:GLU:HG3	1:A:222:ARG:NH1	2.31	0.46
1:A:185:PHE:CD2	1:A:371:LEU:CD2	2.99	0.45
1:A:76:VAL:O	1:A:76:VAL:HG12	2.16	0.45
1:C:163:GLU:OE2	1:C:382:ARG:HD2	2.17	0.44
1:B:32:ARG:HD2	1:B:247:PHE:CE1	2.52	0.44
1:B:474:GLU:O	1:B:475:GLY:C	2.61	0.44
1:C:205:ARG:CB	1:C:206:PRO:CA	2.97	0.43
1:A:452:GLU:HB3	1:A:453:PRO:HD3	2.01	0.43
1:C:205:ARG:HB2	1:C:206:PRO:HA	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:196:LEU:HD21	1:A:365:THR:HG22	2.01	0.43
1:C:447:GLU:OE2	1:C:470:ARG:NH1	2.51	0.43
1:B:253:PRO:HD3	1:B:292:TRP:CD1	2.54	0.42
1:A:298:ASP:OD2	4:A:901:HOH:O	2.22	0.42
1:B:327:PHE:N	1:B:328:PRO:HD2	2.34	0.42
1:C:387:PRO:O	1:C:390:LEU:HB2	2.20	0.42
1:A:31:GLN:HG3	2:A:802:GOL:C3	2.50	0.42
1:B:266:PHE:CE1	1:B:268:ASN:HB2	2.55	0.42
1:A:31:GLN:CG	2:A:802:GOL:H32	2.49	0.42
1:C:452:GLU:HB3	1:C:453:PRO:HD3	2.02	0.42
1:A:205:ARG:NH2	1:A:344:ASP:CG	2.77	0.41
1:A:224:ALA:HB1	1:A:274:THR:HG21	2.02	0.41
1:A:31:GLN:HG3	2:A:802:GOL:H32	2.02	0.41
1:B:42:HIS:CD2	1:C:252:GLY:HA3	2.55	0.41
1:C:302:LEU:O	1:C:306:GLU:HG2	2.20	0.41
1:A:14:GLN:HA	1:A:14:GLN:OE1	2.20	0.41
1:C:207:ASP:CG	1:C:210:ILE:HG23	2.46	0.41
1:B:335:ALA:O	1:B:337:LEU:N	2.53	0.41
1:B:427:PHE:N	1:B:428:PRO:CD	2.83	0.41
1:C:357:ILE:HD12	1:C:357:ILE:N	2.36	0.41
1:B:205:ARG:HB3	1:B:206:PRO:HD2	2.03	0.41
1:B:387:PRO:O	1:B:390:LEU:HB2	2.21	0.41
1:A:163:GLU:OE1	1:A:382:ARG:HD3	2.21	0.40
1:C:30:ASP:HB3	1:C:43:ARG:HH21	1.86	0.40
1:C:207:ASP:OD2	1:C:210:ILE:HG23	2.21	0.40
1:A:196:LEU:HD11	1:A:354:PRO:HG3	2.03	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1042:HOH:O	4:A:1042:HOH:O[4_555]	1.83	0.37
4:A:1032:HOH:O	4:A:1039:HOH:O[3_655]	2.07	0.13

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	508/510 (100%)	499 (98%)	8 (2%)	1 (0%)	43	66
1	B	508/510 (100%)	479 (94%)	24 (5%)	5 (1%)	12	28
1	C	508/510 (100%)	494 (97%)	12 (2%)	2 (0%)	30	51
All	All	1524/1530 (100%)	1472 (97%)	44 (3%)	8 (0%)	24	46

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	205	ARG
1	C	205	ARG
1	C	508	LEU
1	B	206	PRO
1	B	214	PRO
1	B	336	SER
1	B	215	TYR
1	B	213	ARG

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	412/412 (100%)	402 (98%)	10 (2%)	43	70
1	B	412/412 (100%)	400 (97%)	12 (3%)	37	65
1	C	412/412 (100%)	384 (93%)	28 (7%)	14	32
All	All	1236/1236 (100%)	1186 (96%)	50 (4%)	28	55

All (50) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	103	ARG

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Mol	Chain	Res	Type
1	A	196	LEU
1	A	200	LEU
1	A	205	ARG
1	A	249	ILE
1	A	261	ARG
1	A	305	HIS
1	A	337	LEU
1	A	372	VAL
1	A	407	LYS
1	B	22	SER
1	B	56	GLN
1	B	126	ASP
1	B	129	ARG
1	B	187	GLU
1	B	196	LEU
1	B	197	ASP
1	B	211	LEU
1	B	277	GLU
1	B	372	VAL
1	B	468	ARG
1	B	486	ARG
1	C	103	ARG
1	C	106	VAL
1	C	121	GLU
1	C	129	ARG
1	C	132	LEU
1	C	142	THR
1	C	148	VAL
1	C	149	LEU
1	C	152	LEU
1	C	188	LEU
1	C	193	LYS
1	C	196	LEU
1	C	202	SER
1	C	204	LYS
1	C	205	ARG
1	C	211	LEU
1	C	217	VAL
1	C	251	ILE
1	C	260	THR
1	C	264	GLU
1	C	290	GLU

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Mol	Chain	Res	Type
1	C	305	HIS
1	C	311	THR
1	C	371	LEU
1	C	378	LEU
1	C	382	ARG
1	C	390	LEU
1	C	413	VAL

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	42	HIS
1	A	92	GLN
1	A	212	HIS
1	A	346	HIS
1	A	442	GLN
1	B	8	GLN
1	B	31	GLN
1	B	40	HIS
1	B	77	GLN
1	B	212	HIS
1	C	245	HIS
1	C	442	GLN

5.3.3 RNA [i](#)

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](#)

Of 7 ligands modelled in this entry, 3 are monoatomic - leaving 4 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	$\# Z > 2$
2	GOL	A	802	-	5,5,5	0.67	0	5,5,5	1.29	0
2	GOL	A	803	-	5,5,5	0.52	0	5,5,5	0.23	0
2	GOL	A	801	-	5,5,5	0.91	0	5,5,5	0.94	0
2	GOL	C	601	-	5,5,5	0.57	0	5,5,5	0.29	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
2	GOL	A	802	-	-	3/4/4/4	-
2	GOL	A	803	-	-	2/4/4/4	-
2	GOL	A	801	-	-	4/4/4/4	-
2	GOL	C	601	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	801	GOL	O1-C1-C2-C3
2	A	801	GOL	O2-C2-C3-O3
2	A	802	GOL	O1-C1-C2-O2
2	A	802	GOL	O1-C1-C2-C3
2	A	803	GOL	O2-C2-C3-O3
2	A	801	GOL	C1-C2-C3-O3
2	A	803	GOL	C1-C2-C3-O3
2	A	801	GOL	O1-C1-C2-O2
2	A	802	GOL	O2-C2-C3-O3

There are no ring outliers.

2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	802	GOL	6	0
2	A	803	GOL	1	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	510/510 (100%)	-0.58	4 (0%) 82 80	18, 32, 51, 75	0
1	B	510/510 (100%)	0.28	16 (3%) 51 45	30, 52, 84, 106	0
1	C	510/510 (100%)	-0.05	11 (2%) 62 57	28, 46, 73, 102	0
All	All	1530/1530 (100%)	-0.12	31 (2%) 65 60	18, 44, 77, 106	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	205	ARG	3.2
1	B	269	ALA	3.1
1	B	129	ARG	3.0
1	C	205	ARG	3.0
1	B	206	PRO	3.0
1	C	203	GLY	2.9
1	C	340	VAL	2.9
1	B	266	PHE	2.9
1	B	214	PRO	2.8
1	B	320	LEU	2.8
1	B	215	TYR	2.8
1	C	334	PHE	2.5
1	B	124	PRO	2.4
1	C	407	LYS	2.4
1	B	336	SER	2.3
1	A	392	GLU	2.3
1	B	136	LYS	2.3
1	B	405	ALA	2.2
1	C	204	LYS	2.2
1	B	510	GLY	2.2
1	B	265	ASP	2.2
1	B	508	LEU	2.2
1	C	337	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	200	LEU	2.1
1	A	407	LYS	2.1
1	C	1	MET	2.1
1	B	134	TYR	2.1
1	B	359	VAL	2.1
1	C	405	ALA	2.0
1	C	193	LYS	2.0
1	C	510	GLY	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
2	GOL	A	801	6/6	0.90	0.18	33,38,48,53	0
2	GOL	A	802	6/6	0.91	0.19	42,45,48,48	0
2	GOL	C	601	6/6	0.91	0.22	63,84,88,89	0
2	GOL	A	803	6/6	0.94	0.23	81,85,88,88	0
3	ZN	B	601	1/1	0.97	0.05	83,83,83,83	0
3	ZN	C	602	1/1	0.97	0.04	61,61,61,61	0
3	ZN	A	804	1/1	0.98	0.04	53,53,53,53	0

6.5 Other polymers [i](#)

There are no such residues in this entry.