



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 09:33 PM UTC

PDB ID : 6EU7 / pdb_00006eu7
Title : Structure of the arsenite-bound form of AioX from Rhizobium sp. str. NT-26
Authors : Djordjevic, S.; Badilla, C.; Cole, A.; Santini, J.
Deposited on : 2017-10-28
Resolution : 3.00 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
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

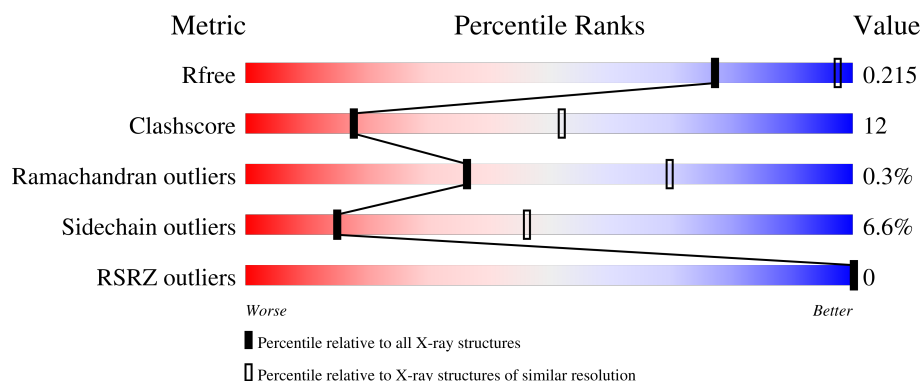
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	283	
1	B	283	
1	C	283	
1	D	283	
1	E	283	

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Mol	Chain	Length	Quality of chain
1	F	283	 A horizontal bar chart showing the quality of the chain. The bar is divided into four segments: green (72%), yellow (15%), orange (9%), and grey (4%). The percentages are labeled below the bar: 72%, 15%, 9%, and 4%.

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 12169 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 Putative periplasmic phosphite-binding-like protein (Pbl) PtxB-like protein designated AioX.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	260	Total	As	C	N	O	S	0	0	0
			2035	1	1289	353	386	6			
1	B	261	Total	As	C	N	O	S	0	0	0
			2040	1	1292	354	387	6			
1	C	260	Total	As	C	N	O	S	0	0	0
			2035	1	1289	353	386	6			
1	D	257	Total	As	C	N	O	S	0	0	0
			2019	1	1279	350	383	6			
1	E	257	Total	As	C	N	O	S	0	0	0
			2019	1	1279	350	383	6			
1	F	257	Total	As	C	N	O	S	0	0	0
			2019	1	1279	350	383	6			

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	22	GLY	-	expression tag	UNP L0NML6
A	23	ALA	-	expression tag	UNP L0NML6
A	24	MET	-	expression tag	UNP L0NML6
A	25	GLY	-	expression tag	UNP L0NML6
A	26	SER	-	expression tag	UNP L0NML6
B	22	GLY	-	expression tag	UNP L0NML6
B	23	ALA	-	expression tag	UNP L0NML6
B	24	MET	-	expression tag	UNP L0NML6
B	25	GLY	-	expression tag	UNP L0NML6
B	26	SER	-	expression tag	UNP L0NML6
C	22	GLY	-	expression tag	UNP L0NML6
C	23	ALA	-	expression tag	UNP L0NML6
C	24	MET	-	expression tag	UNP L0NML6
C	25	GLY	-	expression tag	UNP L0NML6
C	26	SER	-	expression tag	UNP L0NML6
D	22	GLY	-	expression tag	UNP L0NML6

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Chain	Residue	Modelled	Actual	Comment	Reference
D	23	ALA	-	expression tag	UNP L0NML6
D	24	MET	-	expression tag	UNP L0NML6
D	25	GLY	-	expression tag	UNP L0NML6
D	26	SER	-	expression tag	UNP L0NML6
E	22	GLY	-	expression tag	UNP L0NML6
E	23	ALA	-	expression tag	UNP L0NML6
E	24	MET	-	expression tag	UNP L0NML6
E	25	GLY	-	expression tag	UNP L0NML6
E	26	SER	-	expression tag	UNP L0NML6
F	22	GLY	-	expression tag	UNP L0NML6
F	23	ALA	-	expression tag	UNP L0NML6
F	24	MET	-	expression tag	UNP L0NML6
F	25	GLY	-	expression tag	UNP L0NML6
F	26	SER	-	expression tag	UNP L0NML6

- Molecule 2 is water.

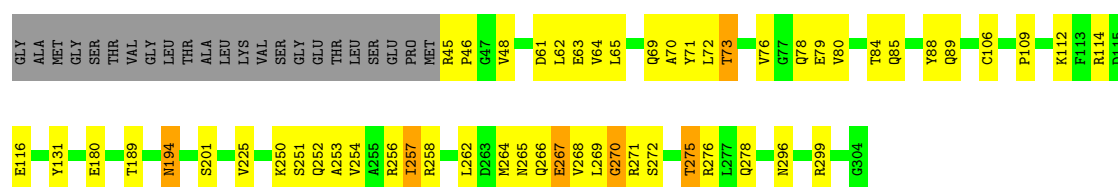
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	D	1	Total O 1 1	0	0
2	E	1	Total O 1 1	0	0

3 Residue-property plots

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.

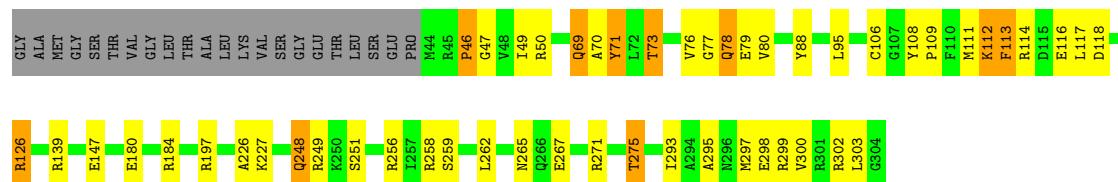
- Molecule 1: Putative periplasmic phosphite-binding-like protein (Pbl) PtxB-like protein designated AioX

Chain A: 



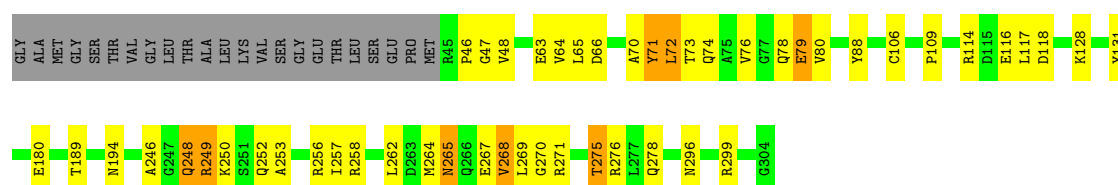
- Molecule 1: Putative periplasmic phosphite-binding-like protein (Pbl) PtxB-like protein designated AioX

Chain B: 



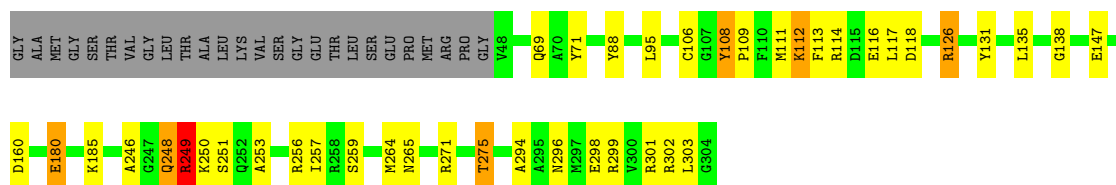
- Molecule 1: Putative periplasmic phosphite-binding-like protein (Pbl) PtxB-like protein designated AioX

Chain C: 



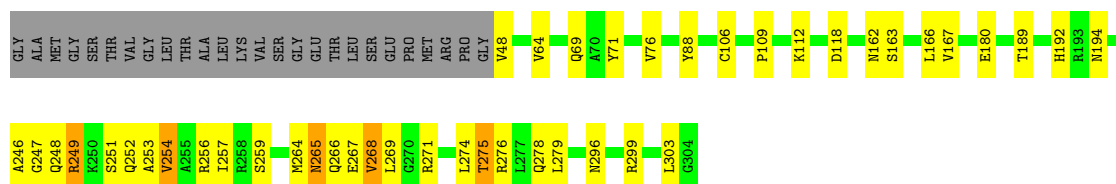
- Molecule 1: Putative periplasmic phosphite-binding-like protein (Pbl) PtxB-like protein designated AioX

Chain D: 



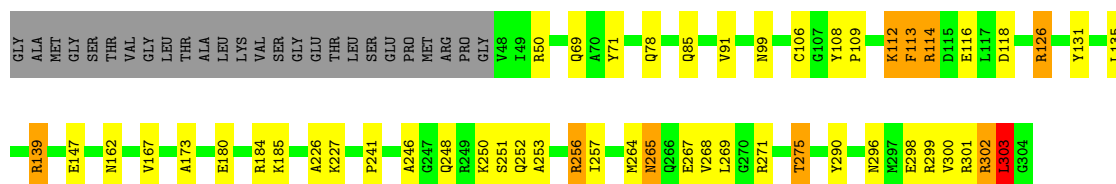
- Molecule 1: Putative periplasmic phosphite-binding-like protein (Pbl) PtxB-like protein designated AioX

Chain E: 75% 14% 9%



- Molecule 1: Putative periplasmic phosphite-binding-like protein (Pbl) PtxB-like protein designated AioX

Chain F: 72% 15% 9%



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	202.36Å 116.92Å 136.84Å 90.00° 90.02° 90.00°	Depositor
Resolution (Å)	136.84 – 3.00 136.84 – 3.00	Depositor EDS
% Data completeness (in resolution range)	97.7 (136.84-3.00) 97.5 (136.84-3.00)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.46 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.8.0103	Depositor
R, R_{free}	0.192 , 0.215 0.192 , 0.215	Depositor DCC
R_{free} test set	3194 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	57.5	Xtriage
Anisotropy	0.361	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 14.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.027 for -1/2*h+3/2*k,1/2*h+1/2*k,-l 0.027 for -1/2*h-3/2*k,-1/2*h+1/2*k,-l 0.457 for 1/2*h+3/2*k,1/2*h-1/2*k,-l 0.450 for 1/2*h-3/2*k,-1/2*h-1/2*k,-l 0.026 for -h,-k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	12169	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.12% 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: CZ2

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	0.95	0/2066	1.06	1/2801 (0.0%)
1	B	0.94	0/2071	1.06	1/2808 (0.0%)
1	C	0.94	0/2066	1.10	1/2801 (0.0%)
1	D	0.91	1/2049 (0.0%)	1.05	3/2777 (0.1%)
1	E	0.92	0/2049	1.06	1/2777 (0.0%)
1	F	0.94	0/2049	1.08	2/2777 (0.1%)
All	All	0.93	1/12350 (0.0%)	1.07	9/16741 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	108	TYR	N-CA	-6.16	1.42	1.46

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	126	ARG	CG-CD-NE	6.32	125.91	112.00
1	D	126	ARG	CG-CD-NE	6.22	125.68	112.00
1	F	126	ARG	CG-CD-NE	6.10	125.42	112.00
1	D	249	ARG	N-CA-C	5.79	117.67	111.36
1	C	248	GLN	N-CA-C	-5.68	102.79	110.68
1	D	138	GLY	N-CA-C	-5.48	106.30	112.33
1	F	303	LEU	N-CA-C	5.45	117.22	111.28
1	A	194	ASN	N-CA-C	5.41	117.18	111.28
1	E	166	LEU	N-CA-C	5.13	116.87	111.28

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	2035	0	2003	64	0
1	B	2040	0	2005	58	0
1	C	2035	0	2003	58	0
1	D	2019	0	1991	38	0
1	E	2019	0	1991	45	0
1	F	2019	0	1991	42	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
All	All	12169	0	11984	297	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 12.

All (297) 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:E:249:ARG:HH11	1:E:249:ARG:HB2	1.15	1.09
1:A:73:THR:HG22	1:A:78:GLN:O	1.53	1.08
1:A:73:THR:CG2	1:A:79:GLU:HA	1.87	1.03
1:E:249:ARG:HH11	1:E:249:ARG:CB	1.74	0.99
1:A:253:ALA:O	1:A:257:ILE:HG13	1.60	0.98
1:A:73:THR:HG21	1:A:79:GLU:HA	1.44	0.96
1:C:71:TYR:HD2	1:C:71:TYR:O	1.47	0.96
1:A:71:TYR:OH	1:A:264:MET:HA	1.67	0.93
1:E:118:ASP:OD2	1:E:249:ARG:HG3	1.73	0.86
1:E:267:GLU:O	1:E:271:ARG:HG3	1.75	0.85
1:D:246:ALA:O	1:D:249:ARG:HD3	1.77	0.85
1:B:248:GLN:HG2	1:B:251:SER:HB2	1.59	0.84
1:B:139:ARG:HD3	1:B:226:ALA:O	1.79	0.83
1:A:73:THR:CG2	1:A:78:GLN:O	2.26	0.83
1:F:139:ARG:HG2	1:F:139:ARG:HH21	1.43	0.83
1:B:112:LYS:HD2	1:B:113:PHE:HE2	1.45	0.82
1:E:249:ARG:HB2	1:E:249:ARG:NH1	1.95	0.82
1:A:267:GLU:O	1:A:271:ARG:CZ	2.28	0.81
1:A:252:GLN:NE2	1:A:256:ARG:HH21	1.78	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:246:ALA:O	1:E:249:ARG:HB2	1.80	0.80
1:B:73:THR:CG2	1:B:79:GLU:HA	2.11	0.80
1:C:71:TYR:HD2	1:C:71:TYR:C	1.90	0.80
1:B:295:ALA:O	1:B:299:ARG:HG3	1.82	0.79
1:B:112:LYS:HD2	1:B:113:PHE:CE2	2.18	0.79
1:B:299:ARG:O	1:B:303:LEU:HB2	1.83	0.79
1:F:268:VAL:HG23	1:F:269:LEU:N	1.98	0.78
1:C:253:ALA:O	1:C:257:ILE:HG13	1.87	0.75
1:C:71:TYR:C	1:C:71:TYR:CD2	2.63	0.75
1:F:173:ALA:O	1:F:303:LEU:HD22	1.86	0.75
1:B:112:LYS:C	1:B:113:PHE:CD2	2.66	0.74
1:A:267:GLU:O	1:A:271:ARG:NH2	2.21	0.73
1:C:71:TYR:O	1:C:71:TYR:CD2	2.38	0.73
1:A:71:TYR:CZ	1:A:264:MET:HA	2.23	0.73
1:E:162:ASN:O	1:E:167:VAL:HG23	1.88	0.72
1:F:139:ARG:HG2	1:F:139:ARG:NH2	2.02	0.72
1:F:299:ARG:HG3	1:F:302:ARG:NH2	2.05	0.72
1:E:248:GLN:HG3	1:E:251:SER:HB2	1.71	0.71
1:A:73:THR:HG23	1:A:80:VAL:N	2.05	0.71
1:A:73:THR:HG23	1:A:80:VAL:H	1.54	0.70
1:D:118:ASP:OD2	1:D:246:ALA:HA	1.91	0.70
1:A:71:TYR:OH	1:A:264:MET:CA	2.40	0.69
1:A:73:THR:CG2	1:A:79:GLU:CA	2.70	0.69
1:D:114:ARG:HD2	1:D:114:ARG:O	1.94	0.68
1:E:266:GLN:O	1:E:267:GLU:CD	2.37	0.67
1:D:112:LYS:HD2	1:D:113:PHE:CE2	2.30	0.67
1:F:112:LYS:HD2	1:F:113:PHE:HE2	1.60	0.67
1:C:114:ARG:NH1	1:C:117:LEU:O	2.27	0.67
1:D:296:ASN:OD1	1:D:299:ARG:NH1	2.29	0.66
1:C:71:TYR:HE1	1:C:264:MET:HG3	1.60	0.66
1:F:268:VAL:HG23	1:F:269:LEU:H	1.59	0.66
1:C:258:ARG:HB2	1:C:258:ARG:NH1	2.12	0.65
1:A:251:SER:HB3	1:A:254:VAL:HG23	1.77	0.64
1:B:184:ARG:HH11	1:B:184:ARG:HG2	1.62	0.64
1:F:296:ASN:OD1	1:F:299:ARG:NH1	2.30	0.64
1:A:61:ASP:CG	1:A:64:VAL:HG23	2.22	0.64
1:B:46:PRO:CD	1:B:47:GLY:H	2.13	0.62
1:C:71:TYR:OH	1:C:264:MET:HA	1.99	0.62
1:B:112:LYS:C	1:B:113:PHE:HD2	2.08	0.62
1:A:73:THR:HG22	1:A:78:GLN:C	2.24	0.62
1:D:246:ALA:O	1:D:249:ARG:CD	2.47	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:73:THR:HG23	1:C:78:GLN:O	1.99	0.62
1:C:252:GLN:HG2	1:C:253:ALA:N	2.14	0.62
1:B:73:THR:HG23	1:B:79:GLU:HA	1.81	0.61
1:C:118:ASP:OD2	1:C:249:ARG:HG2	2.00	0.61
1:A:73:THR:HG23	1:A:80:VAL:HG23	1.81	0.61
1:C:265:ASN:OD1	1:C:265:ASN:N	2.31	0.61
1:D:108:TYR:HB3	1:D:109:PRO:HD3	1.83	0.61
1:E:246:ALA:O	1:E:249:ARG:NH1	2.34	0.61
1:C:63:GLU:OE1	1:C:276:ARG:NH2	2.34	0.61
1:B:46:PRO:HD2	1:B:47:GLY:H	1.66	0.61
1:B:73:THR:O	1:B:77:GLY:N	2.34	0.60
1:B:76:VAL:HG12	1:B:78:GLN:HG3	1.82	0.60
1:C:76:VAL:HG13	1:C:256:ARG:HD2	1.82	0.60
1:C:71:TYR:CE1	1:C:264:MET:HG3	2.37	0.60
1:C:252:GLN:O	1:C:256:ARG:N	2.25	0.60
1:F:248:GLN:HG2	1:F:251:SER:HB2	1.84	0.60
1:A:267:GLU:C	1:A:271:ARG:NH2	2.60	0.59
1:D:249:ARG:HH11	1:D:249:ARG:CG	2.15	0.59
1:C:258:ARG:HH11	1:C:258:ARG:CB	2.16	0.59
1:A:269:LEU:O	1:A:272:SER:N	2.36	0.59
1:E:76:VAL:HG13	1:E:256:ARG:HD2	1.82	0.59
1:F:112:LYS:HB3	1:F:113:PHE:CD2	2.37	0.59
1:A:71:TYR:CE1	1:A:270:GLY:HA3	2.37	0.59
1:C:72:LEU:O	1:C:76:VAL:HG23	2.03	0.59
1:F:268:VAL:CG2	1:F:269:LEU:N	2.66	0.59
1:D:249:ARG:HG2	1:D:249:ARG:NH1	2.17	0.59
1:E:248:GLN:O	1:E:248:GLN:HG2	2.02	0.58
1:A:252:GLN:HE21	1:A:256:ARG:HH21	1.49	0.58
1:B:73:THR:CG2	1:B:78:GLN:O	2.52	0.58
1:E:267:GLU:O	1:E:271:ARG:CG	2.49	0.58
1:B:118:ASP:OD2	1:B:249:ARG:NE	2.27	0.58
1:C:118:ASP:OD2	1:C:249:ARG:CG	2.51	0.58
1:D:112:LYS:HD2	1:D:113:PHE:HE2	1.68	0.58
1:D:299:ARG:O	1:D:303:LEU:HB2	2.04	0.58
1:A:296:ASN:OD1	1:A:299:ARG:NH1	2.36	0.57
1:C:76:VAL:O	1:C:76:VAL:HG12	2.03	0.57
1:C:296:ASN:OD1	1:C:299:ARG:NH1	2.37	0.57
1:D:118:ASP:OD2	1:D:249:ARG:HD2	2.05	0.57
1:E:248:GLN:CG	1:E:251:SER:HB2	2.34	0.57
1:C:267:GLU:O	1:C:271:ARG:CZ	2.53	0.57
1:D:114:ARG:HD2	1:D:114:ARG:C	2.30	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:256:ARG:O	1:B:259:SER:HB2	2.05	0.56
1:B:76:VAL:HG12	1:B:76:VAL:O	2.04	0.56
1:A:71:TYR:HD2	1:A:72:LEU:HD23	1.70	0.56
1:C:249:ARG:CG	1:C:249:ARG:HH11	2.17	0.56
1:E:296:ASN:OD1	1:E:299:ARG:NH1	2.38	0.56
1:A:265:ASN:OD1	1:A:265:ASN:N	2.36	0.56
1:B:73:THR:HG21	1:B:79:GLU:HA	1.88	0.56
1:B:76:VAL:HG13	1:B:256:ARG:HD2	1.86	0.56
1:E:278:GLN:OE1	1:F:126:ARG:NH2	2.38	0.56
1:A:266:GLN:C	1:A:271:ARG:HH21	2.14	0.55
1:A:64:VAL:HG22	1:A:276:ARG:HD3	1.88	0.55
1:A:71:TYR:CE1	1:A:264:MET:HA	2.41	0.55
1:C:73:THR:HG23	1:C:79:GLU:HA	1.86	0.55
1:D:106:CZ2:HB2	1:D:109:PRO:HD2	1.88	0.55
1:F:113:PHE:CD2	1:F:113:PHE:N	2.74	0.55
1:B:139:ARG:CD	1:B:226:ALA:O	2.54	0.55
1:B:258:ARG:O	1:B:262:LEU:HD12	2.07	0.55
1:B:113:PHE:CD2	1:B:113:PHE:N	2.74	0.55
1:B:184:ARG:HG2	1:B:184:ARG:NH1	2.21	0.55
1:C:48:VAL:HG13	1:C:48:VAL:O	2.06	0.55
1:E:265:ASN:OD1	1:E:265:ASN:N	2.39	0.55
1:C:71:TYR:CE1	1:C:264:MET:HA	2.43	0.54
1:E:266:GLN:O	1:E:267:GLU:OE2	2.24	0.54
1:F:253:ALA:O	1:F:257:ILE:N	2.39	0.54
1:A:71:TYR:CD1	1:A:270:GLY:CA	2.91	0.54
1:A:252:GLN:NE2	1:A:256:ARG:NH2	2.54	0.54
1:D:302:ARG:O	1:D:302:ARG:HG2	2.08	0.54
1:E:64:VAL:HG22	1:E:276:ARG:HD3	1.90	0.54
1:E:249:ARG:HH11	1:E:249:ARG:CG	2.19	0.54
1:D:249:ARG:HH11	1:D:249:ARG:HG2	1.73	0.54
1:A:76:VAL:HG12	1:A:76:VAL:O	2.08	0.53
1:B:71:TYR:C	1:B:71:TYR:CD2	2.85	0.53
1:F:299:ARG:O	1:F:303:LEU:HB2	2.09	0.53
1:A:71:TYR:C	1:A:71:TYR:CD2	2.86	0.53
1:C:278:GLN:OE1	1:D:126:ARG:NH2	2.42	0.53
1:D:248:GLN:HG2	1:D:251:SER:HB2	1.90	0.53
1:F:71:TYR:OH	1:F:264:MET:HA	2.08	0.53
1:F:118:ASP:OD2	1:F:246:ALA:HA	2.09	0.53
1:B:73:THR:HG23	1:B:78:GLN:O	2.09	0.52
1:E:254:VAL:O	1:E:257:ILE:N	2.41	0.52
1:A:278:GLN:OE1	1:B:126:ARG:NH2	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:71:TYR:OH	1:E:264:MET:HA	2.08	0.52
1:E:247:GLY:C	1:E:249:ARG:H	2.17	0.52
1:A:268:VAL:HA	1:A:271:ARG:HH12	1.75	0.52
1:A:201:SER:HB3	1:D:180:GLU:CB	2.40	0.52
1:F:268:VAL:CG2	1:F:269:LEU:H	2.20	0.52
1:E:266:GLN:C	1:E:267:GLU:CD	2.78	0.52
1:F:139:ARG:HH21	1:F:139:ARG:CG	2.18	0.51
1:C:249:ARG:NH1	1:C:249:ARG:HG3	2.24	0.51
1:C:71:TYR:HD1	1:C:270:GLY:HA2	1.75	0.51
1:F:112:LYS:HB3	1:F:113:PHE:HD2	1.75	0.51
1:F:184:ARG:HG3	1:F:184:ARG:HH11	1.74	0.51
1:D:298:GLU:CD	1:D:301:ARG:HH21	2.18	0.51
1:B:293:ILE:O	1:B:297:MET:HG3	2.11	0.51
1:A:88:TYR:OH	1:A:106:CZ2:O1	2.25	0.50
1:C:64:VAL:HG22	1:C:276:ARG:HD3	1.93	0.50
1:D:112:LYS:C	1:D:113:PHE:CD2	2.89	0.50
1:E:251:SER:HB3	1:E:254:VAL:HG23	1.94	0.50
1:F:78:GLN:OE1	1:F:256:ARG:NH2	2.44	0.50
1:A:84:THR:O	1:A:85:GLN:NE2	2.25	0.50
1:F:162:ASN:O	1:F:167:VAL:HG23	2.12	0.50
1:B:46:PRO:CG	1:B:47:GLY:N	2.75	0.50
1:E:88:TYR:OH	1:E:106:CZ2:O1	2.22	0.50
1:F:302:ARG:CG	1:F:303:LEU:N	2.75	0.50
1:D:249:ARG:CG	1:D:249:ARG:NH1	2.74	0.49
1:B:88:TYR:OH	1:B:106:CZ2:O1	2.24	0.49
1:B:106:CZ2:HB2	1:B:109:PRO:HD2	1.94	0.49
1:A:268:VAL:HA	1:A:271:ARG:NH1	2.28	0.49
1:C:246:ALA:O	1:C:249:ARG:HB2	2.12	0.49
1:E:274:LEU:HB3	1:E:279:LEU:O	2.12	0.49
1:F:298:GLU:CD	1:F:301:ARG:HH21	2.20	0.49
1:F:265:ASN:OD1	1:F:265:ASN:N	2.35	0.49
1:C:258:ARG:NH1	1:C:258:ARG:CB	2.75	0.49
1:D:88:TYR:OH	1:D:106:CZ2:O1	2.23	0.49
1:D:71:TYR:OH	1:D:264:MET:HA	2.12	0.49
1:B:76:VAL:HG12	1:B:78:GLN:CG	2.42	0.48
1:F:112:LYS:HD2	1:F:113:PHE:CE2	2.46	0.48
1:C:70:ALA:HB3	1:C:269:LEU:HD21	1.94	0.48
1:E:71:TYR:HB2	1:E:269:LEU:HD23	1.95	0.48
1:E:266:GLN:C	1:E:267:GLU:OE2	2.57	0.48
1:B:73:THR:HG22	1:B:78:GLN:O	2.14	0.48
1:C:252:GLN:CG	1:C:253:ALA:N	2.76	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:258:ARG:HG2	1:C:262:LEU:CD1	2.44	0.48
1:B:46:PRO:CG	1:B:47:GLY:H	2.27	0.48
1:A:71:TYR:CD1	1:A:270:GLY:HA3	2.49	0.48
1:B:73:THR:HG23	1:B:80:VAL:N	2.30	0.47
1:A:48:VAL:HG13	1:A:48:VAL:O	2.14	0.47
1:B:112:LYS:HB3	1:B:113:PHE:CD2	2.49	0.47
1:F:71:TYR:C	1:F:71:TYR:CD2	2.92	0.47
1:A:276:ARG:HG2	1:A:276:ARG:HH11	1.78	0.47
1:A:254:VAL:O	1:A:258:ARG:N	2.35	0.47
1:A:268:VAL:HG13	1:A:269:LEU:N	2.30	0.47
1:B:46:PRO:CD	1:B:47:GLY:N	2.77	0.47
1:F:241:PRO:HB3	1:F:290:TYR:OH	2.15	0.47
1:A:201:SER:HB3	1:D:180:GLU:HB3	1.97	0.47
1:C:249:ARG:HH11	1:C:249:ARG:CB	2.27	0.47
1:C:258:ARG:HB2	1:C:258:ARG:HH11	1.77	0.47
1:E:71:TYR:C	1:E:71:TYR:CD2	2.92	0.47
1:F:271:ARG:O	1:F:275:THR:OG1	2.33	0.46
1:B:73:THR:HG23	1:B:80:VAL:H	1.79	0.46
1:B:111:MET:C	1:B:113:PHE:N	2.73	0.46
1:A:276:ARG:HG2	1:A:276:ARG:NH1	2.29	0.46
1:A:62:LEU:HD12	1:D:302:ARG:HA	1.97	0.46
1:A:63:GLU:OE2	1:A:276:ARG:NH2	2.48	0.46
1:E:249:ARG:NH1	1:E:249:ARG:CG	2.78	0.46
1:F:106:CZ2:HB2	1:F:109:PRO:HD2	1.96	0.46
1:C:63:GLU:O	1:C:66:ASP:HB2	2.15	0.46
1:E:48:VAL:O	1:E:48:VAL:HG13	2.16	0.46
1:B:271:ARG:O	1:B:275:THR:OG1	2.33	0.46
1:D:271:ARG:O	1:D:275:THR:OG1	2.34	0.46
1:E:268:VAL:HG13	1:E:271:ARG:HH22	1.80	0.46
1:C:88:TYR:OH	1:C:106:CZ2:O1	2.23	0.45
1:F:173:ALA:O	1:F:303:LEU:CD2	2.62	0.45
1:A:271:ARG:O	1:A:275:THR:OG1	2.32	0.45
1:B:184:ARG:HH11	1:B:184:ARG:CG	2.28	0.45
1:A:262:LEU:N	1:A:262:LEU:HD12	2.30	0.45
1:C:73:THR:HA	1:C:80:VAL:HG23	1.98	0.45
1:A:114:ARG:O	1:A:114:ARG:NH1	2.46	0.45
1:D:109:PRO:HD3	1:D:160:ASP:O	2.17	0.45
1:C:271:ARG:O	1:C:275:THR:OG1	2.34	0.45
1:E:247:GLY:C	1:E:249:ARG:N	2.75	0.45
1:C:267:GLU:O	1:C:271:ARG:NH2	2.50	0.45
1:D:71:TYR:CD2	1:D:71:TYR:C	2.93	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:106:CZ2:HB2	1:A:109:PRO:HD2	1.99	0.44
1:B:113:PHE:HD2	1:B:113:PHE:N	2.13	0.44
1:E:106:CZ2:HB2	1:E:109:PRO:HD2	2.00	0.44
1:E:163:SER:OG	1:E:192:HIS:CE1	2.70	0.44
1:E:268:VAL:CG1	1:E:271:ARG:NH2	2.81	0.44
1:B:69:GLN:O	1:B:73:THR:OG1	2.35	0.44
1:C:249:ARG:HH11	1:C:249:ARG:HG3	1.82	0.44
1:B:265:ASN:OD1	1:B:265:ASN:N	2.48	0.44
1:D:298:GLU:OE2	1:D:301:ARG:NH2	2.47	0.44
1:F:139:ARG:CZ	1:F:226:ALA:O	2.66	0.44
1:C:106:CZ2:HB2	1:C:109:PRO:HD2	2.00	0.44
1:C:268:VAL:HG23	1:C:269:LEU:H	1.83	0.44
1:F:113:PHE:N	1:F:113:PHE:HD2	2.14	0.44
1:B:108:TYR:HB3	1:B:109:PRO:HD3	2.00	0.44
1:D:111:MET:HE3	1:D:294:ALA:HB2	1.99	0.44
1:A:201:SER:HB3	1:D:180:GLU:HB2	1.99	0.44
1:B:95:LEU:CD2	1:B:117:LEU:HD22	2.48	0.44
1:C:258:ARG:O	1:C:262:LEU:HD12	2.18	0.44
1:D:253:ALA:O	1:D:257:ILE:HG13	2.18	0.44
1:A:88:TYR:O	1:A:89:GLN:C	2.61	0.43
1:B:69:GLN:HG3	1:B:70:ALA:N	2.33	0.43
1:A:71:TYR:CD2	1:A:72:LEU:HD23	2.53	0.43
1:A:272:SER:O	1:A:275:THR:OG1	2.36	0.43
1:B:95:LEU:HD23	1:B:117:LEU:HD22	2.00	0.43
1:B:298:GLU:C	1:B:300:VAL:N	2.76	0.43
1:F:298:GLU:OE2	1:F:301:ARG:NH2	2.41	0.43
1:B:73:THR:HG23	1:B:79:GLU:CA	2.47	0.43
1:C:71:TYR:HE1	1:C:264:MET:HA	1.83	0.43
1:E:71:TYR:CA	1:E:269:LEU:HD23	2.48	0.42
1:C:71:TYR:CD1	1:C:270:GLY:CA	3.02	0.42
1:D:108:TYR:HB3	1:D:109:PRO:CD	2.48	0.42
1:C:258:ARG:HG2	1:C:262:LEU:HD12	2.02	0.42
1:F:50:ARG:NH2	1:F:99:ASN:OD1	2.40	0.42
1:C:76:VAL:CG1	1:C:256:ARG:HD2	2.49	0.42
1:D:112:LYS:HB3	1:D:113:PHE:CD2	2.54	0.42
1:A:225:VAL:O	1:A:225:VAL:HG12	2.20	0.41
1:B:112:LYS:O	1:B:113:PHE:CD2	2.73	0.41
1:C:47:GLY:O	1:C:78:GLN:HB2	2.20	0.41
1:C:71:TYR:CZ	1:C:264:MET:HA	2.54	0.41
1:D:265:ASN:OD1	1:D:265:ASN:N	2.51	0.41
1:B:197:ARG:CZ	1:E:303:LEU:HD22	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:249:ARG:HH11	1:C:249:ARG:HB2	1.85	0.41
1:A:62:LEU:HA	1:A:62:LEU:HD23	1.79	0.41
1:A:76:VAL:HG13	1:A:256:ARG:HD2	2.02	0.41
1:B:73:THR:HA	1:B:80:VAL:HG23	2.02	0.41
1:E:189:THR:HB	1:E:194:ASN:HB3	2.02	0.41
1:B:112:LYS:HB3	1:B:113:PHE:CE2	2.55	0.41
1:C:252:GLN:O	1:C:253:ALA:C	2.63	0.41
1:E:269:LEU:HD12	1:E:269:LEU:HA	1.80	0.41
1:E:271:ARG:O	1:E:275:THR:OG1	2.39	0.41
1:D:113:PHE:CD2	1:D:113:PHE:N	2.88	0.41
1:A:45:ARG:N	1:A:46:PRO:CD	2.84	0.41
1:B:113:PHE:HB2	1:B:117:LEU:HD12	2.02	0.41
1:A:189:THR:HB	1:A:194:ASN:HB3	2.03	0.41
1:F:184:ARG:HG3	1:F:184:ARG:NH1	2.35	0.41
1:C:267:GLU:O	1:C:271:ARG:NH1	2.54	0.41
1:E:252:GLN:O	1:E:253:ALA:C	2.64	0.41
1:F:112:LYS:C	1:F:113:PHE:CD2	2.99	0.41
1:B:49:ILE:HG22	1:B:50:ARG:N	2.35	0.40
1:A:267:GLU:C	1:A:271:ARG:HH22	2.30	0.40
1:C:73:THR:CG2	1:C:79:GLU:HA	2.52	0.40
1:C:189:THR:HB	1:C:194:ASN:HB3	2.03	0.40
1:E:248:GLN:CG	1:E:251:SER:CB	2.98	0.40
1:F:85:GLN:HB2	1:F:91:VAL:HG23	2.04	0.40
1:A:70:ALA:HB3	1:A:269:LEU:HD21	2.03	0.40
1:A:268:VAL:CG1	1:A:269:LEU:N	2.84	0.40
1:F:108:TYR:HB3	1:F:109:PRO:HD3	2.02	0.40
1:F:114:ARG:O	1:F:114:ARG:NH1	2.55	0.40
1:A:269:LEU:O	1:A:271:ARG:N	2.54	0.40
1:B:298:GLU:O	1:B:299:ARG:C	2.61	0.40
1:F:302:ARG:HG2	1:F:303:LEU:H	1.86	0.40
1:D:95:LEU:CD2	1:D:117:LEU:HD22	2.51	0.40
1:E:268:VAL:HG13	1:E:271:ARG:NH2	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	257/283 (91%)	244 (95%)	12 (5%)	1 (0%)	30	65
1	B	258/283 (91%)	244 (95%)	13 (5%)	1 (0%)	30	65
1	C	257/283 (91%)	251 (98%)	5 (2%)	1 (0%)	30	65
1	D	254/283 (90%)	239 (94%)	15 (6%)	0	100	100
1	E	254/283 (90%)	242 (95%)	11 (4%)	1 (0%)	30	65
1	F	254/283 (90%)	243 (96%)	11 (4%)	0	100	100
All	All	1534/1698 (90%)	1463 (95%)	67 (4%)	4 (0%)	36	70

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	46	PRO
1	C	46	PRO
1	A	270	GLY
1	E	254	VAL

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	213/231 (92%)	202 (95%)	11 (5%)	21	55
1	B	213/231 (92%)	198 (93%)	15 (7%)	14	44
1	C	213/231 (92%)	198 (93%)	15 (7%)	14	44
1	D	212/231 (92%)	198 (93%)	14 (7%)	15	46
1	E	212/231 (92%)	204 (96%)	8 (4%)	29	63
1	F	212/231 (92%)	191 (90%)	21 (10%)	7	30
All	All	1275/1386 (92%)	1191 (93%)	84 (7%)	15	46

All (84) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	65	LEU
1	A	69	GLN
1	A	73	THR
1	A	112	LYS
1	A	116	GLU
1	A	131	TYR
1	A	180	GLU
1	A	250	LYS
1	A	257	ILE
1	A	267	GLU
1	A	275	THR
1	B	69	GLN
1	B	71	TYR
1	B	73	THR
1	B	78	GLN
1	B	112	LYS
1	B	113	PHE
1	B	114	ARG
1	B	116	GLU
1	B	147	GLU
1	B	180	GLU
1	B	227	LYS
1	B	248	GLN
1	B	267	GLU
1	B	275	THR
1	B	302	ARG
1	C	65	LEU
1	C	71	TYR
1	C	72	LEU
1	C	74	GLN
1	C	79	GLU
1	C	116	GLU
1	C	128	LYS
1	C	131	TYR
1	C	180	GLU
1	C	248	GLN
1	C	249	ARG
1	C	250	LYS
1	C	265	ASN
1	C	268	VAL
1	C	275	THR
1	D	69	GLN

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Mol	Chain	Res	Type
1	D	112	LYS
1	D	116	GLU
1	D	131	TYR
1	D	135	LEU
1	D	147	GLU
1	D	180	GLU
1	D	185	LYS
1	D	248	GLN
1	D	249	ARG
1	D	250	LYS
1	D	256	ARG
1	D	259	SER
1	D	275	THR
1	E	69	GLN
1	E	112	LYS
1	E	180	GLU
1	E	249	ARG
1	E	259	SER
1	E	265	ASN
1	E	268	VAL
1	E	275	THR
1	F	69	GLN
1	F	112	LYS
1	F	113	PHE
1	F	114	ARG
1	F	116	GLU
1	F	131	TYR
1	F	135	LEU
1	F	139	ARG
1	F	147	GLU
1	F	180	GLU
1	F	185	LYS
1	F	227	LYS
1	F	250	LYS
1	F	252	GLN
1	F	256	ARG
1	F	265	ASN
1	F	267	GLU
1	F	275	THR
1	F	300	VAL
1	F	302	ARG
1	F	303	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	69	GLN
1	A	132	GLN
1	A	162	ASN
1	A	252	GLN
1	B	89	GLN
1	B	132	GLN
1	B	162	ASN
1	B	248	GLN
1	B	252	GLN
1	C	74	GLN
1	C	78	GLN
1	C	132	GLN
1	C	162	ASN
1	D	85	GLN
1	D	89	GLN
1	D	132	GLN
1	D	162	ASN
1	D	248	GLN
1	E	132	GLN
1	E	252	GLN
1	F	85	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

6 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	CZ2	A	106	1	3,8,9	1.03	0	1,9,11	0.88	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	CZ2	E	106	1	3,8,9	0.75	0	1,9,11	1.10	0
1	CZ2	D	106	1	3,8,9	0.83	0	1,9,11	0.79	0
1	CZ2	C	106	1	3,8,9	0.84	0	1,9,11	1.04	0
1	CZ2	F	106	1	3,8,9	0.81	0	1,9,11	0.90	0
1	CZ2	B	106	1	3,8,9	0.94	0	1,9,11	0.95	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
1	CZ2	A	106	1	-	0/0/7/9	-
1	CZ2	E	106	1	-	0/0/7/9	-
1	CZ2	D	106	1	-	0/0/7/9	-
1	CZ2	C	106	1	-	0/0/7/9	-
1	CZ2	F	106	1	-	0/0/7/9	-
1	CZ2	B	106	1	-	0/0/7/9	-

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.

6 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	106	CZ2	2	0
1	E	106	CZ2	2	0
1	D	106	CZ2	2	0
1	C	106	CZ2	2	0
1	F	106	CZ2	1	0
1	B	106	CZ2	2	0

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	259/283 (91%)	-1.55	0 100 100	25, 54, 104, 134	0
1	B	260/283 (91%)	-1.52	0 100 100	30, 59, 106, 165	0
1	C	259/283 (91%)	-1.54	0 100 100	27, 52, 103, 154	0
1	D	256/283 (90%)	-1.53	0 100 100	30, 57, 103, 135	0
1	E	256/283 (90%)	-1.56	0 100 100	27, 52, 104, 138	0
1	F	256/283 (90%)	-1.53	0 100 100	31, 57, 105, 136	0
All	All	1546/1698 (91%)	-1.54	0 100 100	25, 55, 105, 165	0

There are no RSRZ outliers to report.

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	CZ2	A	106	9/10	1.00	0.01	38,51,55,57	0
1	CZ2	B	106	9/10	1.00	0.01	41,45,53,58	0
1	CZ2	C	106	9/10	1.00	0.02	38,48,53,57	0
1	CZ2	D	106	9/10	1.00	0.01	41,46,51,51	0
1	CZ2	E	106	9/10	1.00	0.01	40,51,56,57	0
1	CZ2	F	106	9/10	1.00	0.01	40,45,53,57	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.