



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:15 AM GMT

PDB ID : 3A3T
Title : The oxidoreductase NmDsbA1 from *N. meningitidis*
Authors : Vivian, J.P.; Scoullar, J.; Bushell, S.; Beddoe, T.; Wilce, M.C.J.; Byres, E.; Boyle, T.P.; Rimmer, K.; Doak, B.; Simpson, J.S.; Graham, B.; Heras, B.; Kahler, C.M.; Rossjohn, J.; Scanlon, M.J.
Deposited on : 2009-06-19
Resolution : 2.10 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

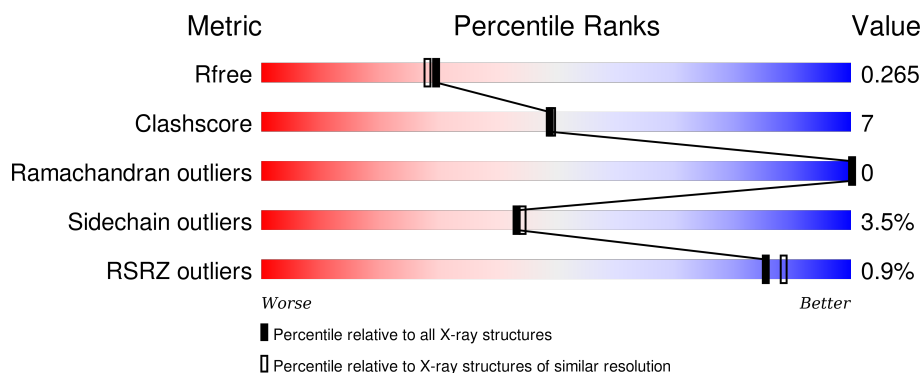
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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}	91344	3939 (2.10-2.10)
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (2.10-2.10)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	210	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 12%, green 79%, grey 8%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 79% 12% 8% </div> </div>
1	B	210	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, yellow 13%, green 77%, orange 8%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 77% 13% 8% </div> </div>
1	C	210	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 10%, green 80%, grey 8%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 80% 10% 8% </div> </div>
1	D	210	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, yellow 14%, green 76%, orange 8%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 76% 14% 8% </div> </div>
1	E	210	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, yellow 11%, green 79%, orange 8%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 79% 11% 8% </div> </div>

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Mol	Chain	Length	Quality of chain
1	F	210	<div><div></div><div>2%</div><div>77%</div><div>14%</div><div>8%</div></div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 9950 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 Thiol:disulfide interchange protein DsbA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	193	Total	C	N	O	S	0	1	0
			1521	964	254	294	9			
1	B	193	Total	C	N	O	S	0	1	0
			1521	964	254	294	9			
1	C	193	Total	C	N	O	S	0	1	0
			1521	964	254	294	9			
1	D	193	Total	C	N	O	S	0	1	0
			1521	964	254	294	9			
1	E	193	Total	C	N	O	S	0	1	0
			1521	964	254	294	9			
1	F	193	Total	C	N	O	S	0	1	0
			1521	964	254	294	9			

There are 114 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	EXPRESSION TAG	UNP Q9K189
A	-18	ALA	-	EXPRESSION TAG	UNP Q9K189
A	-17	HIS	-	EXPRESSION TAG	UNP Q9K189
A	-16	HIS	-	EXPRESSION TAG	UNP Q9K189
A	-15	HIS	-	EXPRESSION TAG	UNP Q9K189
A	-14	HIS	-	EXPRESSION TAG	UNP Q9K189
A	-13	HIS	-	EXPRESSION TAG	UNP Q9K189
A	-12	HIS	-	EXPRESSION TAG	UNP Q9K189
A	-11	VAL	-	EXPRESSION TAG	UNP Q9K189
A	-10	GLY	-	EXPRESSION TAG	UNP Q9K189
A	-9	THR	-	EXPRESSION TAG	UNP Q9K189
A	-8	GLY	-	EXPRESSION TAG	UNP Q9K189
A	-7	SER	-	EXPRESSION TAG	UNP Q9K189
A	-6	ASN	-	EXPRESSION TAG	UNP Q9K189
A	-5	ASP	-	EXPRESSION TAG	UNP Q9K189
A	-4	ASP	-	EXPRESSION TAG	UNP Q9K189
A	-3	ASP	-	EXPRESSION TAG	UNP Q9K189

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	ASP	-	EXPRESSION TAG	UNP Q9K189
A	-1	LYS	-	EXPRESSION TAG	UNP Q9K189
B	-19	MET	-	EXPRESSION TAG	UNP Q9K189
B	-18	ALA	-	EXPRESSION TAG	UNP Q9K189
B	-17	HIS	-	EXPRESSION TAG	UNP Q9K189
B	-16	HIS	-	EXPRESSION TAG	UNP Q9K189
B	-15	HIS	-	EXPRESSION TAG	UNP Q9K189
B	-14	HIS	-	EXPRESSION TAG	UNP Q9K189
B	-13	HIS	-	EXPRESSION TAG	UNP Q9K189
B	-12	HIS	-	EXPRESSION TAG	UNP Q9K189
B	-11	VAL	-	EXPRESSION TAG	UNP Q9K189
B	-10	GLY	-	EXPRESSION TAG	UNP Q9K189
B	-9	THR	-	EXPRESSION TAG	UNP Q9K189
B	-8	GLY	-	EXPRESSION TAG	UNP Q9K189
B	-7	SER	-	EXPRESSION TAG	UNP Q9K189
B	-6	ASN	-	EXPRESSION TAG	UNP Q9K189
B	-5	ASP	-	EXPRESSION TAG	UNP Q9K189
B	-4	ASP	-	EXPRESSION TAG	UNP Q9K189
B	-3	ASP	-	EXPRESSION TAG	UNP Q9K189
B	-2	ASP	-	EXPRESSION TAG	UNP Q9K189
B	-1	LYS	-	EXPRESSION TAG	UNP Q9K189
C	-19	MET	-	EXPRESSION TAG	UNP Q9K189
C	-18	ALA	-	EXPRESSION TAG	UNP Q9K189
C	-17	HIS	-	EXPRESSION TAG	UNP Q9K189
C	-16	HIS	-	EXPRESSION TAG	UNP Q9K189
C	-15	HIS	-	EXPRESSION TAG	UNP Q9K189
C	-14	HIS	-	EXPRESSION TAG	UNP Q9K189
C	-13	HIS	-	EXPRESSION TAG	UNP Q9K189
C	-12	HIS	-	EXPRESSION TAG	UNP Q9K189
C	-11	VAL	-	EXPRESSION TAG	UNP Q9K189
C	-10	GLY	-	EXPRESSION TAG	UNP Q9K189
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C	-6	ASN	-	EXPRESSION TAG	UNP Q9K189
C	-5	ASP	-	EXPRESSION TAG	UNP Q9K189
C	-4	ASP	-	EXPRESSION TAG	UNP Q9K189
C	-3	ASP	-	EXPRESSION TAG	UNP Q9K189
C	-2	ASP	-	EXPRESSION TAG	UNP Q9K189
C	-1	LYS	-	EXPRESSION TAG	UNP Q9K189
D	-19	MET	-	EXPRESSION TAG	UNP Q9K189
D	-18	ALA	-	EXPRESSION TAG	UNP Q9K189

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-17	HIS	-	EXPRESSION TAG	UNP Q9K189
D	-16	HIS	-	EXPRESSION TAG	UNP Q9K189
D	-15	HIS	-	EXPRESSION TAG	UNP Q9K189
D	-14	HIS	-	EXPRESSION TAG	UNP Q9K189
D	-13	HIS	-	EXPRESSION TAG	UNP Q9K189
D	-12	HIS	-	EXPRESSION TAG	UNP Q9K189
D	-11	VAL	-	EXPRESSION TAG	UNP Q9K189
D	-10	GLY	-	EXPRESSION TAG	UNP Q9K189
D	-9	THR	-	EXPRESSION TAG	UNP Q9K189
D	-8	GLY	-	EXPRESSION TAG	UNP Q9K189
D	-7	SER	-	EXPRESSION TAG	UNP Q9K189
D	-6	ASN	-	EXPRESSION TAG	UNP Q9K189
D	-5	ASP	-	EXPRESSION TAG	UNP Q9K189
D	-4	ASP	-	EXPRESSION TAG	UNP Q9K189
D	-3	ASP	-	EXPRESSION TAG	UNP Q9K189
D	-2	ASP	-	EXPRESSION TAG	UNP Q9K189
D	-1	LYS	-	EXPRESSION TAG	UNP Q9K189
E	-19	MET	-	EXPRESSION TAG	UNP Q9K189
E	-18	ALA	-	EXPRESSION TAG	UNP Q9K189
E	-17	HIS	-	EXPRESSION TAG	UNP Q9K189
E	-16	HIS	-	EXPRESSION TAG	UNP Q9K189
E	-15	HIS	-	EXPRESSION TAG	UNP Q9K189
E	-14	HIS	-	EXPRESSION TAG	UNP Q9K189
E	-13	HIS	-	EXPRESSION TAG	UNP Q9K189
E	-12	HIS	-	EXPRESSION TAG	UNP Q9K189
E	-11	VAL	-	EXPRESSION TAG	UNP Q9K189
E	-10	GLY	-	EXPRESSION TAG	UNP Q9K189
E	-9	THR	-	EXPRESSION TAG	UNP Q9K189
E	-8	GLY	-	EXPRESSION TAG	UNP Q9K189
E	-7	SER	-	EXPRESSION TAG	UNP Q9K189
E	-6	ASN	-	EXPRESSION TAG	UNP Q9K189
E	-5	ASP	-	EXPRESSION TAG	UNP Q9K189
E	-4	ASP	-	EXPRESSION TAG	UNP Q9K189
E	-3	ASP	-	EXPRESSION TAG	UNP Q9K189
E	-2	ASP	-	EXPRESSION TAG	UNP Q9K189
E	-1	LYS	-	EXPRESSION TAG	UNP Q9K189
F	-19	MET	-	EXPRESSION TAG	UNP Q9K189
F	-18	ALA	-	EXPRESSION TAG	UNP Q9K189
F	-17	HIS	-	EXPRESSION TAG	UNP Q9K189
F	-16	HIS	-	EXPRESSION TAG	UNP Q9K189
F	-15	HIS	-	EXPRESSION TAG	UNP Q9K189
F	-14	HIS	-	EXPRESSION TAG	UNP Q9K189

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-13	HIS	-	EXPRESSION TAG	UNP Q9K189
F	-12	HIS	-	EXPRESSION TAG	UNP Q9K189
F	-11	VAL	-	EXPRESSION TAG	UNP Q9K189
F	-10	GLY	-	EXPRESSION TAG	UNP Q9K189
F	-9	THR	-	EXPRESSION TAG	UNP Q9K189
F	-8	GLY	-	EXPRESSION TAG	UNP Q9K189
F	-7	SER	-	EXPRESSION TAG	UNP Q9K189
F	-6	ASN	-	EXPRESSION TAG	UNP Q9K189
F	-5	ASP	-	EXPRESSION TAG	UNP Q9K189
F	-4	ASP	-	EXPRESSION TAG	UNP Q9K189
F	-3	ASP	-	EXPRESSION TAG	UNP Q9K189
F	-2	ASP	-	EXPRESSION TAG	UNP Q9K189
F	-1	LYS	-	EXPRESSION TAG	UNP Q9K189

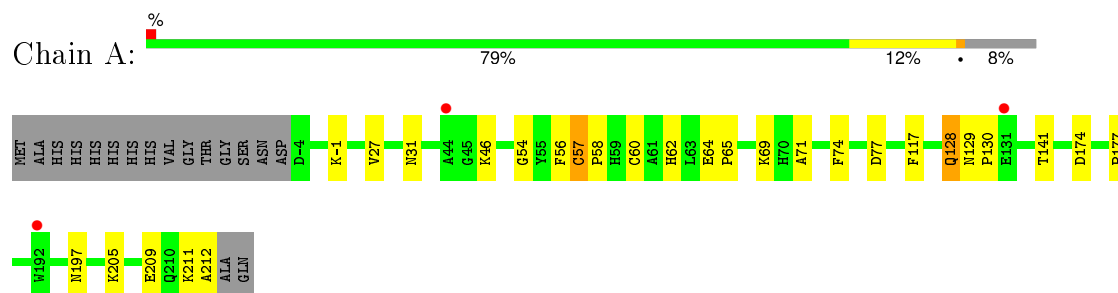
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	143	Total O 143 143	0	0
2	B	123	Total O 123 123	0	0
2	C	159	Total O 159 159	0	0
2	D	163	Total O 163 163	0	0
2	E	133	Total O 133 133	0	0
2	F	103	Total O 103 103	0	0

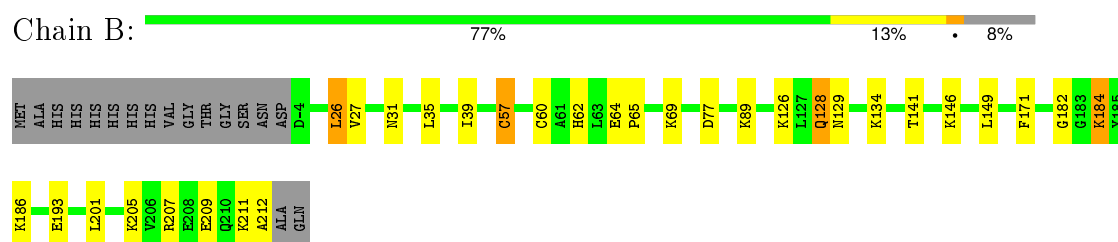
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 ($\text{RSRZ} > 2$). 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.

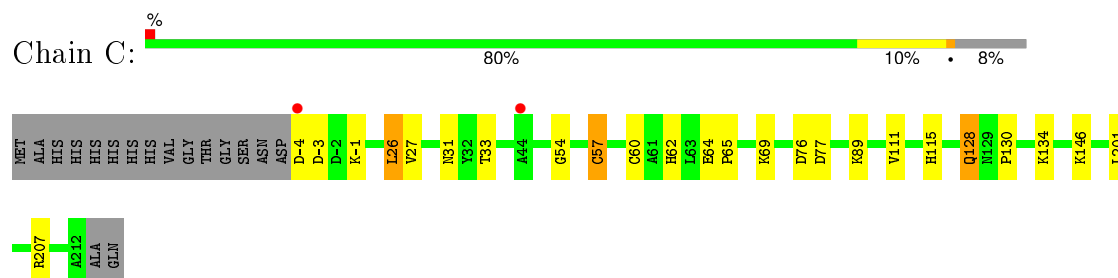
- Molecule 1: Thiol:disulfide interchange protein DsbA



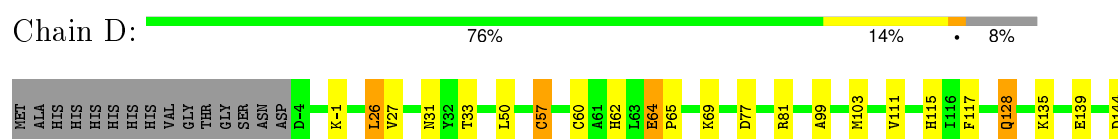
- Molecule 1: Thiol:disulfide interchange protein DsbA



- Molecule 1: Thiol:disulfide interchange protein DsbA

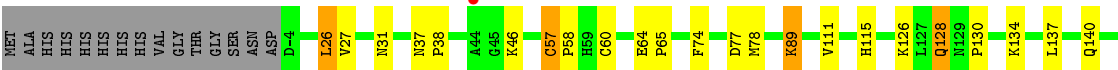
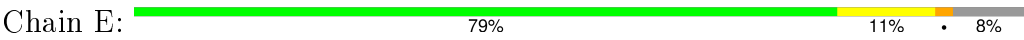


- Molecule 1: Thiol:disulfide interchange protein DsbA

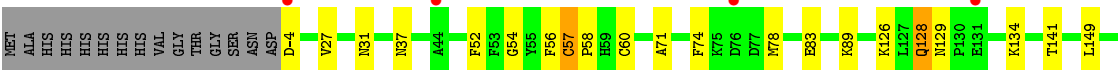
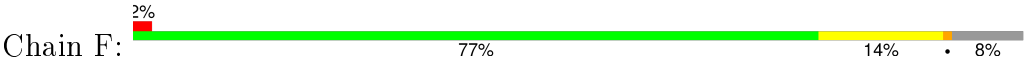




• Molecule 1: Thiol:disulfide interchange protein DsbA



• Molecule 1: Thiol:disulfide interchange protein DsbA



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	88.21Å 59.30Å 126.52Å 90.00° 108.92° 90.00°	Depositor
Resolution (Å)	48.06 – 2.10 48.06 – 2.10	Depositor EDS
% Data completeness (in resolution range)	98.0 (48.06-2.10) 98.0 (48.06-2.10)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.94 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.5.0088	Depositor
R, R_{free}	0.189 , 0.246 0.201 , 0.265	Depositor DCC
R_{free} test set	3604 reflections (5.33%)	DCC
Wilson B-factor (Å ²)	32.8	Xtriage
Anisotropy	0.040	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 38.4	EDS
Estimated twinning fraction	0.024 for h,-k,-h-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	12 of 71253 reflections (0.017%)	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9950	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 50.71 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 6.2235e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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	0.29	0/1554	0.44	0/2101
1	B	0.28	0/1554	0.45	0/2101
1	C	0.29	0/1554	0.45	0/2101
1	D	0.31	0/1554	0.46	0/2101
1	E	0.29	0/1554	0.45	0/2101
1	F	0.28	0/1554	0.43	0/2101
All	All	0.29	0/9324	0.45	0/12606

There are no bond length outliers.

There are no bond angle outliers.

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	1521	0	1498	23	0
1	B	1521	0	1498	23	0
1	C	1521	0	1498	18	0
1	D	1521	0	1498	26	0
1	E	1521	0	1498	20	0
1	F	1521	0	1498	24	0
2	A	143	0	0	4	0
2	B	123	0	0	4	0
2	C	159	0	0	2	0
2	D	163	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	133	0	0	1	0
2	F	103	0	0	0	0
All	All	9950	0	8988	131	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 (131) 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:128:GLN:H	1:A:128:GLN:HE21	1.04	1.03
1:D:128:GLN:HE21	1:D:128:GLN:H	1.04	1.00
1:D:211:LYS:O	1:D:212:ALA:HB2	1.60	0.97
1:F:27:VAL:H	1:F:31:ASN:HD22	1.08	0.95
1:C:128:GLN:HE21	1:C:128:GLN:H	1.16	0.94
1:E:128:GLN:H	1:E:128:GLN:HE21	1.12	0.93
1:F:128:GLN:HE21	1:F:128:GLN:H	1.17	0.91
1:D:27:VAL:H	1:D:31:ASN:HD22	1.15	0.91
1:B:128:GLN:HE21	1:B:128:GLN:H	1.21	0.89
1:D:211:LYS:O	1:D:212:ALA:CB	2.20	0.87
1:A:27:VAL:H	1:A:31:ASN:HD22	1.24	0.81
1:C:146:LYS:HD2	2:C:408:HOH:O	1.83	0.78
1:E:27:VAL:H	1:E:31:ASN:HD22	1.30	0.77
1:A:211:LYS:O	1:A:212:ALA:HB2	1.83	0.77
1:C:27:VAL:H	1:C:31:ASN:HD22	1.32	0.74
1:B:211:LYS:O	1:B:212:ALA:HB2	1.90	0.70
1:C:111:VAL:O	1:C:115:HIS:HD2	1.74	0.70
1:A:197:ASN:HB3	2:A:427:HOH:O	1.92	0.69
1:A:64:GLU:HG3	1:A:117:PHE:CE2	2.27	0.69
1:D:144:ASP:CG	1:F:37:ASN:HD21	1.96	0.67
1:F:128:GLN:NE2	1:F:128:GLN:H	1.91	0.67
1:C:128:GLN:NE2	1:C:128:GLN:H	1.92	0.67
1:D:128:GLN:N	1:D:128:GLN:HE21	1.85	0.67
1:B:27:VAL:H	1:B:31:ASN:HD22	1.42	0.66
1:C:128:GLN:N	1:C:128:GLN:HE21	1.93	0.65
1:F:128:GLN:HE21	1:F:128:GLN:N	1.92	0.65
1:F:27:VAL:N	1:F:31:ASN:HD22	1.88	0.64
1:C:26:LEU:HG	1:C:201:LEU:HB3	1.80	0.62
1:A:128:GLN:N	1:A:128:GLN:HE21	1.87	0.62
1:C:77:ASP:OD1	1:C:207:ARG:HD3	2.01	0.61
1:E:128:GLN:HE21	1:E:128:GLN:N	1.92	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:111:VAL:O	1:D:115:HIS:HD2	1.83	0.61
1:D:99:ALA:HB1	1:D:160:ARG:HD2	1.83	0.61
1:F:126:LYS:HE2	1:F:129:ASN:HB2	1.85	0.59
1:B:126:LYS:HD3	1:B:129:ASN:HB2	1.83	0.58
1:E:77:ASP:OD1	1:E:207:ARG:HD3	2.04	0.58
1:B:134:LYS:HG2	1:B:149:LEU:HD11	1.86	0.57
1:A:211:LYS:O	1:A:212:ALA:CB	2.51	0.57
1:C:64:GLU:HB3	1:C:65:PRO:HD3	1.86	0.56
1:C:130:PRO:O	1:C:134:LYS:HG3	2.06	0.56
1:D:204:ASP:O	1:D:208:GLU:HG2	2.07	0.55
1:B:211:LYS:O	1:B:212:ALA:CB	2.54	0.55
1:A:205:LYS:O	1:A:209:GLU:HG3	2.06	0.55
1:A:46:LYS:HD3	2:A:672:HOH:O	2.07	0.54
1:B:205:LYS:O	1:B:209:GLU:HG3	2.08	0.53
1:D:77:ASP:OD1	1:D:207:ARG:HD3	2.09	0.53
1:A:54:GLY:O	1:A:57[A]:CYS:HB3	2.08	0.53
1:C:54:GLY:O	1:C:57[A]:CYS:HB3	2.07	0.53
1:D:62:HIS:O	1:D:65:PRO:HD2	2.08	0.53
1:F:57[A]:CYS:SG	1:F:60:CYS:N	2.75	0.53
1:B:64:GLU:HB3	1:B:65:PRO:HD3	1.89	0.53
1:A:46:LYS:HB3	1:A:77:ASP:C	2.29	0.53
1:C:-4:ASP:CG	1:C:-3:ASP:H	2.11	0.53
1:B:57[A]:CYS:SG	1:B:60:CYS:N	2.78	0.52
1:B:62:HIS:O	1:B:65:PRO:HD2	2.09	0.52
1:A:71:ALA:O	1:A:74:PHE:HB2	2.10	0.52
1:B:57[B]:CYS:HB3	1:B:60:CYS:SG	2.50	0.51
1:A:57[B]:CYS:SG	1:A:60:CYS:SG	3.02	0.51
1:E:57[A]:CYS:SG	1:E:60:CYS:N	2.81	0.51
1:D:65:PRO:O	1:D:69:LYS:HD3	2.09	0.51
1:A:62:HIS:O	1:A:65:PRO:HD2	2.11	0.51
1:D:64:GLU:HG2	1:D:117:PHE:CE2	2.45	0.51
1:F:71:ALA:O	1:F:74:PHE:HB2	2.11	0.51
1:D:115:HIS:HE1	2:D:10:HOH:O	1.93	0.50
1:A:-1:LYS:HE2	2:A:303:HOH:O	2.11	0.50
1:D:50:LEU:HD13	1:D:81:ARG:HD3	1.94	0.50
1:A:57[A]:CYS:SG	1:A:60:CYS:N	2.81	0.50
1:D:135:LYS:O	1:D:139:GLU:HG3	2.12	0.49
1:C:57[B]:CYS:SG	1:C:60:CYS:SG	3.08	0.49
1:F:57[B]:CYS:SG	1:F:60:CYS:SG	3.07	0.49
1:C:115:HIS:HE1	2:C:385:HOH:O	1.96	0.48
1:E:140:GLN:HG3	1:E:143:PHE:CZ	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:58:PRO:HD2	2:E:398:HOH:O	2.14	0.48
1:F:205:LYS:O	1:F:209:GLU:HG3	2.14	0.48
1:C:62:HIS:O	1:C:65:PRO:HD2	2.14	0.47
1:E:64:GLU:HB3	1:E:65:PRO:HD3	1.96	0.47
1:D:64:GLU:CB	1:D:65:PRO:HD3	2.44	0.47
1:D:57[A]:CYS:SG	1:D:60:CYS:N	2.81	0.47
1:B:141:THR:HG23	2:B:232:HOH:O	2.14	0.47
1:E:111:VAL:O	1:E:115:HIS:HD2	1.97	0.47
1:B:146:LYS:HE3	2:B:450:HOH:O	2.15	0.47
1:B:182:GLY:O	1:B:184:LYS:HG3	2.14	0.47
1:B:193:GLU:HG3	2:B:515:HOH:O	2.14	0.47
1:C:57[B]:CYS:HB3	1:C:60:CYS:SG	2.54	0.46
1:B:128:GLN:HE21	1:B:128:GLN:N	2.01	0.46
1:A:71:ALA:HA	1:A:74:PHE:CD2	2.51	0.46
1:B:77:ASP:OD1	1:B:207:ARG:HD3	2.16	0.46
1:F:78:MET:HE3	1:F:203:ALA:HB2	1.97	0.46
1:E:204:ASP:O	1:E:208:GLU:HG2	2.16	0.46
1:B:35:LEU:HD11	1:B:186:LYS:HB2	1.98	0.45
1:F:149:LEU:O	1:F:153:GLU:HG3	2.17	0.45
1:F:134:LYS:HG2	1:F:149:LEU:HD11	1.98	0.45
1:F:56:PHE:O	1:F:58:PRO:HD3	2.16	0.45
1:D:64:GLU:CG	1:D:117:PHE:CE2	3.00	0.45
1:E:46:LYS:HB3	1:E:77:ASP:O	2.17	0.45
1:B:207:ARG:NH2	2:B:219:HOH:O	2.50	0.45
1:E:89:LYS:HB3	1:E:89:LYS:NZ	2.32	0.45
1:A:46:LYS:HB3	1:A:77:ASP:O	2.17	0.44
1:D:57[B]:CYS:SG	1:D:60:CYS:SG	3.11	0.44
1:C:27:VAL:N	1:C:31:ASN:HD22	2.06	0.44
1:F:54:GLY:O	1:F:57[A]:CYS:HB3	2.17	0.44
1:C:57[A]:CYS:SG	1:C:60:CYS:N	2.86	0.44
1:B:39:ILE:HG12	1:B:171:PHE:CG	2.52	0.44
1:E:130:PRO:O	1:E:134:LYS:HG3	2.18	0.44
1:B:26:LEU:HG	1:B:201:LEU:HB3	1.99	0.44
1:E:126:LYS:O	1:E:126:LYS:HG2	2.18	0.43
1:D:99:ALA:O	1:D:103:MET:HG3	2.17	0.43
1:F:57[B]:CYS:HB3	1:F:60:CYS:SG	2.58	0.43
1:B:126:LYS:CD	1:B:129:ASN:HB2	2.48	0.43
1:D:26:LEU:HG	1:D:201:LEU:HB3	2.01	0.43
1:A:64:GLU:HG3	1:A:117:PHE:HE2	1.78	0.43
1:D:64:GLU:HB3	1:D:65:PRO:HD3	2.01	0.43
1:D:184:LYS:HE2	1:D:185:TYR:CZ	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:37:ASN:HD21	1:F:156:GLU:HG3	1.84	0.43
1:F:202:LEU:O	1:F:206:VAL:HG23	2.19	0.43
1:D:144:ASP:OD2	1:D:147:LYS:HB2	2.19	0.42
1:E:137:LEU:HD23	1:E:137:LEU:HA	1.89	0.42
1:F:27:VAL:H	1:F:31:ASN:ND2	1.92	0.42
1:E:37:ASN:ND2	1:F:156:GLU:HG3	2.34	0.42
1:E:74:PHE:HB3	1:E:78:MET:HB3	2.00	0.42
1:E:37:ASN:HA	1:E:38:PRO:HD3	1.87	0.42
1:F:210:GLN:O	1:F:212:ALA:N	2.51	0.41
1:A:57[B]:CYS:HB3	1:A:60:CYS:SG	2.61	0.41
1:A:129:ASN:HA	1:A:130:PRO:HD3	1.90	0.41
1:F:189:PHE:CE1	1:F:195:GLY:HA3	2.56	0.41
1:D:211:LYS:HE3	1:D:211:LYS:HB2	1.70	0.41
1:F:52:PHE:HA	1:F:83:GLU:O	2.21	0.41
1:B:128:GLN:H	1:B:128:GLN:NE2	2.03	0.40
1:A:56:PHE:O	1:A:58:PRO:HD3	2.21	0.40
1:E:26:LEU:HG	1:E:201:LEU:HB3	2.03	0.40
1:A:174:ASP:HB3	2:A:469:HOH:O	2.20	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	192/210 (91%)	186 (97%)	6 (3%)	0	100	100
1	B	192/210 (91%)	190 (99%)	2 (1%)	0	100	100
1	C	192/210 (91%)	188 (98%)	4 (2%)	0	100	100
1	D	192/210 (91%)	187 (97%)	5 (3%)	0	100	100
1	E	192/210 (91%)	188 (98%)	4 (2%)	0	100	100
1	F	192/210 (91%)	184 (96%)	8 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1152/1260 (91%)	1123 (98%)	29 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	162/174 (93%)	156 (96%)	6 (4%)	41	41
1	B	162/174 (93%)	155 (96%)	7 (4%)	35	34
1	C	162/174 (93%)	153 (94%)	9 (6%)	26	22
1	D	162/174 (93%)	155 (96%)	7 (4%)	35	34
1	E	162/174 (93%)	157 (97%)	5 (3%)	47	50
1	F	162/174 (93%)	156 (96%)	6 (4%)	41	41
All	All	972/1044 (93%)	932 (96%)	40 (4%)	43	36

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	57[A]	CYS
1	A	57[B]	CYS
1	A	69	LYS
1	A	128	GLN
1	A	141	THR
1	A	177	PRO
1	B	26	LEU
1	B	57[A]	CYS
1	B	57[B]	CYS
1	B	69	LYS
1	B	89	LYS
1	B	128	GLN
1	B	184	LYS
1	C	-1	LYS

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Mol	Chain	Res	Type
1	C	26	LEU
1	C	33	THR
1	C	57[A]	CYS
1	C	57[B]	CYS
1	C	69	LYS
1	C	76	ASP
1	C	89	LYS
1	C	128	GLN
1	D	-1	LYS
1	D	26	LEU
1	D	33	THR
1	D	57[A]	CYS
1	D	57[B]	CYS
1	D	64	GLU
1	D	128	GLN
1	E	26	LEU
1	E	57[A]	CYS
1	E	57[B]	CYS
1	E	89	LYS
1	E	128	GLN
1	F	-4	ASP
1	F	57[A]	CYS
1	F	57[B]	CYS
1	F	89	LYS
1	F	128	GLN
1	F	141	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (35) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	30	GLN
1	A	31	ASN
1	A	88	GLN
1	A	122	ASN
1	A	128	GLN
1	A	197	ASN
1	B	31	ASN
1	B	88	GLN
1	B	122	ASN
1	B	128	GLN
1	C	31	ASN
1	C	88	GLN

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Mol	Chain	Res	Type
1	C	115	HIS
1	C	122	ASN
1	C	123	GLN
1	C	128	GLN
1	C	197	ASN
1	D	31	ASN
1	D	88	GLN
1	D	115	HIS
1	D	122	ASN
1	D	128	GLN
1	D	197	ASN
1	E	31	ASN
1	E	37	ASN
1	E	88	GLN
1	E	115	HIS
1	E	122	ASN
1	E	128	GLN
1	E	197	ASN
1	F	31	ASN
1	F	37	ASN
1	F	88	GLN
1	F	122	ASN
1	F	128	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates 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 ⓘ

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	193/210 (91%)	0.02	3 (1%) 74 79	13, 19, 33, 60	0
1	B	193/210 (91%)	-0.01	0 100 100	12, 20, 33, 62	0
1	C	193/210 (91%)	-0.17	2 (1%) 84 87	14, 20, 31, 44	0
1	D	193/210 (91%)	-0.13	0 100 100	14, 20, 31, 52	0
1	E	193/210 (91%)	-0.14	1 (0%) 91 93	15, 20, 31, 51	0
1	F	193/210 (91%)	0.04	4 (2%) 67 72	10, 21, 38, 59	0
All	All	1158/1260 (91%)	-0.06	10 (0%) 85 88	10, 20, 34, 62	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	44	ALA	4.1
1	F	76	ASP	3.3
1	A	192	TRP	3.0
1	C	44	ALA	2.4
1	F	44	ALA	2.2
1	A	131	GLU	2.2
1	F	-4	ASP	2.2
1	F	131	GLU	2.1
1	C	-4	ASP	2.1
1	E	44	ALA	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates 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.