



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 09:25 PM EDT

PDB ID : 7F90 / pdb_00007f90
Title : Crystal structure of SARS auxiliary protein in complex with human nuclear protein
Authors : Gao, X.; Cui, S.
Deposited on : 2021-07-03
Resolution : 2.39 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
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

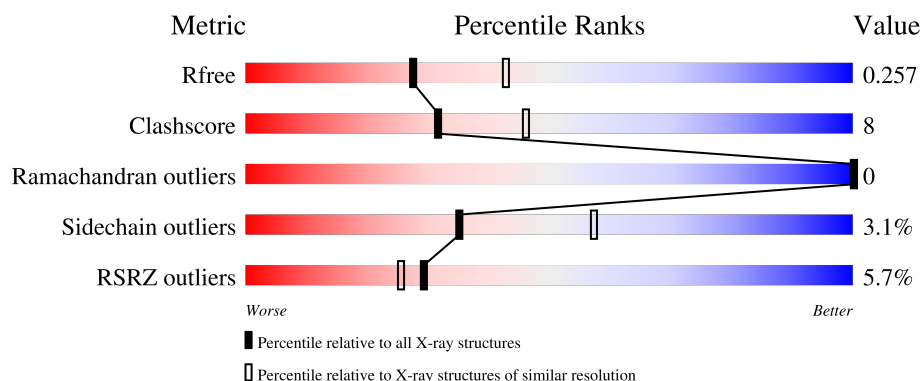
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.39 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.



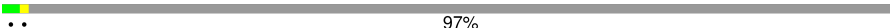
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	E	63	5% (red) 8% (orange) 8% (yellow) 84% (green)
1	F	63	11% (red) 11% (orange) 8% (yellow) 81% (green)
2	A	368	3% (red) 74% (green) 14% (yellow) 11% (grey)
2	C	368	2% (red) 73% (green) 16% (yellow) 11% (grey)
3	B	1817	0% (red) 98% (green)

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Mol	Chain	Length	Quality of chain
3	D	1817	 97%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 12124 atoms, of which 5832 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 ORF6 protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	E	10	Total	C	H	N	O	S	0	0	0
			151	52	65	10	23	1			
1	F	12	Total	C	H	N	O	S	0	0	0
			162	63	61	12	25	1			

- Molecule 2 is a protein called mRNA export factor.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	A	328	Total	C	H	N	O	S	0	0	0
			5096	1645	2499	452	483	17			
2	C	327	Total	C	H	N	O	S	0	1	0
			5086	1643	2494	449	483	17			

- Molecule 3 is a protein called Nuclear pore complex protein Nup98-Nup96.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	B	45	Total	C	H	N	O	S	0	0	0
			713	221	353	62	75	2			
3	D	46	Total	C	H	N	O	S	0	0	0
			727	225	360	63	77	2			

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	E	2	Total	O	0	0
			2	2		
4	F	1	Total	O	0	0
			1	1		
4	A	83	Total	O	0	0
			83	83		
4	C	90	Total	O	0	0
			90	90		

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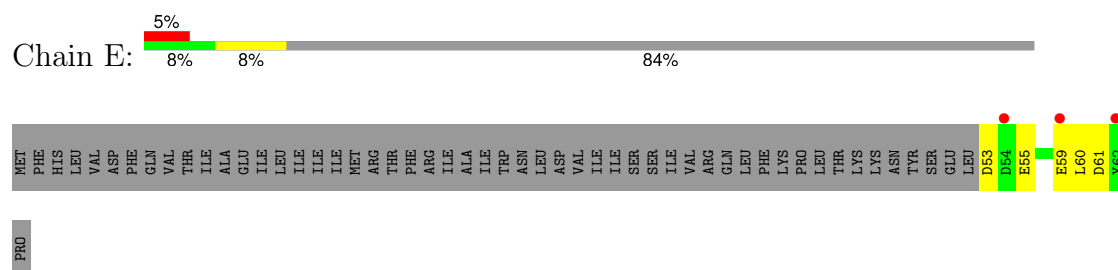
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	5	Total	O	0	0
			5	5		
4	D	8	Total	O	0	0
			8	8		

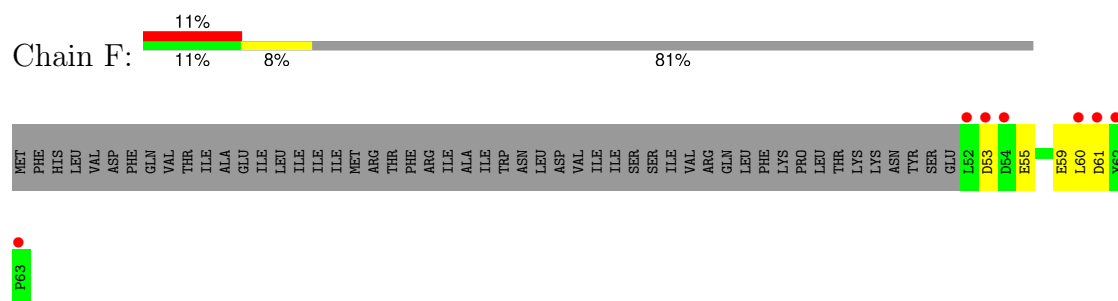
3 Residue-property plots [i](#)

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.

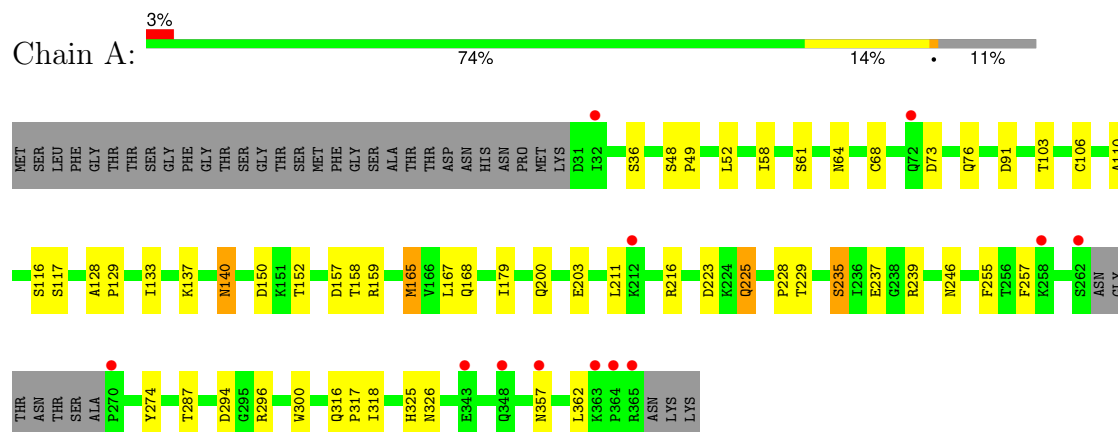
- Molecule 1: ORF6 protein



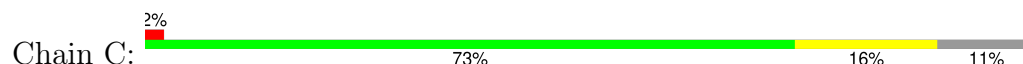
- Molecule 1: ORF6 protein

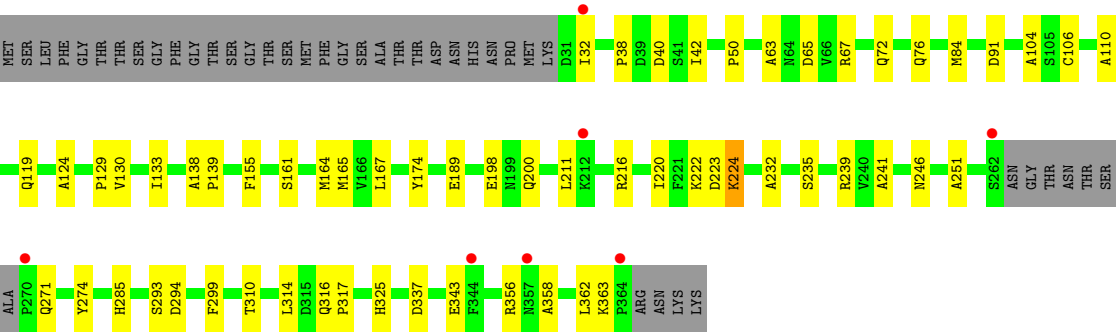


- Molecule 2: mRNA export factor

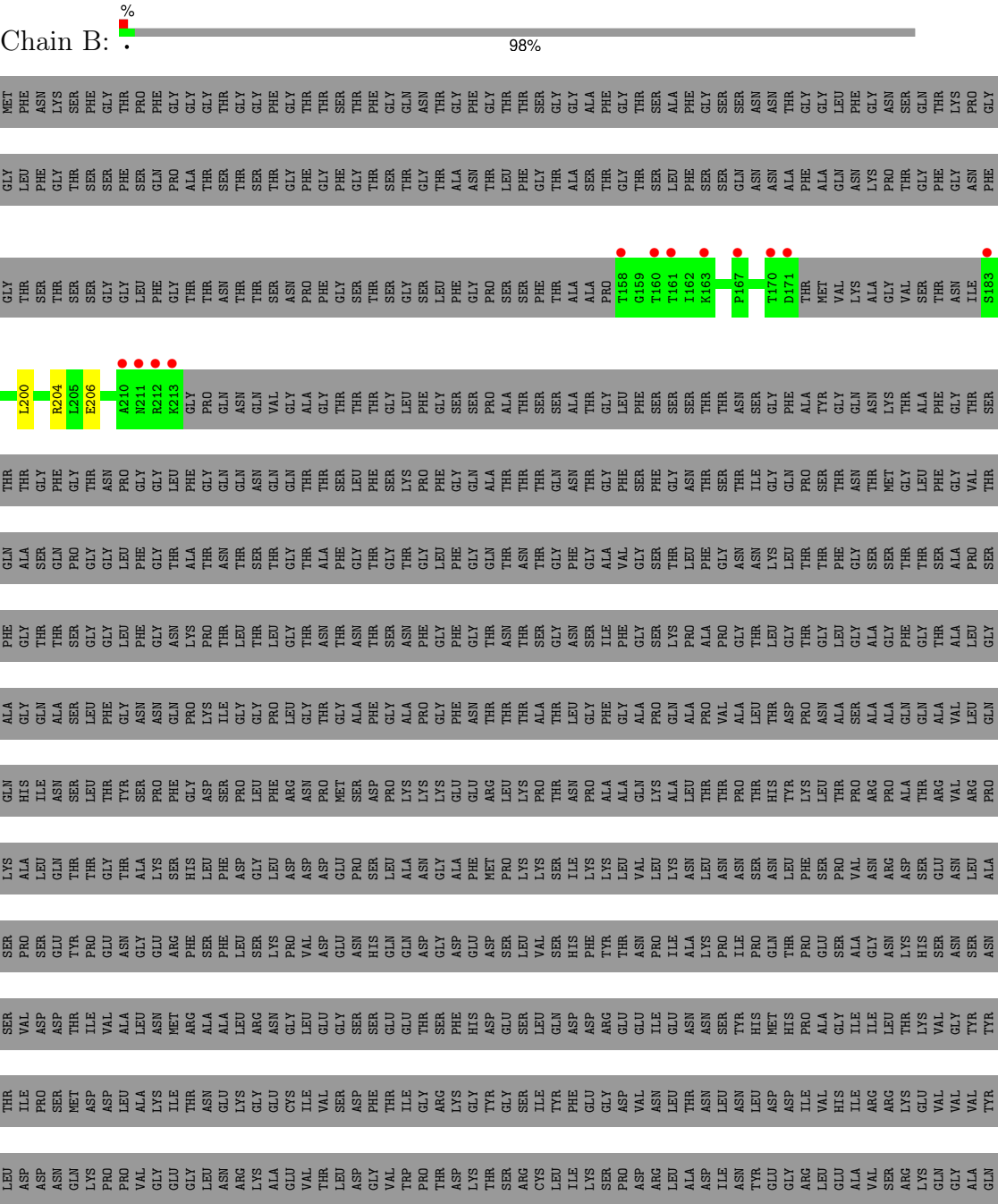


- Molecule 2: mRNA export factor





● Molecule 3: Nuclear pore complex protein Nup98-Nup96







[illegible]

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	189.33Å 86.79Å 47.91Å 90.00° 92.09° 90.00°	Depositor
Resolution (Å)	47.87 – 2.39 47.87 – 2.39	Depositor EDS
% Data completeness (in resolution range)	99.7 (47.87-2.39) 99.8 (47.87-2.39)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.80 (at 2.39Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.220 , 0.258 0.222 , 0.257	Depositor DCC
R_{free} test set	1603 reflections (5.22%)	wwPDB-VP
Wilson B-factor (Å ²)	31.2	Xtriage
Anisotropy	1.016	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 40.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.086 for -h,-k,l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	12124	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.00% 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](#)

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	E	0.22	0/87	0.40	0/117
1	F	0.37	0/103	0.67	0/140
2	A	0.34	1/2672 (0.0%)	0.54	0/3631
2	C	0.26	0/2670	0.48	0/3629
3	B	0.17	0/364	0.35	0/487
3	D	0.17	0/371	0.38	0/497
All	All	0.29	1/6267 (0.0%)	0.50	0/8501

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	64	ASN	C-O	-7.46	1.14	1.24

There are no bond angle outliers.

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	E	86	65	65	7	0
1	F	101	61	83	1	0
2	A	2597	2499	2499	39	0
2	C	2592	2494	2494	45	0
3	B	360	353	352	3	0
3	D	367	360	359	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	83	0	0	13	0
4	B	5	0	0	2	0
4	C	90	0	0	12	1
4	D	8	0	0	5	0
4	E	2	0	0	1	0
4	F	1	0	0	0	0
All	All	6292	5832	5852	97	1

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 8.

All (97) 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)
2:A:246:ASN:OD1	4:A:401:HOH:O	1.83	0.95
2:C:76:GLN:OE1	4:C:401:HOH:O	1.85	0.95
2:C:220:ILE:O	4:C:402:HOH:O	1.88	0.91
1:E:61:ASP:OD1	2:A:239:ARG:NH1	2.05	0.89
2:A:150:ASP:OD1	2:A:152:THR:OG1	1.91	0.88
2:A:357:ASN:ND2	4:A:403:HOH:O	1.96	0.87
2:A:76:GLN:NE2	4:A:406:HOH:O	2.12	0.82
3:D:161:THR:OG1	4:D:1901:HOH:O	1.98	0.80
3:D:158:THR:O	4:D:1901:HOH:O	1.99	0.79
3:D:187:GLN:O	4:D:1902:HOH:O	2.02	0.78
2:A:91:ASP:HB3	2:A:133:ILE:HG22	1.68	0.74
3:D:200:LEU:H	3:D:200:LEU:HD12	1.56	0.69
2:C:84:MET:O	4:C:403:HOH:O	2.09	0.69
2:C:161:SER:OG	4:C:404:HOH:O	2.10	0.69
3:D:158:THR:HA	4:D:1903:HOH:O	1.92	0.68
2:C:222:LYS:O	4:C:406:HOH:O	2.13	0.67
2:A:326:ASN:ND2	4:A:405:HOH:O	2.05	0.66
2:C:211:LEU:HD13	2:C:235:SER:HB3	1.79	0.65
2:C:246:ASN:OD1	4:C:407:HOH:O	2.15	0.65
2:C:310:THR:HG21	4:C:412:HOH:O	1.95	0.64
2:A:179:ILE:HG22	2:A:228:PRO:HG3	1.82	0.61
1:F:61:ASP:OD1	2:C:239:ARG:NH1	2.32	0.61
2:C:310:THR:CB	4:C:412:HOH:O	2.49	0.61
2:A:223:ASP:OD2	4:A:407:HOH:O	2.16	0.61
3:B:204:ARG:NH1	4:B:1902:HOH:O	2.32	0.60
2:C:356:ARG:HG2	2:C:358:ALA:HB2	1.84	0.60
2:A:203:GLU:OE1	4:A:408:HOH:O	2.17	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:225:GLN:NE2	4:A:407:HOH:O	2.36	0.58
2:A:73:ASP:OD1	4:A:409:HOH:O	2.17	0.58
2:A:140:ASN:HB2	4:A:426:HOH:O	2.06	0.56
2:C:165:MET:HE3	2:C:167:LEU:HD21	1.87	0.56
3:D:194:GLU:OE2	3:D:194:GLU:N	2.33	0.56
2:C:316:GLN:HB2	2:C:317:PRO:HD2	1.89	0.55
2:A:157:ASP:O	2:A:158:THR:OG1	2.22	0.55
3:D:212:ARG:NH2	4:D:1901:HOH:O	2.41	0.52
2:C:299:PHE:CG	2:C:362:LEU:HD21	2.45	0.52
1:E:61:ASP:CG	2:A:239:ARG:HH11	2.18	0.51
2:C:174:TYR:CZ	3:D:199:SER:HB3	2.46	0.51
2:C:110:ALA:HB3	2:C:124:ALA:HB3	1.93	0.51
2:A:165:MET:HE3	2:A:167:LEU:HG	1.94	0.50
2:C:138:ALA:HB1	2:C:139:PRO:HD2	1.94	0.50
2:A:211:LEU:HD13	2:A:235:SER:HB3	1.94	0.49
2:A:316:GLN:HB3	2:A:317:PRO:HD2	1.93	0.49
2:C:32:ILE:H	2:C:32:ILE:HD12	1.78	0.49
2:C:38:PRO:HD2	2:C:42:ILE:HD11	1.94	0.48
1:E:61:ASP:O	4:E:101:HOH:O	2.19	0.48
2:C:274:TYR:CD1	2:C:294:ASP:HB3	2.49	0.48
2:C:119:GLN:NE2	4:C:410:HOH:O	2.22	0.48
2:C:293:SER:OG	2:C:337:ASP:OD2	2.26	0.48
1:E:60:LEU:HD23	2:A:257:PHE:HB3	1.96	0.48
2:C:216:ARG:NH1	3:D:200:LEU:HD13	2.29	0.47
2:C:224:LYS:N	2:C:224:LYS:HD3	2.30	0.47
2:C:274:TYR:HB3	2:C:293:SER:HB2	1.96	0.47
2:C:40:ASP:HB2	2:C:63:ALA:HB2	1.96	0.47
1:E:61:ASP:CG	2:A:239:ARG:NH1	2.73	0.46
2:A:48:SER:HB2	2:A:52:LEU:HD12	1.97	0.46
2:A:211:LEU:HD13	2:A:235:SER:CB	2.45	0.46
2:C:50:PRO:HG3	2:C:325:HIS:HB2	1.98	0.46
2:C:310:THR:CG2	4:C:412:HOH:O	2.58	0.46
2:A:106:CYS:HA	2:A:129:PRO:HB3	1.96	0.46
2:A:274:TYR:CD2	2:A:294:ASP:HB3	2.51	0.45
2:C:271:GLN:HB3	3:D:184:THR:HG22	1.98	0.45
2:A:103:THR:O	2:A:110:ALA:HA	2.17	0.45
2:C:91:ASP:HB3	2:C:133:ILE:HG22	1.98	0.45
2:C:65:ASP:OD2	2:C:67:ARG:NE	2.48	0.44
2:C:189:GLU:OE2	4:C:409:HOH:O	2.21	0.44
2:A:128:ALA:HB1	2:A:129:PRO:HD2	1.99	0.44
2:C:232:ALA:HA	2:C:241:ALA:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:296:ARG:C	2:A:318:ILE:HD12	2.43	0.44
2:A:137:LYS:O	4:A:410:HOH:O	2.21	0.44
1:E:60:LEU:HD22	2:A:255:PHE:CD2	2.53	0.43
2:A:150:ASP:OD1	2:A:150:ASP:C	2.61	0.43
2:A:357:ASN:ND2	4:A:417:HOH:O	2.36	0.43
2:A:58:ILE:HD13	2:A:68:CYS:HB2	2.00	0.43
2:A:216:ARG:CZ	3:B:200:LEU:HD12	2.48	0.43
2:A:325:HIS:CE1	4:A:405:HOH:O	2.71	0.43
2:C:155:PHE:O	2:C:164:MET:HG2	2.18	0.43
2:A:116:SER:OG	2:A:117:SER:N	2.52	0.43
2:C:165:MET:CE	2:C:167:LEU:HD21	2.48	0.43
2:C:343:GLU:OE2	3:D:163:LYS:HG3	2.19	0.43
2:C:198:GLU:O	2:C:200:GLN:N	2.51	0.43
3:D:171:ASP:OD1	3:D:172:THR:N	2.51	0.43
2:C:299:PHE:CG	2:C:362:LEU:CD2	3.02	0.42
2:C:251:ALA:HB3	4:C:432:HOH:O	2.18	0.42
2:C:223:ASP:C	2:C:223:ASP:OD1	2.62	0.42
2:A:48:SER:HB2	2:A:49:PRO:HD2	2.01	0.42
2:C:293:SER:HA	2:C:317:PRO:HB3	2.02	0.42
2:A:140:ASN:ND2	4:A:426:HOH:O	2.52	0.42
3:D:168:THR:HG22	3:D:185:LYS:HE2	2.02	0.42
2:C:104:ALA:HB1	2:C:130:VAL:HG12	2.01	0.41
3:D:170:THR:HG22	3:D:171:ASP:N	2.35	0.41
2:C:285:HIS:CD2	2:C:363:LYS:HG3	2.55	0.41
2:C:314:LEU:HD12	2:C:314:LEU:N	2.35	0.41
3:B:206:GLU:OE2	4:B:1901:HOH:O	2.22	0.41
1:E:60:LEU:HD22	2:A:255:PHE:HD2	1.86	0.41
2:A:287:THR:HB	2:A:300:TRP:O	2.21	0.41
2:C:106:CYS:HA	2:C:129:PRO:HB3	2.03	0.41

All (1) 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:C:411:HOH:O	4:C:437:HOH:O[2_556]	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	E	8/63 (13%)	8 (100%)	0	0	100	100
1	F	10/63 (16%)	10 (100%)	0	0	100	100
2	A	324/368 (88%)	305 (94%)	19 (6%)	0	100	100
2	C	324/368 (88%)	311 (96%)	13 (4%)	0	100	100
3	B	41/1817 (2%)	41 (100%)	0	0	100	100
3	D	42/1817 (2%)	42 (100%)	0	0	100	100
All	All	749/4496 (17%)	717 (96%)	32 (4%)	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	E	10/61 (16%)	7 (70%)	3 (30%)	0	0
1	F	12/61 (20%)	8 (67%)	4 (33%)	0	0
2	A	285/317 (90%)	273 (96%)	12 (4%)	26	45
2	C	285/317 (90%)	283 (99%)	2 (1%)	76	88
3	B	41/1543 (3%)	41 (100%)	0	100	100
3	D	42/1543 (3%)	42 (100%)	0	100	100
All	All	675/3842 (18%)	654 (97%)	21 (3%)	35	57

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	53	ASP
1	E	55	GLU
1	E	59	GLU
1	F	53	ASP
1	F	55	GLU
1	F	59	GLU
1	F	60	LEU
2	A	36	SER
2	A	61	SER
2	A	140	ASN
2	A	159	ARG
2	A	165	MET
2	A	168	GLN
2	A	200	GLN
2	A	225	GLN
2	A	229	THR
2	A	235	SER
2	A	237	GLU
2	A	362	LEU
2	C	72	GLN
2	C	224	LYS

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

Mol	Chain	Res	Type
2	A	316	GLN
2	C	119	GLN
2	C	214	GLN
2	C	246	ASN
2	C	249	ASN

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	E	10/63 (15%)	1.38	3 (30%) 1 1	52, 62, 96, 97	0
1	F	12/63 (19%)	2.75	7 (58%) 0 0	47, 77, 106, 125	0
2	A	328/368 (89%)	0.44	12 (3%) 45 41	26, 39, 65, 100	0
2	C	327/368 (88%)	0.34	7 (2%) 63 59	24, 37, 59, 73	1 (0%)
3	B	45/1817 (2%)	1.35	12 (26%) 1 1	39, 64, 88, 95	0
3	D	46/1817 (2%)	0.79	3 (6%) 25 21	33, 51, 76, 83	0
All	All	768/4496 (17%)	0.52	44 (5%) 29 25	24, 39, 72, 125	1 (0%)

All (44) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	63	PRO	7.9
2	A	262	SER	6.9
1	F	52	LEU	6.0
2	C	262	SER	5.9
3	D	172	THR	5.3
3	B	171	ASP	4.9
2	A	270	PRO	4.7
1	F	62	TYR	4.2
1	E	62	TYR	3.7
2	C	357	ASN	3.4
2	C	364	PRO	3.3
3	B	158	THR	3.2
2	A	365	ARG	3.1
2	A	258	LYS	3.1
3	B	163	LYS	3.1
3	D	171	ASP	2.9
1	F	53	ASP	2.9
2	A	357	ASN	2.8
3	B	183	SER	2.8

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Mol	Chain	Res	Type	RSRZ
1	F	54	ASP	2.7
1	F	61	ASP	2.7
2	A	364	PRO	2.7
2	A	348	GLN	2.6
3	D	183	SER	2.6
2	C	270	PRO	2.6
2	C	32	ILE	2.5
3	B	167	PRO	2.5
2	A	212	LYS	2.5
3	B	211	ASN	2.5
1	E	59	GLU	2.4
3	B	170	THR	2.4
3	B	161	THR	2.4
2	A	32	ILE	2.3
3	B	210	ALA	2.3
2	C	344	PHE	2.2
2	A	363	LYS	2.2
2	A	343	GLU	2.1
3	B	213	LYS	2.1
3	B	212	ARG	2.1
2	A	72	GLN	2.1
2	C	212	LYS	2.1
3	B	160	THR	2.1
1	E	54	ASP	2.1
1	F	60	LEU	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.