Full wwPDB X-ray Structure Validation Report ⓘ

Dec 17, 2023 – 09:10 AM EST

PDB ID	:	4WA6
Title	:	Structure of yeast SAGA DUBm with Sgf73 N59D mutant at 2.36 angstroms resolution
Authors	:	Wolberger, C.; Yan, M.
Deposited on	:	2014-08-28
Resolution	:	2.36 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:

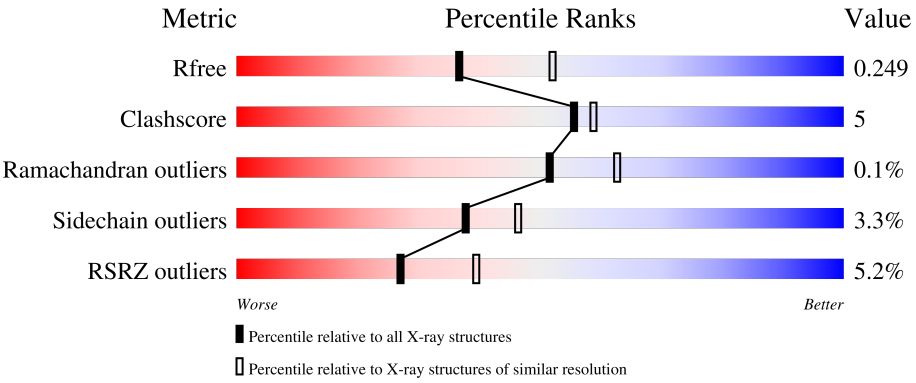
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.36 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}	130704	1164 (2.36-2.36)
Clashscore	141614	1232 (2.36-2.36)
Ramachandran outliers	138981	1211 (2.36-2.36)
Sidechain outliers	138945	1212 (2.36-2.36)
RSRZ outliers	127900	1150 (2.36-2.36)

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 <=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	476	3% 79% 13% • 8%
1	D	476	3% 74% 12% • 13%
2	B	96	3% 85% 14% •
2	F	96	2% 86% 9% • •
3	C	99	12% 68% 15% 17%

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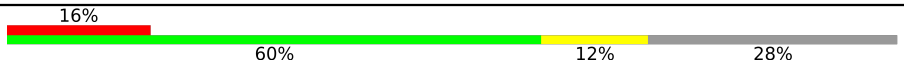
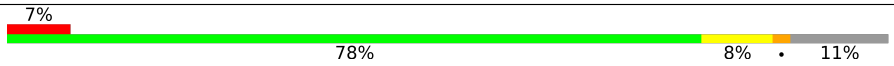
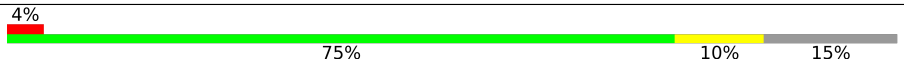
Mol	Chain	Length	Quality of chain
3	G	99	
4	E	96	
4	H	96	

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 11129 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 Ubiquitin carboxyl-terminal hydrolase 8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	440	Total	C	N	O	S	0	4	0
			3548	2256	604	652	36			
1	D	415	Total	C	N	O	S	0	1	0
			3338	2128	568	610	32			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	GLY	-	expression tag	UNP P50102
A	-3	ALA	-	expression tag	UNP P50102
A	-2	ALA	-	expression tag	UNP P50102
A	-1	ALA	-	expression tag	UNP P50102
A	0	ALA	-	expression tag	UNP P50102
D	-4	GLY	-	expression tag	UNP P50102
D	-3	ALA	-	expression tag	UNP P50102
D	-2	ALA	-	expression tag	UNP P50102
D	-1	ALA	-	expression tag	UNP P50102
D	0	ALA	-	expression tag	UNP P50102

- Molecule 2 is a protein called Transcription and mRNA export factor SUS1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	96	Total	C	N	O	S	0	1	0
			780	487	126	163	4			
2	F	93	Total	C	N	O	S	0	0	0
			750	468	122	157	3			

- Molecule 3 is a protein called SAGA-associated factor 11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	82	Total	C	N	O	S	0	0	0
			652	405	116	130	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	G	71	Total	C	N	O	S	0	0	0
			564	344	104	112	4			

- Molecule 4 is a protein called SAGA-associated factor 73.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	85	Total	C	N	O	S	0	1	0
			687	434	114	135	4			
4	H	82	Total	C	N	O	S	0	0	0
			656	414	109	129	4			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	59	ASP	ASN	engineered mutation	UNP P53165
H	59	ASP	ASN	engineered mutation	UNP P53165

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	6	Total	Zn	0	0
			6	6		
5	C	1	Total	Zn	0	0
			1	1		
5	E	1	Total	Zn	0	0
			1	1		
5	D	5	Total	Zn	0	0
			5	5		
5	G	1	Total	Zn	0	0
			1	1		
5	H	1	Total	Zn	0	0
			1	1		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	49	Total	O	0	0
			49	49		
6	B	8	Total	O	0	0
			8	8		
6	C	3	Total	O	0	0
			3	3		

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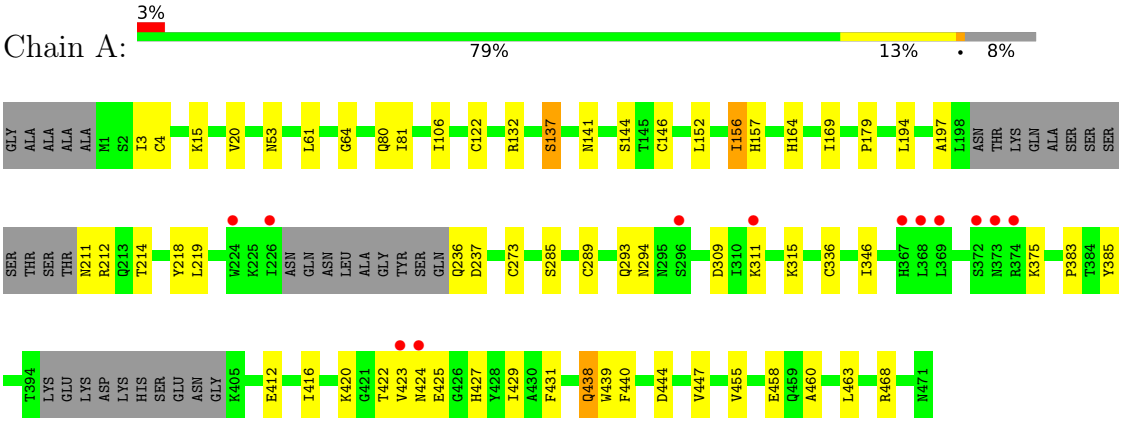
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	E	8	Total O 8 8	0	0
6	D	49	Total O 49 49	0	0
6	F	6	Total O 6 6	0	0
6	G	3	Total O 3 3	0	0
6	H	13	Total O 13 13	0	0

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.

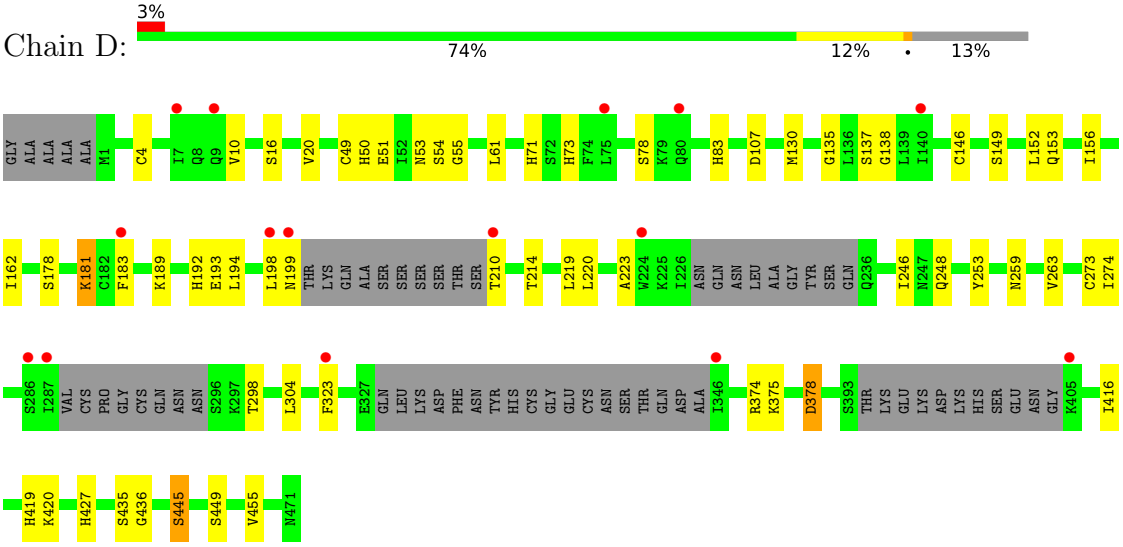
• Molecule 1: Ubiquitin carboxyl-terminal hydrolase 8

Chain A:



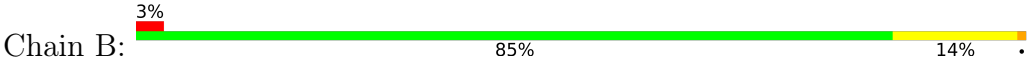
• Molecule 1: Ubiquitin carboxyl-terminal hydrolase 8

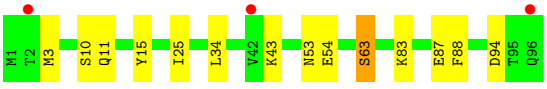
Chain D:



• Molecule 2: Transcription and mRNA export factor SUS1

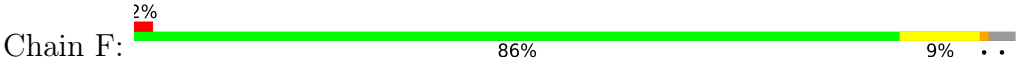
Chain B:





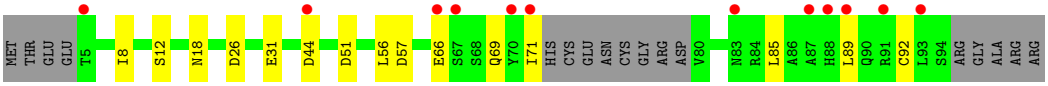
• Molecule 2: Transcription and mRNA export factor SUS1

Chain F:



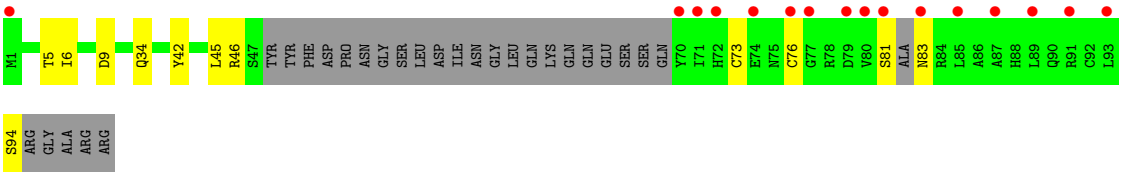
• Molecule 3: SAGA-associated factor 11

Chain C:



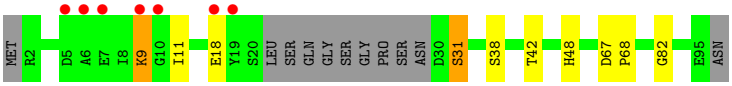
• Molecule 3: SAGA-associated factor 11

Chain G:



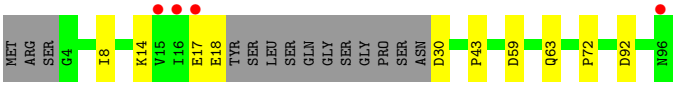
• Molecule 4: SAGA-associated factor 73

Chain E:



• Molecule 4: SAGA-associated factor 73

Chain H:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	81.08Å 68.00Å 137.86Å 90.00° 106.75° 90.00°	Depositor
Resolution (Å)	47.41 – 2.36 47.36 – 2.36	Depositor EDS
% Data completeness (in resolution range)	99.8 (47.41-2.36) 99.8 (47.36-2.36)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.99 (at 2.37Å)	Xtriage
Refinement program	REFMAC 5.7.0029, PHENIX	Depositor
R, R_{free}	0.183 , 0.244 0.191 , 0.249	Depositor DCC
R_{free} test set	2993 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å^2)	46.5	Xtriage
Anisotropy	0.360	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 49.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.013 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	11129	wwPDB-VP
Average B, all atoms (Å^2)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.97% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: ZN

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	0/3634	0.81	3/4895 (0.1%)
1	D	0.69	0/3412	0.80	0/4591
2	B	0.75	0/789	0.82	0/1062
2	F	0.64	0/756	0.75	0/1019
3	C	0.68	0/658	0.79	1/891 (0.1%)
3	G	0.58	0/566	0.79	0/763
4	E	0.65	0/703	0.83	0/946
4	H	0.77	0/668	0.90	1/898 (0.1%)
All	All	0.70	0/11186	0.81	5/15065 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	132	ARG	NE-CZ-NH1	5.84	123.22	120.30
4	H	59	ASP	C-N-CD	5.77	140.51	128.40
1	A	237	ASP	CB-CG-OD1	5.74	123.47	118.30
3	C	26	ASP	CB-CG-OD1	5.46	123.21	118.30
1	A	122	CYS	CA-CB-SG	-5.08	104.85	114.00

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	3548	0	3480	40	0
1	D	3338	0	3287	40	0
2	B	780	0	792	9	0
2	F	750	0	754	9	0
3	C	652	0	655	10	0
3	G	564	0	568	7	0
4	E	687	0	682	8	0
4	H	656	0	652	8	0
5	A	6	0	0	0	0
5	C	1	0	0	0	0
5	D	5	0	0	0	0
5	E	1	0	0	0	0
5	G	1	0	0	0	0
5	H	1	0	0	0	0
6	A	49	0	0	2	0
6	B	8	0	0	1	0
6	C	3	0	0	0	0
6	D	49	0	0	3	0
6	E	8	0	0	0	0
6	F	6	0	0	0	0
6	G	3	0	0	0	0
6	H	13	0	0	0	0
All	All	11129	0	10870	112	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 5.

All (112) 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:D:146:CYS:HG	1:D:427:HIS:CE1	1.86	0.92
1:D:427:HIS:CE1	6:D:643:HOH:O	2.28	0.85
1:A:146:CYS:HG	1:A:427:HIS:CE1	2.05	0.75
1:D:146:CYS:SG	1:D:427:HIS:CE1	2.82	0.72
2:F:5:THR:HG22	3:G:6:ILE:HG12	1.75	0.68
1:D:156:ILE:O	1:D:162:ILE:HD11	1.95	0.67
1:A:422:THR:OG1	1:A:425:GLU:O	2.09	0.65
1:A:3:ILE:HG23	1:A:106:ILE:HD11	1.79	0.65
1:A:157:HIS:HD2	6:A:641:HOH:O	1.81	0.63
3:G:73:CYS:O	3:G:76:CYS:O	2.18	0.62
6:B:108:HOH:O	4:E:48:HIS:HB3	2.00	0.62
1:A:420:LYS:NZ	1:A:458:GLU:OE1	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:32:ARG:NH2	2:F:80:THR:HG21	2.16	0.60
1:D:436:GLY:O	2:F:47:LYS:NZ	2.32	0.60
2:F:86:ARG:HD3	3:G:9:ASP:OD1	2.02	0.59
1:A:385:TYR:CE1	2:B:34[A]:LEU:HD11	2.38	0.59
3:C:8:ILE:O	3:C:12:SER:OG	2.17	0.59
1:A:460:ALA:HB1	1:A:463:LEU:HD21	1.86	0.58
1:D:416:ILE:HD12	1:D:455:VAL:HG13	1.86	0.56
1:A:416[A]:ILE:HB	1:A:431:PHE:HB2	1.88	0.56
1:A:146:CYS:SG	1:A:427:HIS:CE1	2.98	0.56
4:E:38:SER:O	4:E:42:THR:OG1	2.20	0.55
1:A:164:HIS:CD2	1:A:169:ILE:HG21	2.43	0.54
1:A:438[A]:GLN:HG3	1:A:440:PHE:CE2	2.41	0.54
3:G:81:SER:O	3:G:83:ASN:N	2.40	0.54
3:C:66:GLU:HA	3:C:69:GLN:CG	2.39	0.53
1:A:447:VAL:O	3:C:57:ASP:HB2	2.09	0.52
1:A:214:THR:HG22	1:A:218:TYR:CE2	2.43	0.52
1:A:293:GLN:O	1:A:294:ASN:C	2.46	0.52
1:D:193:GLU:OE2	1:D:214:THR:HB	2.09	0.52
1:A:152:LEU:HD11	1:A:219:LEU:HD22	1.92	0.52
1:A:420:LYS:HD3	1:A:429:ILE:HD12	1.92	0.52
1:D:51:GLU:HB2	1:D:54:SER:HB2	1.92	0.52
2:F:93:VAL:CG1	4:H:8:ILE:HG23	2.40	0.52
4:H:17:GLU:O	4:H:18:GLU:CG	2.58	0.51
1:A:211:ASN:OD1	1:A:212:ARG:N	2.40	0.51
1:A:438[A]:GLN:OE1	1:A:439:TRP:N	2.43	0.51
1:D:246:ILE:HD12	1:D:246:ILE:C	2.31	0.50
1:D:20:VAL:HG13	1:D:61:LEU:HD21	1.94	0.50
1:D:51:GLU:OE1	1:D:71:HIS:HE1	1.95	0.50
4:H:17:GLU:O	4:H:18:GLU:HG3	2.12	0.50
1:D:181:LYS:NZ	6:D:601:HOH:O	2.45	0.50
1:D:220:LEU:O	1:D:223:ALA:HB3	2.12	0.49
3:C:57:ASP:OD1	3:C:57:ASP:C	2.51	0.49
1:A:460:ALA:CB	1:A:463:LEU:HD21	2.42	0.49
2:B:83:LYS:HE2	2:B:87:GLU:OE2	2.13	0.49
3:C:44:ASP:OD1	3:C:44:ASP:N	2.41	0.48
1:A:64:GLY:HA3	4:E:31:SER:HB2	1.95	0.48
1:A:141:ASN:HD22	1:A:427:HIS:HE1	1.62	0.48
1:A:20:VAL:HG13	1:A:61:LEU:HD21	1.95	0.47
1:D:246:ILE:HD11	1:D:304:LEU:HD13	1.96	0.47
2:F:93:VAL:HG13	4:H:8:ILE:HG23	1.95	0.47
1:A:416[B]:ILE:HG23	1:A:431:PHE:HB2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:15:TYR:CE2	4:E:11:ILE:HD13	2.49	0.47
3:C:85:LEU:HD23	3:C:89:LEU:HD12	1.97	0.47
1:A:164:HIS:CD2	1:A:169:ILE:CG2	2.97	0.46
1:A:416[B]:ILE:CD1	1:A:460:ALA:HB2	2.46	0.46
3:G:34:GLN:NE2	4:H:72:PRO:HG2	2.30	0.46
1:A:375:LYS:HB2	1:A:423:VAL:HG13	1.96	0.46
1:D:416:ILE:HD12	1:D:455:VAL:CG1	2.45	0.46
1:A:53:ASN:O	3:C:18:ASN:HB3	2.16	0.45
3:C:71:ILE:O	3:C:71:ILE:HG22	2.16	0.45
1:D:146:CYS:HG	1:D:427:HIS:CG	2.32	0.45
1:A:423:VAL:HG23	1:A:424:ASN:N	2.31	0.45
1:D:149:SER:O	1:D:153:GLN:HG2	2.17	0.45
4:H:17:GLU:O	4:H:18:GLU:OE2	2.35	0.45
1:D:259:ASN:O	1:D:263:VAL:HG23	2.17	0.44
2:B:63:SER:HG	1:D:374:ARG:HH21	1.62	0.44
1:D:146:CYS:HB3	1:D:427:HIS:NE2	2.32	0.44
1:A:80:GLN:HB2	1:A:81:ILE:HD12	2.00	0.44
2:B:25:ILE:HD11	2:B:88:PHE:HD2	1.83	0.44
1:A:141:ASN:HB2	1:A:444:ASP:OD2	2.17	0.44
1:D:130:MET:HB2	3:G:42:TYR:CD1	2.53	0.44
1:D:210:THR:O	1:D:210:THR:OG1	2.27	0.43
1:D:53:ASN:O	1:D:55:GLY:N	2.51	0.43
2:F:25:ILE:HD11	2:F:88:PHE:HD2	1.83	0.43
2:B:53:ASN:O	2:B:54:GLU:C	2.57	0.43
1:D:71:HIS:HB2	1:D:73:HIS:CE1	2.54	0.43
1:D:435:SER:CB	4:H:72:PRO:HA	2.48	0.43
2:F:92:ILE:HG22	2:F:93:VAL:HG23	2.00	0.43
4:E:67:ASP:N	4:E:68:PRO:CD	2.82	0.43
1:D:427:HIS:HE1	6:D:643:HOH:O	1.85	0.43
1:A:416[B]:ILE:HD12	1:A:460:ALA:HB2	2.00	0.43
1:D:78:SER:HA	1:D:83:HIS:O	2.18	0.43
1:A:315:LYS:NZ	6:A:601:HOH:O	2.50	0.43
1:A:197:ALA:O	4:E:82:GLY:HA3	2.19	0.42
2:B:43:LYS:HE3	3:C:31:GLU:OE2	2.19	0.42
1:D:253:TYR:CD1	1:D:273:CYS:HB3	2.55	0.42
1:A:137:SER:HB3	1:A:194:LEU:HG	2.01	0.42
2:B:11:GLN:HB3	4:E:11:ILE:CD1	2.50	0.42
2:F:32:ARG:CZ	2:F:80:THR:HG21	2.49	0.42
1:A:156:ILE:C	1:A:156:ILE:HD12	2.40	0.42
3:C:51:ASP:HB2	3:C:56:LEU:HB2	2.01	0.42
1:A:383:PRO:HB2	1:A:385:TYR:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:274:ILE:HD12	4:H:63:GLN:NE2	2.35	0.42
1:D:378:ASP:OD1	1:D:378:ASP:N	2.52	0.42
1:D:183:PHE:CE2	1:D:248:GLN:HG3	2.55	0.42
1:D:135:GLY:HA2	1:D:194:LEU:O	2.19	0.42
1:D:375:LYS:NZ	1:D:419:HIS:O	2.53	0.41
1:D:10:VAL:HG13	1:D:16:SER:HB3	2.02	0.41
2:B:94:ASP:O	4:E:9:LYS:N	2.53	0.41
1:D:138:GLY:HA3	1:D:445:SER:HA	2.02	0.41
1:A:179:PRO:O	1:A:218:TYR:HB3	2.20	0.41
3:G:45:LEU:HD12	3:G:46:ARG:H	1.86	0.41
1:D:189:LYS:O	1:D:192:HIS:HB3	2.20	0.41
1:A:80:GLN:CB	1:A:81:ILE:HD12	2.50	0.40
1:D:49:CYS:O	1:D:50:HIS:HB2	2.21	0.40
1:A:412:GLU:OE2	1:A:468:ARG:NH1	2.54	0.40
1:D:198:LEU:O	1:D:199:ASN:C	2.59	0.40
1:A:431:PHE:HA	1:A:440:PHE:O	2.21	0.40
1:D:152:LEU:HD23	1:D:152:LEU:HA	1.86	0.40
1:D:416:ILE:CD1	1:D:455:VAL:CG1	2.99	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	436/476 (92%)	415 (95%)	20 (5%)	1 (0%)	47 56
1	D	404/476 (85%)	394 (98%)	10 (2%)	0	100 100
2	B	95/96 (99%)	94 (99%)	1 (1%)	0	100 100
2	F	91/96 (95%)	91 (100%)	0	0	100 100
3	C	78/99 (79%)	73 (94%)	5 (6%)	0	100 100
3	G	65/99 (66%)	59 (91%)	6 (9%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
4	E	82/96 (85%)	78 (95%)	4 (5%)	0	100 100
4	H	78/96 (81%)	74 (95%)	4 (5%)	0	100 100
All	All	1329/1534 (87%)	1278 (96%)	50 (4%)	1 (0%)	51 63

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	137	SER

5.3.2 Protein sidechains (i)

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	406/429 (95%)	391 (96%)	15 (4%)	34 42
1	D	381/429 (89%)	369 (97%)	12 (3%)	40 48
2	B	92/91 (101%)	89 (97%)	3 (3%)	38 46
2	F	88/91 (97%)	86 (98%)	2 (2%)	50 61
3	C	75/89 (84%)	74 (99%)	1 (1%)	69 80
3	G	66/89 (74%)	64 (97%)	2 (3%)	41 50
4	E	78/86 (91%)	75 (96%)	3 (4%)	33 41
4	H	74/86 (86%)	70 (95%)	4 (5%)	22 25
All	All	1260/1390 (91%)	1218 (97%)	42 (3%)	38 46

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	CYS
1	A	15	LYS
1	A	144	SER
1	A	156	ILE
1	A	236	GLN
1	A	273	CYS

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Mol	Chain	Res	Type
1	A	285	SER
1	A	289	CYS
1	A	309	ASP
1	A	311	LYS
1	A	336	CYS
1	A	346	ILE
1	A	438[A]	GLN
1	A	438[B]	GLN
1	A	455	VAL
2	B	3	MET
2	B	10	SER
2	B	63	SER
3	C	92	CYS
4	E	9	LYS
4	E	18	GLU
4	E	31	SER
1	D	4	CYS
1	D	107	ASP
1	D	137	SER
1	D	178	SER
1	D	181	LYS
1	D	219	LEU
1	D	298	THR
1	D	323	PHE
1	D	378	ASP
1	D	420	LYS
1	D	445	SER
1	D	449	SER
2	F	5	THR
2	F	10	SER
3	G	5	THR
3	G	94	SER
4	H	14	LYS
4	H	30	ASP
4	H	43	PRO
4	H	92	ASP

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

Mol	Chain	Res	Type
1	A	42	ASN
1	D	12	GLN

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Mol	Chain	Res	Type
1	D	71	HIS
1	D	80	GLN
3	G	34	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 monosaccharides in this entry.

5.6 Ligand geometry

Of 15 ligands modelled in this entry, 15 are monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.

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, 95^{th} 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	440/476 (92%)	0.29	12 (2%) 54 64	32, 52, 78, 117	0
1	D	415/476 (87%)	0.36	15 (3%) 42 55	30, 56, 86, 108	1 (0%)
2	B	96/96 (100%)	0.35	3 (3%) 49 61	37, 49, 69, 98	0
2	F	93/96 (96%)	0.44	2 (2%) 62 72	50, 66, 80, 91	0
3	C	82/99 (82%)	0.94	12 (14%) 2 3	33, 66, 106, 113	0
3	G	71/99 (71%)	1.02	16 (22%) 0 1	50, 68, 110, 124	0
4	E	85/96 (88%)	0.45	7 (8%) 11 17	44, 59, 86, 96	0
4	H	82/96 (85%)	0.34	4 (4%) 29 42	37, 57, 86, 98	0
All	All	1364/1534 (88%)	0.41	71 (5%) 27 39	30, 56, 87, 124	1 (0%)

All (71) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	71	ILE	7.0
3	G	70	TYR	6.5
1	A	367	HIS	5.8
1	D	199	ASN	5.8
1	D	210	THR	5.6
3	C	93	LEU	5.3
1	A	368	LEU	5.1
3	C	70	TYR	4.8
3	G	91	ARG	4.4
4	H	15	VAL	4.4
4	H	16	ILE	4.4
1	A	296	SER	4.3
3	G	77	GLY	4.2
1	A	224	TRP	4.2
1	A	369	LEU	4.2
2	F	15	TYR	4.1

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Mol	Chain	Res	Type	RSRZ
1	D	286	SER	3.9
1	D	346	ILE	3.6
3	G	71	ILE	3.6
2	B	96	GLN	3.5
3	C	5	THR	3.5
3	G	80	VAL	3.4
4	E	9	LYS	3.4
3	G	81	SER	3.4
3	G	74	GLU	3.2
1	A	372	SER	3.2
3	G	93	LEU	3.2
1	D	198	LEU	3.1
3	G	1	MET	3.1
3	C	89	LEU	3.1
4	H	96	ASN	3.1
1	D	323	PHE	3.1
1	D	9	GLN	3.0
1	D	75	LEU	3.0
1	A	373	ASN	3.0
4	E	19	TYR	2.8
1	A	311	LYS	2.8
1	D	80	GLN	2.7
3	G	76	CYS	2.7
3	G	85	LEU	2.7
3	C	67	SER	2.6
3	G	79	ASP	2.6
1	A	424	ASN	2.6
1	D	224	TRP	2.6
1	D	405	LYS	2.5
3	C	87	ALA	2.5
3	C	66	GLU	2.4
1	D	183	PHE	2.4
3	C	44	ASP	2.3
2	F	92	ILE	2.3
3	G	87	ALA	2.3
4	E	18	GLU	2.3
4	H	17	GLU	2.3
3	G	72	HIS	2.3
3	C	83	ASN	2.3
3	G	89	LEU	2.3
3	C	91	ARG	2.3
3	G	83	ASN	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	423	VAL	2.2
1	A	374	ARG	2.2
2	B	2	THR	2.2
4	E	6	ALA	2.2
1	D	7	ILE	2.2
4	E	5	ASP	2.1
1	A	226	ILE	2.1
2	B	42	VAL	2.1
4	E	7	GLU	2.1
1	D	287	ILE	2.0
1	D	140	ILE	2.0
3	C	88	HIS	2.0
4	E	10	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 monosaccharides 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, 95^{th} 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
5	ZN	G	101	1/1	0.94	0.05	102,102,102,102	0
5	ZN	C	101	1/1	0.95	0.03	90,90,90,90	0
5	ZN	D	502	1/1	0.97	0.11	65,65,65,65	0
5	ZN	E	101	1/1	0.99	0.12	63,63,63,63	0
5	ZN	D	501	1/1	0.99	0.08	78,78,78,78	0
5	ZN	A	506	1/1	0.99	0.06	70,70,70,70	0
5	ZN	D	503	1/1	0.99	0.12	71,71,71,71	0
5	ZN	D	504	1/1	0.99	0.12	53,53,53,53	0
5	ZN	A	505	1/1	0.99	0.13	47,47,47,47	0
5	ZN	H	101	1/1	0.99	0.11	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	ZN	A	503	1/1	1.00	0.14	45,45,45,45	0
5	ZN	A	504	1/1	1.00	0.13	52,52,52,52	0
5	ZN	D	505	1/1	1.00	0.12	37,37,37,37	0
5	ZN	A	501	1/1	1.00	0.15	47,47,47,47	0
5	ZN	A	502	1/1	1.00	0.15	41,41,41,41	0

6.5 Other polymers (i)

There are no such residues in this entry.