Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2023 – 06:08 PM JST

PDB ID	:	7Y6E
Title	:	Crystal structure of sDscam FNIII23 domains, isoform Beta2v6
Authors	:	Chen, Q.; Yu, Y.; Cheng, J.
Deposited on	:	2022-06-20
Resolution	:	3.03 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:

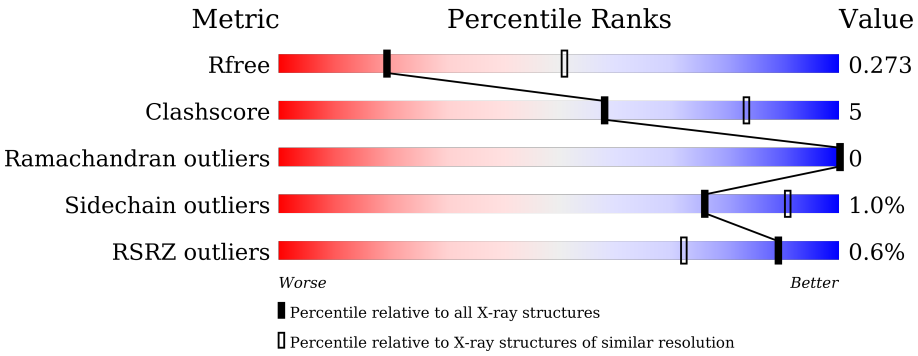
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.32.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.32.2

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 3.03 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	2752 (3.08-3.00)
Clashscore	141614	3096 (3.08-3.00)
Ramachandran outliers	138981	2986 (3.08-3.00)
Sidechain outliers	138945	2988 (3.08-3.00)
RSRZ outliers	127900	2636 (3.08-3.00)

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 <=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	202	88% 9% ·
1	B	202	85% 11% ·
1	C	202	83% 13% ·
1	D	202	2% 88% 10% ·
1	E	202	% 78% 18% ·
1	F	202	83% 12% 5%

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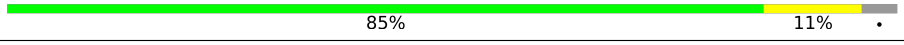
Mol	Chain	Length	Quality of chain
1	G	202	

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 10706 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 Dscam.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	198	Total	C	N	O	S	0	0	0
			1549	993	263	291	2			
1	B	194	Total	C	N	O	S	0	0	0
			1518	975	259	282	2			
1	C	196	Total	C	N	O	S	0	0	0
			1531	981	259	289	2			
1	D	199	Total	C	N	O	S	0	0	0
			1558	995	267	294	2			
1	E	195	Total	C	N	O	S	0	0	0
			1528	980	260	286	2			
1	F	192	Total	C	N	O	S	0	0	0
			1504	964	255	283	2			
1	G	193	Total	C	N	O	S	0	0	0
			1509	970	257	280	2			

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	388	GLY	-	expression tag	UNP A0A161FW14
A	389	ALA	-	expression tag	UNP A0A161FW14
A	390	SER	-	expression tag	UNP A0A161FW14
B	388	GLY	-	expression tag	UNP A0A161FW14
B	389	ALA	-	expression tag	UNP A0A161FW14
B	390	SER	-	expression tag	UNP A0A161FW14
C	388	GLY	-	expression tag	UNP A0A161FW14
C	389	ALA	-	expression tag	UNP A0A161FW14
C	390	SER	-	expression tag	UNP A0A161FW14
D	388	GLY	-	expression tag	UNP A0A161FW14
D	389	ALA	-	expression tag	UNP A0A161FW14
D	390	SER	-	expression tag	UNP A0A161FW14
E	388	GLY	-	expression tag	UNP A0A161FW14
E	389	ALA	-	expression tag	UNP A0A161FW14
E	390	SER	-	expression tag	UNP A0A161FW14

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Chain	Residue	Modelled	Actual	Comment	Reference
F	388	GLY	-	expression tag	UNP A0A161FW14
F	389	ALA	-	expression tag	UNP A0A161FW14
F	390	SER	-	expression tag	UNP A0A161FW14
G	388	GLY	-	expression tag	UNP A0A161FW14
G	389	ALA	-	expression tag	UNP A0A161FW14
G	390	SER	-	expression tag	UNP A0A161FW14

- Molecule 2 is water.

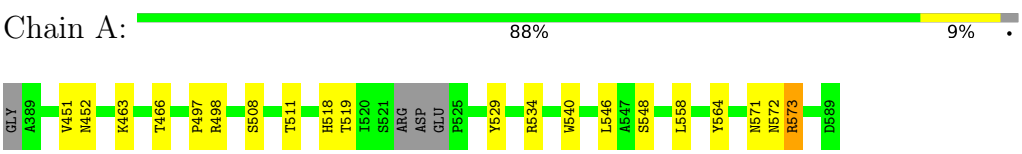
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total O 2 2	0	0
2	B	2	Total O 2 2	0	0
2	C	1	Total O 1 1	0	0
2	D	1	Total O 1 1	0	0
2	E	1	Total O 1 1	0	0
2	F	2	Total O 2 2	0	0

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.

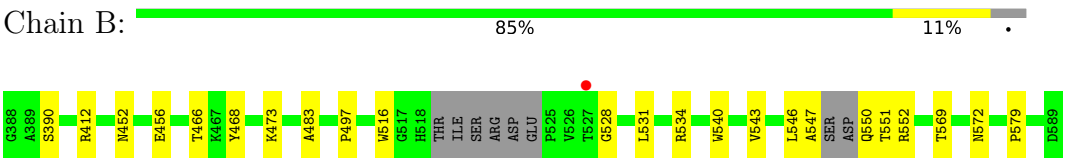
- Molecule 1: Dscam

Chain A:



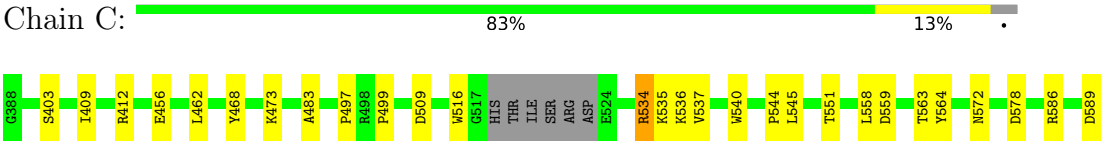
- Molecule 1: Dscam

Chain B:



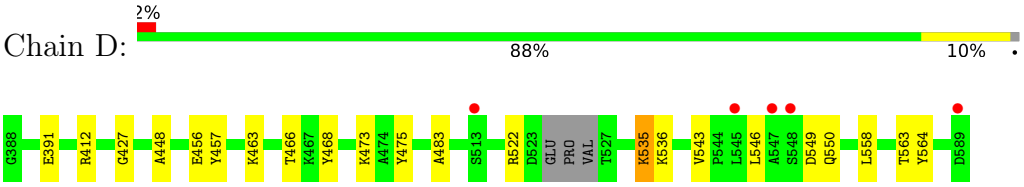
- Molecule 1: Dscam

Chain C:



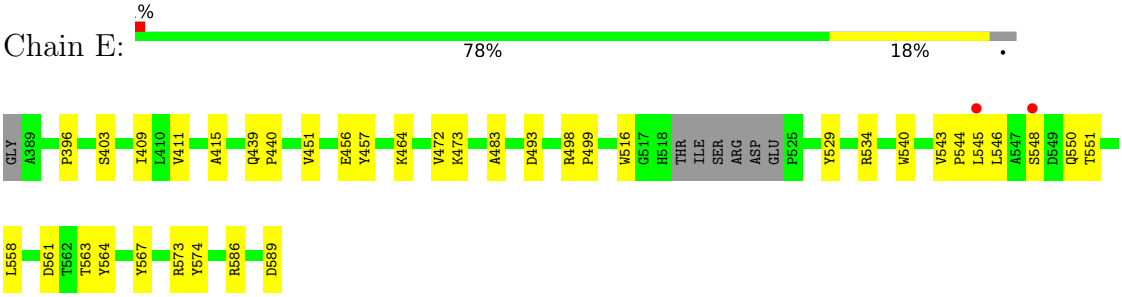
- Molecule 1: Dscam

Chain D:



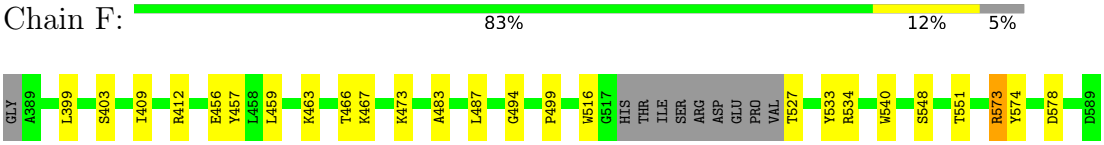
- Molecule 1: Dscam

Chain E:



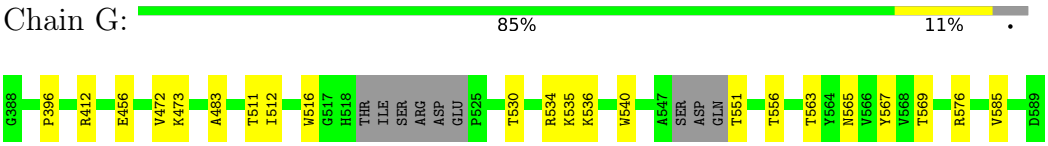
• Molecule 1: Dscam

Chain F:



• Molecule 1: Dscam

Chain G:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	307.02Å 56.22Å 94.84Å 90.00° 105.38° 90.00°	Depositor
Resolution (Å)	48.85 – 3.03 48.85 – 3.03	Depositor EDS
% Data completeness (in resolution range)	84.3 (48.85-3.03) 84.3 (48.85-3.03)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.04 (at 3.01Å)	Xtriage
Refinement program	PHENIX (1.15.2_3472: ???)	Depositor
R, R_{free}	0.234 , 0.272 0.234 , 0.273	Depositor DCC
R_{free} test set	1373 reflections (5.29%)	wwPDB-VP
Wilson B-factor (Å^2)	61.7	Xtriage
Anisotropy	0.287	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 6.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.014 for -h-2*l,-k,l	Xtriage
F_o,F_c correlation	0.89	EDS
Total number of atoms	10706	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 4.03% 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

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	0.25	0/1594	0.50	0/2173
1	B	0.25	0/1562	0.49	0/2127
1	C	0.25	0/1575	0.50	0/2147
1	D	0.25	0/1602	0.51	0/2182
1	E	0.25	0/1573	0.53	0/2144
1	F	0.25	0/1547	0.51	0/2108
1	G	0.25	0/1553	0.49	0/2115
All	All	0.25	0/11006	0.50	0/14996

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	1549	0	1539	13	0
1	B	1518	0	1509	16	0
1	C	1531	0	1517	16	0
1	D	1558	0	1542	14	0
1	E	1528	0	1516	18	0
1	F	1504	0	1492	14	0
1	G	1509	0	1501	13	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	2	0	0	0	0
All	All	10706	0	10616	102	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 (102) 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:451:VAL:HG12	1:A:452:ASN:H	1.48	0.77
1:D:427:GLY:HA2	1:D:448:ALA:HB2	1.71	0.73
1:D:536:LYS:HD3	1:D:563:THR:HB	1.71	0.73
1:C:536:LYS:HD3	1:C:563:THR:HB	1.70	0.72
1:G:512:ILE:HD12	1:G:585:VAL:HG11	1.73	0.71
1:E:439:GLN:HG2	1:E:440:PRO:HD2	1.75	0.68
1:E:464:LYS:HE2	1:E:493:ASP:HA	1.77	0.66
1:B:412:ARG:HG2	1:B:456:GLU:HB3	1.79	0.64
1:C:534:ARG:HB3	1:C:540:TRP:HA	1.80	0.64
1:D:473:LYS:HE2	1:D:483:ALA:HB2	1.80	0.63
1:B:528:GLY:H	1:B:547:ALA:HB2	1.65	0.62
1:C:412:ARG:NH1	1:C:456:GLU:OE1	2.34	0.61
1:G:412:ARG:HG3	1:G:456:GLU:HB3	1.83	0.60
1:A:546:LEU:HG	1:A:548:SER:H	1.65	0.60
1:A:463:LYS:HD2	1:A:466:THR:HG21	1.84	0.60
1:D:391:GLU:OE2	1:F:467:LYS:NZ	2.35	0.58
1:F:516:TRP:O	1:F:551:THR:OG1	2.22	0.58
1:F:499:PRO:HG3	1:F:578:ASP:HB2	1.85	0.58
1:A:451:VAL:HG12	1:A:452:ASN:N	2.18	0.57
1:B:466:THR:HG23	1:B:468:TYR:HE1	1.69	0.56
1:A:518:HIS:ND1	1:A:529:TYR:OH	2.39	0.56
1:D:466:THR:HG23	1:D:468:TYR:HE1	1.71	0.56
1:C:499:PRO:HG3	1:C:578:ASP:HB2	1.87	0.55
1:E:473:LYS:HE2	1:E:483:ALA:HB2	1.89	0.55
1:C:544:PRO:HB2	1:C:545:LEU:HD12	1.88	0.55
1:C:473:LYS:HG2	1:C:483:ALA:HA	1.89	0.54
1:F:473:LYS:HE2	1:F:483:ALA:HB2	1.89	0.54
1:B:531:LEU:HB3	1:B:543:VAL:HG23	1.90	0.54
1:G:473:LYS:HE2	1:G:483:ALA:HB2	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:534:ARG:HG3	1:G:535:LYS:O	2.08	0.53
1:A:571:ASN:OD1	1:A:572:ASN:N	2.42	0.53
1:A:497:PRO:HD3	1:A:572:ASN:HB2	1.91	0.53
1:G:536:LYS:HD2	1:G:563:THR:HB	1.90	0.53
1:F:412:ARG:NH1	1:F:456:GLU:OE1	2.42	0.53
1:B:473:LYS:HE2	1:B:483:ALA:HB2	1.90	0.53
1:D:463:LYS:HB3	1:D:466:THR:HG21	1.91	0.53
1:B:551:THR:HG23	1:B:552:ARG:HD2	1.91	0.52
1:G:512:ILE:HD12	1:G:585:VAL:CG1	2.40	0.51
1:D:549:ASP:OD1	1:D:550:GLN:N	2.43	0.51
1:A:508:SER:OG	1:A:511:THR:HG22	2.11	0.50
1:B:497:PRO:HD3	1:B:572:ASN:HB2	1.92	0.50
1:A:451:VAL:CG1	1:A:452:ASN:H	2.19	0.50
1:G:530:THR:HB	1:G:569:THR:HG22	1.94	0.50
1:E:415:ALA:HB2	1:E:451:VAL:HG12	1.94	0.50
1:D:543:VAL:HG12	1:D:546:LEU:HD11	1.93	0.49
1:B:516:TRP:O	1:B:551:THR:OG1	2.31	0.49
1:E:563:THR:OG1	1:E:586:ARG:HG3	2.12	0.49
1:F:403:SER:HA	1:F:409:ILE:HA	1.94	0.49
1:C:536:LYS:HG3	1:C:537:VAL:HG13	1.95	0.49
1:F:463:LYS:HD3	1:F:466:THR:HG21	1.94	0.49
1:E:543:VAL:HG12	1:E:546:LEU:HD11	1.95	0.48
1:G:511:THR:HG22	1:G:556:THR:HA	1.95	0.48
1:G:534:ARG:NE	1:G:565:ASN:HD22	2.12	0.48
1:E:544:PRO:HB2	1:E:545:LEU:HD12	1.95	0.48
1:D:558:LEU:HD22	1:D:564:TYR:CE2	2.48	0.47
1:G:516:TRP:O	1:G:551:THR:OG1	2.32	0.47
1:B:534:ARG:HD3	1:B:540:TRP:CE2	2.49	0.47
1:C:509:ASP:HA	1:C:589:ASP:H	1.78	0.47
1:C:497:PRO:HD3	1:C:572:ASN:ND2	2.29	0.47
1:F:494:GLY:HA3	1:F:574:TYR:CE2	2.50	0.47
1:F:573:ARG:HD3	1:F:574:TYR:CE2	2.49	0.47
1:C:403:SER:HA	1:C:409:ILE:HA	1.96	0.47
1:D:473:LYS:HG2	1:D:483:ALA:HA	1.97	0.47
1:E:534:ARG:HD3	1:E:540:TRP:CE2	2.49	0.47
1:A:558:LEU:HD22	1:A:564:TYR:CE2	2.50	0.47
1:E:529:TYR:HE1	1:E:548:SER:HA	1.80	0.47
1:E:561:ASP:HB2	1:E:589:ASP:HB3	1.97	0.46
1:B:550:GLN:HG3	1:B:552:ARG:H	1.79	0.46
1:C:558:LEU:HD22	1:C:564:TYR:CE2	2.51	0.46
1:F:534:ARG:HD3	1:F:540:TRP:CE2	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:558:LEU:HD22	1:E:564:TYR:CE2	2.50	0.46
1:G:534:ARG:HD3	1:G:540:TRP:CE2	2.51	0.46
1:E:403:SER:HA	1:E:409:ILE:HA	1.98	0.45
1:A:534:ARG:HD3	1:A:540:TRP:CE2	2.52	0.45
1:A:572:ASN:OD1	1:A:573:ARG:N	2.47	0.45
1:D:427:GLY:HA2	1:D:448:ALA:CB	2.46	0.45
1:E:498:ARG:HD2	1:E:499:PRO:HD2	1.99	0.45
1:C:534:ARG:HG2	1:C:540:TRP:CD2	2.53	0.44
1:G:569:THR:HG21	1:G:576:ARG:HD3	2.00	0.44
1:B:550:GLN:HG3	1:B:551:THR:N	2.33	0.44
1:A:498:ARG:HD2	1:A:519:THR:O	2.17	0.44
1:E:473:LYS:HG2	1:E:483:ALA:HA	2.00	0.44
1:G:396:PRO:HG2	1:G:472:VAL:HG12	1.99	0.43
1:C:516:TRP:O	1:C:551:THR:OG1	2.36	0.43
1:D:391:GLU:H	1:D:391:GLU:HG2	1.66	0.43
1:E:411:VAL:O	1:E:456:GLU:HA	2.19	0.43
1:D:535:LYS:H	1:D:535:LYS:HD2	1.84	0.43
1:B:452:ASN:N	1:B:452:ASN:OD1	2.41	0.42
1:B:473:LYS:HG2	1:B:483:ALA:HA	2.01	0.42
1:F:527:THR:HG23	1:F:548:SER:HB3	2.01	0.42
1:B:546:LEU:HD13	1:B:547:ALA:N	2.35	0.42
1:E:516:TRP:O	1:E:551:THR:HG23	2.19	0.42
1:D:412:ARG:HG2	1:D:456:GLU:HB3	2.01	0.41
1:C:462:LEU:HD22	1:C:468:TYR:CE2	2.56	0.41
1:F:473:LYS:HG2	1:F:483:ALA:HA	2.02	0.41
1:B:390:SER:HB3	1:C:586:ARG:HH12	1.86	0.41
1:F:399:LEU:HG	1:F:487:LEU:HD12	2.03	0.41
1:E:396:PRO:HG2	1:E:472:VAL:HG12	2.02	0.41
1:E:573:ARG:HD2	1:E:574:TYR:CZ	2.56	0.41
1:C:535:LYS:NZ	1:C:559:ASP:OD2	2.34	0.40
1:B:569:THR:HG22	1:B:579:PRO:HA	2.03	0.40
1:F:457:TYR:HE2	1:F:459:LEU:HD23	1.86	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	194/202 (96%)	187 (96%)	7 (4%)	0	100	100
1	B	188/202 (93%)	185 (98%)	3 (2%)	0	100	100
1	C	192/202 (95%)	189 (98%)	3 (2%)	0	100	100
1	D	195/202 (96%)	190 (97%)	5 (3%)	0	100	100
1	E	191/202 (95%)	185 (97%)	6 (3%)	0	100	100
1	F	188/202 (93%)	184 (98%)	4 (2%)	0	100	100
1	G	187/202 (93%)	185 (99%)	2 (1%)	0	100	100
All	All	1335/1414 (94%)	1305 (98%)	30 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	171/174 (98%)	170 (99%)	1 (1%)	86	94
1	B	166/174 (95%)	166 (100%)	0	100	100
1	C	168/174 (97%)	167 (99%)	1 (1%)	86	94
1	D	171/174 (98%)	167 (98%)	4 (2%)	50	78
1	E	168/174 (97%)	165 (98%)	3 (2%)	59	83
1	F	165/174 (95%)	163 (99%)	2 (1%)	71	89
1	G	165/174 (95%)	164 (99%)	1 (1%)	86	94
All	All	1174/1218 (96%)	1162 (99%)	12 (1%)	76	91

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	573	ARG
1	C	534	ARG
1	D	457	TYR
1	D	475	TYR
1	D	522	ARG
1	D	535	LYS
1	E	457	TYR
1	E	550	GLN
1	E	567	TYR
1	F	533	TYR
1	F	573	ARG
1	G	567	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	565	ASN
1	G	565	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides 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, 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	198/202 (98%)	-0.29	0 100 100	39, 49, 74, 87	0
1	B	194/202 (96%)	-0.14	1 (0%) 91 75	39, 56, 89, 98	0
1	C	196/202 (97%)	-0.26	0 100 100	40, 56, 72, 89	0
1	D	199/202 (98%)	-0.18	5 (2%) 57 28	40, 59, 85, 104	0
1	E	195/202 (96%)	-0.13	2 (1%) 82 59	41, 58, 80, 97	0
1	F	192/202 (95%)	-0.24	0 100 100	41, 59, 78, 99	0
1	G	193/202 (95%)	-0.27	0 100 100	44, 60, 77, 99	0
All	All	1367/1414 (96%)	-0.21	8 (0%) 89 72	39, 57, 80, 104	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	545	LEU	5.1
1	D	547	ALA	3.9
1	E	545	LEU	3.8
1	E	548	SER	3.1
1	D	513	SER	2.5
1	D	589	ASP	2.4
1	B	527	THR	2.4
1	D	548	SER	2.3

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

There are no monosaccharides in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.