



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 26, 2014 – 08:06 PM GMT

PDB ID : 1T2K
Title : Structure Of The DNA Binding Domains Of IRF3, ATF-2 and Jun Bound To DNA
Authors : Panne, D.; Maniatis, T.; Harrison, S.C.
Deposited on : 2004-04-21
Resolution : 3.00 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

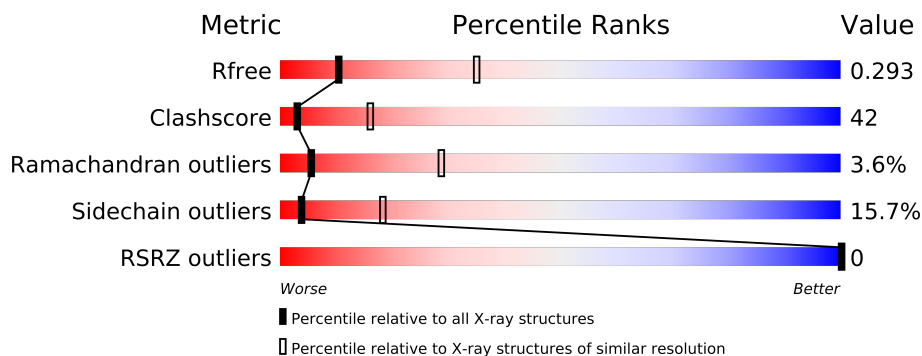
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

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}	66092	1216 (3.00-3.00)
Clashscore	79885	1594 (3.00-3.00)
Ramachandran outliers	78287	1537 (3.00-3.00)
Sidechain outliers	78261	1540 (3.00-3.00)
RSRZ outliers	66119	1217 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	E	31	
2	F	31	
3	A	112	
3	B	112	
4	C	62	
5	D	61	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 4034 atoms, of which 0 are hydrogen and 0 are deuterium.

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 DNA chain called 31-MER.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	E	31	Total	C	N	O	P	0	0	0
			649	308	139	172	30			

- Molecule 2 is a DNA chain called 31-MER.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	F	31	Total	C	N	O	P	0	0	0
			616	301	89	196	30			

- Molecule 3 is a protein called Interferon regulatory factor 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	110	Total	C	N	O		0	0	0
			912	581	172	159				
3	B	108	Total	C	N	O		0	0	0
			888	568	166	154				

- Molecule 4 is a protein called Transcription factor AP-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	C	62	Total	C	N	O	S	0	0	0
			484	293	99	89	3			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	253	MET	ILE	CLONING ARTIFACT	UNP P05412
C	269	SER	CYS	ENGINEERED	UNP P05412

- Molecule 5 is a protein called Cyclic-AMP-dependent transcription factor ATF-2.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	D	61	Total	C	N	O	0	0	0
			477	292	98	87			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	351	SER	CYS	ENGINEERED	UNP P15336

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	3	Total	O	0	0
			3	3		
6	E	2	Total	O	0	0
			2	2		
6	F	3	Total	O	0	0
			3	3		

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 ($RSRZ > 2$). 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.

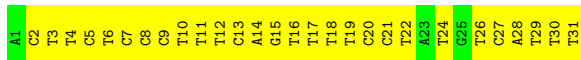
- Molecule 1: 31-MER

Chain E: 



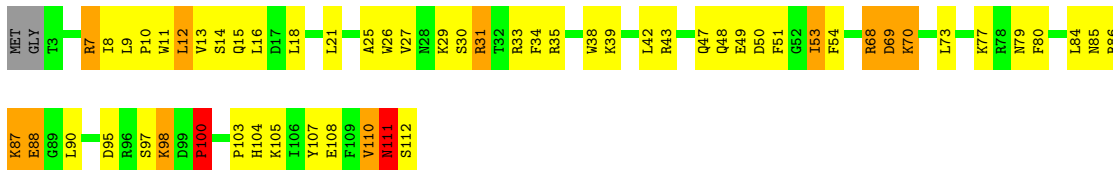
- Molecule 2: 31-MER

Chain F: 



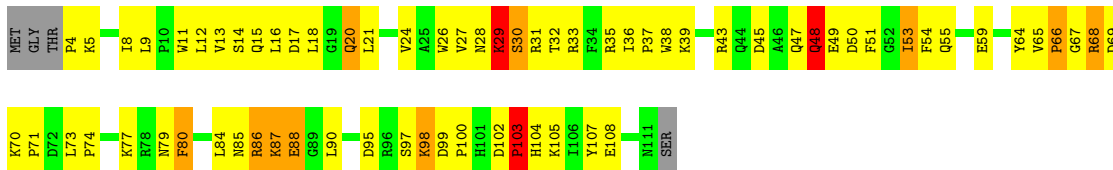
- Molecule 3: Interferon regulatory factor 3

Chain A: 



- Molecule 3: Interferon regulatory factor 3

Chain B: 



- Molecule 4: Transcription factor AP-1

Chain C: 



- Molecule 5: Cyclic-AMP-dependent transcription factor ATF-2

Chain D: 

K336	K337	L341	E342	R343	R344	R345	A346	A347	R350	K354	R355	K356	V357	V358	V359	Q360	S361	L362	E363	E367	D368	L369	S370	S371	Q375	L376	Q377	V380	T381	L382	L383	R384	V385	E386	L390	L394	L395	A396
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	186.38Å 65.21Å 83.85Å 90.00° 93.44° 90.00°	Depositor
Resolution (Å)	29.98 – 3.00 44.94 – 3.00	Depositor EDS
% Data completeness (in resolution range)	98.9 (29.98-3.00) 99.0 (44.94-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.06 (at 3.01Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.257 , 0.296 0.249 , 0.293	Depositor DCC
R_{free} test set	1178 reflections (6.21%)	DCC
Wilson B-factor (Å ²)	55.1	Xtriage
Anisotropy	1.286	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 51.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 20151 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4034	wwPDB-VP
Average B, all atoms (Å ²)	87.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.04% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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	E	0.44	0/735	0.74	0/1135
2	F	0.49	0/683	0.76	0/1050
3	A	0.64	1/940 (0.1%)	0.92	2/1273 (0.2%)
3	B	0.53	0/916	0.95	2/1241 (0.2%)
4	C	0.52	0/483	0.76	0/638
5	D	0.52	0/479	0.77	0/638
All	All	0.54	1/4236 (0.0%)	0.84	4/5975 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	E	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	112	SER	C-OXT	-5.63	1.12	1.23

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	103	PRO	CA-N-CD	-13.34	92.83	111.50
3	A	100	PRO	CA-N-CD	-8.65	99.39	111.50
3	A	69	ASP	CA-C-N	-6.04	103.91	117.20
3	B	48	GLN	N-CA-C	5.09	124.75	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	E	6	DG	Sidechain

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	649	0	347	46	0
2	F	616	0	359	70	0
3	A	912	0	893	56	0
3	B	888	0	863	91	0
4	C	484	0	512	31	0
5	D	477	0	483	49	0
6	A	3	0	0	0	0
6	E	2	0	0	0	0
6	F	3	0	0	0	0
All	All	4034	0	3457	309	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 42.

All (309) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:D:347:ALA:HA	5:D:350:ARG:CG	1.77	1.15
2:F:5:DC:H2"	2:F:6:DT:H5"	1.16	1.08
2:F:29:DT:H2"	2:F:30:DT:H5"	1.33	1.07
3:B:99:ASP:O	3:B:103:PRO:HD3	1.54	1.06
3:A:53:ILE:H	3:A:53:ILE:HD12	1.20	1.04
5:D:347:ALA:HA	5:D:350:ARG:HG3	1.39	1.04
3:B:53:ILE:H	3:B:53:ILE:HD12	1.11	1.04
5:D:347:ALA:HA	5:D:350:ARG:CD	1.89	1.01
2:F:5:DC:C2'	2:F:6:DT:H5"	1.90	1.01
2:F:18:DT:H2"	2:F:19:DT:H5'	1.41	1.00
4:C:280:LEU:HD22	5:D:362:LEU:HD21	1.39	1.00
5:D:347:ALA:HA	5:D:350:ARG:HD2	1.48	0.94
3:B:86:ARG:HB3	3:B:86:ARG:NH1	1.84	0.91
3:B:29:LYS:H	3:B:29:LYS:HD3	1.36	0.89

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:D:347:ALA:CA	5:D:350:ARG:HG3	2.03	0.89
4:C:280:LEU:CD2	5:D:362:LEU:HD21	2.03	0.89
5:D:346:ALA:O	5:D:350:ARG:HG2	1.73	0.88
3:A:68:ARG:NH1	3:A:69:ASP:OD2	2.08	0.87
3:B:53:ILE:N	3:B:53:ILE:HD12	1.92	0.85
3:B:86:ARG:HH11	3:B:86:ARG:HB3	1.41	0.84
3:B:29:LYS:HD3	3:B:29:LYS:N	1.93	0.84
2:F:5:DC:H2''	2:F:6:DT:C5'	2.03	0.84
5:D:362:LEU:C	5:D:362:LEU:HD23	1.97	0.83
3:B:20:GLN:HA	3:B:20:GLN:HE21	1.45	0.81
2:F:29:DT:C2'	2:F:30:DT:H5''	2.10	0.81
2:F:10:DT:H2''	2:F:11:DT:C5'	2.11	0.81
3:B:53:ILE:H	3:B:53:ILE:CD1	1.88	0.81
2:F:18:DT:H2''	2:F:19:DT:C5'	2.10	0.81
1:E:3:DA:H2''	1:E:4:DA:H5'	1.61	0.81
1:E:31:DG:H1	2:F:2:DC:H42	1.27	0.80
2:F:10:DT:H3'	3:B:79:ASN:ND2	1.96	0.80
2:F:18:DT:H5'	2:F:18:DT:H6	1.46	0.80
2:F:29:DT:H2''	2:F:30:DT:C5'	2.11	0.79
1:E:17:DA:H2''	1:E:18:DC:O5'	1.82	0.79
3:A:53:ILE:N	3:A:53:ILE:HD12	1.98	0.78
2:F:10:DT:H2''	2:F:11:DT:H5'	1.66	0.78
4:C:267:SER:O	4:C:271:LYS:HG3	1.84	0.77
5:D:362:LEU:HD23	5:D:363:GLU:N	2.00	0.77
2:F:10:DT:H3'	3:B:79:ASN:HD21	1.46	0.77
3:B:51:PHE:CD2	3:B:73:LEU:HB3	2.20	0.77
4:C:312:VAL:HG21	5:D:394:LEU:HB3	1.65	0.76
3:B:47:GLN:O	3:B:49:GLU:N	2.19	0.75
3:B:9:LEU:O	3:B:13:VAL:HG23	1.86	0.75
2:F:14:DA:H2''	2:F:15:DG:H5''	1.69	0.75
5:D:347:ALA:CA	5:D:350:ARG:CG	2.62	0.75
3:A:9:LEU:O	3:A:13:VAL:HG23	1.86	0.74
1:E:3:DA:H2''	1:E:4:DA:C5'	2.17	0.74
5:D:347:ALA:O	5:D:350:ARG:HG3	1.88	0.73
3:A:35:ARG:HG3	3:A:35:ARG:O	1.87	0.73
3:A:53:ILE:H	3:A:53:ILE:CD1	1.88	0.72
1:E:17:DA:H5'	1:E:17:DA:H8	1.56	0.71
3:B:51:PHE:CE2	3:B:73:LEU:HB3	2.26	0.71
2:F:7:DC:H2''	2:F:8:DC:H5'	1.72	0.70
5:D:347:ALA:C	5:D:350:ARG:HG3	2.12	0.69
1:E:7:DA:H2''	1:E:8:DC:H5'	1.74	0.69
5:D:375:GLN:H	5:D:375:GLN:HE21	1.40	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:F:28:DA:H2''	2:F:29:DT:H5''	1.74	0.68
3:B:73:LEU:HB2	3:B:74:PRO:HD3	1.75	0.68
2:F:18:DT:H5'	2:F:18:DT:C6	2.28	0.68
3:A:9:LEU:HD11	3:A:87:LYS:HG3	1.75	0.68
3:A:21:LEU:H	3:A:21:LEU:HD12	1.59	0.68
3:B:28:ASN:CG	3:B:32:THR:HG22	2.14	0.67
2:F:3:DT:H2'	2:F:4:DT:H71	1.75	0.67
2:F:12:DT:H4'	2:F:13:DC:OP1	1.93	0.67
4:C:280:LEU:HD13	5:D:362:LEU:HD22	1.76	0.67
2:F:15:DG:H2''	2:F:16:DT:O5'	1.95	0.67
5:D:375:GLN:N	5:D:375:GLN:HE21	1.93	0.66
3:B:43:ARG:HB3	3:B:45:ASP:OD1	1.94	0.66
3:B:73:LEU:HB2	3:B:74:PRO:CD	2.26	0.66
3:B:73:LEU:H	3:B:73:LEU:HD22	1.59	0.66
4:C:312:VAL:CG2	5:D:394:LEU:HB3	2.24	0.66
3:A:21:LEU:HD12	3:A:21:LEU:N	2.10	0.66
3:B:20:GLN:HA	3:B:20:GLN:NE2	2.10	0.65
3:B:20:GLN:C	3:B:21:LEU:HD12	2.17	0.65
5:D:337:ARG:HG2	5:D:337:ARG:HH11	1.61	0.64
3:B:54:PHE:HD1	3:B:80:PHE:HD2	1.45	0.64
3:B:99:ASP:O	3:B:103:PRO:CD	2.38	0.64
3:A:87:LYS:O	3:A:88:GLU:C	2.36	0.64
2:F:5:DC:C3'	2:F:6:DT:H5''	2.27	0.63
2:F:16:DT:H3'	3:A:79:ASN:ND2	2.13	0.63
1:E:7:DA:H2''	1:E:8:DC:C5'	2.29	0.63
3:B:38:TRP:CD2	3:B:105:LYS:HD2	2.34	0.62
3:A:54:PHE:CD1	3:A:80:PHE:HD2	2.18	0.62
2:F:10:DT:H2''	2:F:11:DT:H5''	1.81	0.62
1:E:28:DG:H1	2:F:5:DC:H42	1.46	0.62
3:B:14:SER:O	3:B:18:LEU:HG	2.00	0.61
3:B:28:ASN:O	3:B:28:ASN:OD1	2.17	0.61
1:E:17:DA:H5'	1:E:17:DA:C8	2.34	0.61
3:B:73:LEU:H	3:B:73:LEU:CD2	2.13	0.61
5:D:371:SER:O	5:D:375:GLN:NE2	2.32	0.61
3:B:54:PHE:HD1	3:B:80:PHE:CD2	2.19	0.61
1:E:7:DA:H1'	1:E:8:DC:H5''	1.83	0.61
4:C:280:LEU:HD13	5:D:362:LEU:CD2	2.31	0.61
3:B:73:LEU:HD22	3:B:73:LEU:N	2.14	0.61
3:B:65:VAL:O	3:B:67:GLY:N	2.34	0.61
5:D:343:ARG:HG3	5:D:343:ARG:HH11	1.66	0.61
2:F:28:DA:C2'	2:F:29:DT:H5''	2.31	0.60
3:B:35:ARG:HH22	3:B:102:ASP:CG	2.05	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:A:110:VAL:O	3:A:111:ASN:HB3	2.01	0.60
3:B:80:PHE:O	3:B:80:PHE:HD1	1.85	0.60
3:A:98:LYS:O	3:A:100:PRO:HD3	2.01	0.60
2:F:6:DT:H2''	2:F:7:DC:C6	2.36	0.60
2:F:27:DC:OP2	5:D:337:ARG:NH2	2.34	0.59
3:A:47:GLN:HG3	3:A:49:GLU:HB3	1.85	0.59
4:C:287:LEU:O	4:C:291:ASN:HB3	2.03	0.59
3:A:73:LEU:HD22	3:A:73:LEU:N	2.17	0.58
4:C:261:ARG:HG2	4:C:261:ARG:HH11	1.68	0.58
2:F:28:DA:H2''	2:F:29:DT:C5'	2.32	0.58
1:E:8:DC:H6	4:C:270:ARG:NH1	2.02	0.58
5:D:377:GLN:HE21	5:D:377:GLN:HA	1.67	0.58
2:F:26:DT:H2''	2:F:27:DC:O5'	2.04	0.58
2:F:20:DC:H2''	2:F:21:DC:C5'	2.34	0.57
3:B:69:ASP:O	3:B:70:LYS:C	2.41	0.57
1:E:23:DA:H2''	1:E:24:DG:H5''	1.86	0.57
1:E:26:DG:H2''	1:E:27:DA:C8	2.39	0.57
1:E:14:DA:H2''	1:E:15:DA:H5'	1.86	0.57
5:D:356:LYS:O	5:D:360:GLN:HG3	2.05	0.57
3:A:48:GLN:NE2	3:A:49:GLU:N	2.53	0.56
5:D:347:ALA:CA	5:D:350:ARG:HD2	2.28	0.56
3:A:48:GLN:NE2	3:A:49:GLU:H	2.03	0.56
3:B:28:ASN:C	3:B:28:ASN:OD1	2.44	0.56
3:A:38:TRP:NE1	3:A:77:LYS:HE3	2.19	0.56
2:F:20:DC:H1'	2:F:21:DC:H5''	1.88	0.56
4:C:291:ASN:HD22	4:C:292:SER:N	2.04	0.56
4:C:299:ASN:O	4:C:303:GLU:HG3	2.06	0.56
2:F:30:DT:H2''	2:F:31:DT:O5'	2.06	0.55
3:A:73:LEU:HD22	3:A:73:LEU:H	1.70	0.55
3:B:35:ARG:NH2	3:B:102:ASP:OD2	2.33	0.55
4:C:274:LEU:HD23	4:C:277:ILE:HD12	1.88	0.55
1:E:19:DT:H2''	1:E:20:DG:C8	2.41	0.55
5:D:377:GLN:HE21	5:D:377:GLN:CA	2.20	0.55
4:C:273:LYS:O	4:C:277:ILE:HG13	2.06	0.55
3:A:39:LYS:HE2	3:A:50:ASP:CG	2.26	0.55
3:B:16:LEU:HB3	3:B:26:TRP:NE1	2.22	0.55
3:A:110:VAL:O	3:A:111:ASN:CB	2.54	0.55
1:E:5:DT:OP1	5:D:354:LYS:NZ	2.36	0.55
3:A:38:TRP:NE1	3:A:77:LYS:CE	2.70	0.55
4:C:280:LEU:HD11	5:D:363:GLU:HG2	1.88	0.55
1:E:28:DG:H2''	1:E:29:DA:C8	2.43	0.54
1:E:9:DA:H1'	1:E:10:DT:H5''	1.89	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:B:29:LYS:CD	3:B:29:LYS:H	2.16	0.54
4:C:304:GLN:HA	4:C:307:GLN:HB3	1.90	0.54
3:A:14:SER:O	3:A:18:LEU:HG	2.08	0.53
3:B:68:ARG:HD3	3:B:68:ARG:O	2.07	0.53
3:B:33:ARG:HG2	3:B:108:GLU:HB2	1.90	0.53
3:A:54:PHE:CD1	3:A:80:PHE:CD2	2.96	0.53
1:E:29:DA:H2''	1:E:30:DA:H5'	1.90	0.53
3:B:65:VAL:O	3:B:69:ASP:HB2	2.09	0.53
4:C:287:LEU:HD23	5:D:369:LEU:CB	2.39	0.53
2:F:3:DT:H5'	2:F:3:DT:H6	1.74	0.53
1:E:25:DG:H2'	1:E:26:DG:C8	2.44	0.53
3:B:64:TYR:O	3:B:66:PRO:HD3	2.08	0.52
3:B:98:LYS:O	3:B:100:PRO:HD3	2.09	0.52
3:A:9:LEU:HD11	3:A:87:LYS:CG	2.39	0.52
3:B:33:ARG:NH1	3:B:108:GLU:OE1	2.43	0.52
2:F:20:DC:H2''	2:F:21:DC:H5''	1.92	0.52
3:A:54:PHE:HD1	3:A:80:PHE:CD2	2.27	0.52
3:A:7:ARG:O	3:A:10:PRO:HD2	2.09	0.52
5:D:346:ALA:O	5:D:350:ARG:CG	2.52	0.52
1:E:8:DC:C6	4:C:270:ARG:NH1	2.77	0.52
2:F:20:DC:C2'	2:F:21:DC:H5''	2.40	0.52
2:F:27:DC:C2'	2:F:28:DA:C8	2.93	0.51
2:F:10:DT:C6	2:F:11:DT:H72	2.46	0.51
1:E:4:DA:H2''	1:E:5:DT:O5'	2.11	0.51
3:B:38:TRP:NE1	3:B:77:LYS:HE3	2.24	0.51
3:B:27:VAL:HG12	3:B:27:VAL:O	2.10	0.51
3:B:68:ARG:HA	3:B:68:ARG:NE	2.25	0.51
3:A:73:LEU:CD2	3:A:73:LEU:H	2.23	0.51
5:D:390:LEU:HD22	5:D:394:LEU:HD13	1.91	0.51
2:F:18:DT:OP1	3:B:98:LYS:HE2	2.10	0.51
5:D:390:LEU:HD22	5:D:394:LEU:CD1	2.41	0.51
1:E:18:DC:H2''	1:E:19:DT:H5'	1.93	0.51
3:B:80:PHE:CD1	3:B:80:PHE:C	2.83	0.51
3:A:54:PHE:CE1	3:A:80:PHE:HD2	2.29	0.51
3:B:32:THR:HG23	3:B:33:ARG:HG3	1.93	0.50
1:E:2:DA:H2''	1:E:3:DA:OP2	2.11	0.50
2:F:27:DC:H2'	2:F:28:DA:C8	2.47	0.50
3:B:84:LEU:HD22	3:B:90:LEU:CD2	2.41	0.50
2:F:10:DT:H5''	3:B:79:ASN:HD22	1.76	0.50
5:D:377:GLN:NE2	5:D:377:GLN:HA	2.27	0.50
3:B:33:ARG:CG	3:B:108:GLU:HG3	2.41	0.49
3:B:33:ARG:HG2	3:B:108:GLU:HG3	1.93	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:A:51:PHE:CE2	3:A:73:LEU:HB3	2.48	0.49
3:B:48:GLN:NE2	3:B:55:GLN:HE22	2.10	0.49
3:B:29:LYS:C	3:B:31:ARG:H	2.15	0.49
2:F:18:DT:H2'	2:F:19:DT:H71	1.94	0.49
3:B:36:ILE:O	3:B:104:HIS:HB2	2.13	0.49
3:B:86:ARG:HB3	3:B:86:ARG:CZ	2.42	0.48
4:C:267:SER:OG	4:C:271:LYS:HE3	2.12	0.48
1:E:25:DG:OP1	1:E:25:DG:H4'	2.13	0.48
3:A:84:LEU:HD22	3:A:90:LEU:CD2	2.43	0.48
3:B:38:TRP:CE3	3:B:105:LYS:HD2	2.48	0.48
1:E:24:DG:H2''	1:E:25:DG:O5'	2.14	0.48
4:C:311:LYS:HB3	5:D:395:LEU:HD11	1.94	0.48
2:F:9:DC:OP2	3:B:87:LYS:HE2	2.12	0.48
3:A:87:LYS:O	3:A:88:GLU:O	2.31	0.48
3:B:73:LEU:CB	3:B:74:PRO:HD3	2.44	0.48
4:C:257:ARG:HG3	4:C:257:ARG:O	2.14	0.48
1:E:31:DG:H1	2:F:2:DC:N4	2.02	0.48
3:A:25:ALA:O	3:A:35:ARG:HG2	2.14	0.47
5:D:359:VAL:O	5:D:363:GLU:HG3	2.13	0.47
1:E:8:DC:H2'	4:C:270:ARG:HH12	1.80	0.47
2:F:10:DT:C3'	3:B:79:ASN:ND2	2.72	0.47
4:C:255:ALA:O	4:C:259:ARG:HG2	2.13	0.47
1:E:13:DG:H2''	1:E:14:DA:C8	2.49	0.47
4:C:291:ASN:C	4:C:291:ASN:ND2	2.67	0.47
1:E:28:DG:H1	2:F:5:DC:N4	2.12	0.47
2:F:27:DC:H2''	2:F:28:DA:C8	2.49	0.47
2:F:9:DC:H2'	2:F:10:DT:H72	1.97	0.47
2:F:14:DA:C2'	2:F:15:DG:H5''	2.41	0.47
3:A:21:LEU:CD1	3:A:21:LEU:H	2.26	0.47
4:C:291:ASN:ND2	4:C:292:SER:N	2.62	0.47
4:C:280:LEU:CD1	5:D:362:LEU:CD2	2.93	0.47
2:F:27:DC:H5	5:D:344:ASN:OD1	1.98	0.47
3:B:21:LEU:HD12	3:B:21:LEU:N	2.30	0.47
1:E:26:DG:H2''	1:E:27:DA:N7	2.30	0.47
3:B:11:TRP:O	3:B:15:GLN:HG2	2.15	0.47
3:B:33:ARG:HG2	3:B:108:GLU:CB	2.44	0.46
3:A:11:TRP:O	3:A:15:GLN:HG2	2.15	0.46
2:F:24:DT:OP1	3:A:98:LYS:HE2	2.15	0.46
3:B:31:ARG:NH1	3:B:31:ARG:HG3	2.31	0.46
3:B:73:LEU:CD2	3:B:73:LEU:N	2.77	0.46
4:C:260:MET:HG2	4:C:263:ARG:NH2	2.31	0.46
4:C:287:LEU:HD23	5:D:369:LEU:HB2	1.98	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:A:39:LYS:HD2	3:A:43:ARG:HD3	1.97	0.45
3:B:73:LEU:CB	3:B:74:PRO:CD	2.90	0.45
2:F:15:DG:OP1	3:A:7:ARG:HA	2.17	0.45
3:B:24:VAL:HG21	3:B:53:ILE:CG1	2.45	0.45
2:F:14:DA:H1'	2:F:15:DG:O4'	2.15	0.45
1:E:12:DG:H2''	1:E:13:DG:OP2	2.17	0.45
3:B:31:ARG:HG3	3:B:31:ARG:HH11	1.82	0.45
1:E:17:DA:H8	1:E:17:DA:C5'	2.27	0.45
1:E:6:DG:H2''	1:E:7:DA:H5'	1.99	0.45
3:B:80:PHE:HE1	3:B:84:LEU:HG	1.80	0.45
2:F:2:DC:H2''	2:F:3:DT:H5''	1.98	0.45
2:F:18:DT:C2'	2:F:19:DT:C5'	2.89	0.45
2:F:10:DT:C3'	3:B:79:ASN:HD21	2.23	0.45
2:F:7:DC:H1'	2:F:8:DC:H5''	1.99	0.45
3:A:87:LYS:HD2	3:A:87:LYS:HA	1.72	0.45
3:A:33:ARG:HG3	3:A:108:GLU:HG3	1.99	0.45
3:B:33:ARG:HG2	3:B:108:GLU:CG	2.47	0.45
1:E:17:DA:C8	1:E:17:DA:C5'	3.00	0.45
3:A:98:LYS:HE3	3:A:98:LYS:HB3	1.71	0.45
2:F:24:DT:H5'	2:F:24:DT:H6	1.82	0.45
5:D:380:VAL:O	5:D:384:ARG:HG3	2.16	0.45
3:B:28:ASN:O	3:B:29:LYS:C	2.55	0.44
1:E:12:DG:H2''	1:E:13:DG:H5'	1.99	0.44
3:B:80:PHE:HD1	3:B:80:PHE:C	2.20	0.44
2:F:30:DT:C6	2:F:31:DT:H72	2.52	0.44
3:B:39:LYS:HA	3:B:103:PRO:CB	2.47	0.44
4:C:287:LEU:HD23	5:D:370:SER:N	2.32	0.44
2:F:16:DT:C6	2:F:17:DT:H72	2.53	0.44
2:F:21:DC:H2''	2:F:22:DT:H6	1.82	0.44
1:E:23:DA:H2''	1:E:24:DG:C5'	2.48	0.44
1:E:12:DG:H1'	1:E:13:DG:H5''	2.00	0.44
3:A:103:PRO:O	3:A:104:HIS:HB3	2.18	0.44
3:B:59:GLU:HG2	3:B:64:TYR:O	2.19	0.43
1:E:7:DA:C1'	1:E:8:DC:H5''	2.48	0.43
1:E:10:DT:H2''	1:E:11:DA:H8	1.84	0.43
2:F:16:DT:H3'	3:A:79:ASN:HD21	1.84	0.43
5:D:390:LEU:O	5:D:390:LEU:HD13	2.18	0.43
1:E:9:DA:C2'	1:E:10:DT:H5''	2.49	0.43
3:B:16:LEU:HB3	3:B:26:TRP:CE2	2.53	0.43
5:D:343:ARG:HH11	5:D:343:ARG:CG	2.31	0.43
1:E:3:DA:H2''	1:E:4:DA:H5''	1.96	0.43
3:A:12:LEU:HD22	3:A:12:LEU:O	2.18	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:A:21:LEU:CD1	3:A:21:LEU:N	2.80	0.42
3:B:90:LEU:HD11	3:B:107:TYR:HB3	2.01	0.42
3:A:42:LEU:HA	3:A:42:LEU:HD23	1.85	0.42
3:A:38:TRP:CD2	3:A:105:LYS:HD2	2.53	0.42
5:D:383:LEU:HA	5:D:386:GLU:HB3	2.01	0.42
3:A:27:VAL:O	3:A:27:VAL:HG12	2.19	0.42
3:B:98:LYS:HB3	3:B:98:LYS:HE3	1.61	0.42
3:A:38:TRP:CE3	3:A:105:LYS:HD2	2.54	0.42
2:F:27:DC:H4'	2:F:27:DC:OP1	2.20	0.42
5:D:390:LEU:O	5:D:394:LEU:HB2	2.18	0.42
3:A:70:LYS:H	3:A:70:LYS:HG2	1.34	0.42
2:F:29:DT:H2'	2:F:30:DT:H71	2.01	0.42
3:B:51:PHE:CD2	3:B:73:LEU:HD12	2.54	0.42
2:F:5:DC:H4'	2:F:5:DC:OP1	2.19	0.42
4:C:280:LEU:HD23	4:C:280:LEU:O	2.19	0.42
1:E:7:DA:C2'	1:E:8:DC:C5'	2.97	0.42
5:D:337:ARG:NH2	5:D:341:LEU:HD11	2.35	0.42
1:E:19:DT:H2''	1:E:20:DG:N7	2.35	0.42
2:F:21:DC:H2''	2:F:22:DT:C6	2.54	0.42
3:B:95:ASP:OD2	3:B:97:SER:HB2	2.19	0.41
3:B:26:TRP:CG	3:B:31:ARG:HD2	2.55	0.41
2:F:13:DC:H2''	2:F:14:DA:O5'	2.19	0.41
3:A:34:PHE:CE1	3:A:107:TYR:HB2	2.55	0.41
1:E:14:DA:H1'	1:E:15:DA:H5''	2.03	0.41
3:A:95:ASP:OD2	3:A:97:SER:CB	2.69	0.41
5:D:337:ARG:HG2	5:D:337:ARG:NH1	2.31	0.41
3:B:80:PHE:CE1	3:B:84:LEU:HG	2.55	0.41
1:E:14:DA:H2''	1:E:15:DA:C5'	2.48	0.41
2:F:16:DT:H5''	2:F:16:DT:H6	1.84	0.41
2:F:15:DG:H2'	2:F:16:DT:H72	2.03	0.41
3:B:28:ASN:O	3:B:31:ARG:N	2.54	0.41
3:B:36:ILE:HA	3:B:37:PRO:HD3	1.91	0.41
3:A:16:LEU:HB3	3:A:26:TRP:NE1	2.36	0.41
5:D:362:LEU:HD23	5:D:363:GLU:CA	2.50	0.41
3:A:111:ASN:O	3:A:111:ASN:ND2	2.54	0.41
3:B:4:PRO:O	3:B:5:LYS:HB3	2.21	0.40
2:F:20:DC:OP1	3:B:43:ARG:HA	2.21	0.40
3:B:30:SER:O	3:B:31:ARG:C	2.58	0.40
4:C:261:ARG:HG2	4:C:261:ARG:NH1	2.34	0.40
3:A:26:TRP:CE3	3:A:31:ARG:HA	2.56	0.40
3:B:17:ASP:OD1	3:B:31:ARG:NH1	2.51	0.40
3:B:99:ASP:O	3:B:100:PRO:C	2.59	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:D:376:LEU:O	5:D:380:VAL:HG23	2.22	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	
3	A	108/112 (96%)	89 (82%)	13 (12%)	6 (6%)	3	16
3	B	106/112 (95%)	88 (83%)	12 (11%)	6 (6%)	3	16
4	C	60/62 (97%)	59 (98%)	1 (2%)	0	100	100
5	D	59/61 (97%)	58 (98%)	1 (2%)	0	100	100
All	All	333/347 (96%)	294 (88%)	27 (8%)	12 (4%)	5	29

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	30	SER
3	A	88	GLU
3	B	48	GLN
3	A	111	ASN
3	B	29	LYS
3	B	66	PRO
3	A	31	ARG
3	B	88	GLU
3	A	29	LYS
3	B	30	SER
3	B	71	PRO
3	A	110	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	
3	A	94/96 (98%)	82 (87%)	12 (13%)	6	27
3	B	90/96 (94%)	75 (83%)	15 (17%)	3	16
4	C	49/54 (91%)	41 (84%)	8 (16%)	3	17
5	D	47/54 (87%)	38 (81%)	9 (19%)	2	12
All	All	280/300 (93%)	236 (84%)	44 (16%)	4	18

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	7	ARG
3	A	8	ILE
3	A	12	LEU
3	A	53	ILE
3	A	68	ARG
3	A	70	LYS
3	A	85	ASN
3	A	86	ARG
3	A	87	LYS
3	A	98	LYS
3	A	100	PRO
3	A	111	ASN
3	B	8	ILE
3	B	12	LEU
3	B	20	GLN
3	B	29	LYS
3	B	48	GLN
3	B	50	ASP
3	B	53	ILE
3	B	68	ARG
3	B	80	PHE
3	B	85	ASN
3	B	86	ARG
3	B	87	LYS
3	B	88	GLU
3	B	98	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	B	103	PRO
4	C	256	GLU
4	C	257	ARG
4	C	259	ARG
4	C	262	ASN
4	C	280	LEU
4	C	291	ASN
4	C	296	SER
4	C	299	ASN
5	D	343	ARG
5	D	345	ARG
5	D	350	ARG
5	D	358	TRP
5	D	367	GLU
5	D	375	GLN
5	D	377	GLN
5	D	382	LEU
5	D	383	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
3	A	40	HIS
3	A	48	GLN
3	A	111	ASN
3	B	20	GLN
3	B	44	GLN
3	B	55	GLN
3	B	79	ASN
4	C	262	ASN
4	C	291	ASN
5	D	375	GLN
5	D	377	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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	E	31/31 (100%)	-0.41	0 100 100	49, 74, 95, 98	0
2	F	31/31 (100%)	-0.38	0 100 100	50, 74, 103, 117	0
3	A	110/112 (98%)	-0.07	0 100 100	44, 66, 97, 102	0
3	B	108/112 (96%)	0.03	0 100 100	67, 101, 118, 128	0
4	C	62/62 (100%)	0.06	0 100 100	96, 122, 137, 145	0
5	D	61/61 (100%)	0.04	0 100 100	47, 109, 133, 145	0
All	All	403/409 (98%)	-0.06	0 100 100	44, 93, 131, 145	0

There are no RSRZ outliers to report.

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 carbohydrates 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.