Full wwPDB X-ray Structure Validation Report ⓘ

May 21, 2020 – 08:08 am BST

PDB ID	:	4R8A
Title	:	Crystal structure of paFAN1 - 5' flap DNA complex
Authors	:	Cho, Y.; Gwon, G.H.; Kim, Y.R.
Deposited on	:	2014-08-30
Resolution	:	3.20 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 following versions of software and data (see references ①) were used in the production of this report:

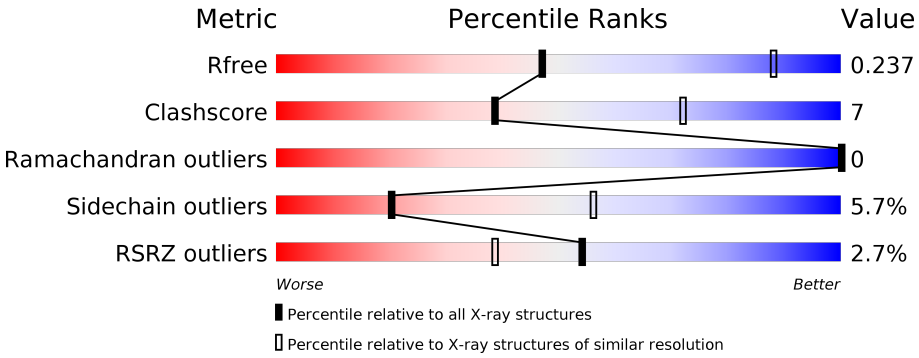
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 3.20 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	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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 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	559	2% 78% 17%
1	F	559	3% 77% 17%
2	B	15	47% 53%
2	G	15	7% 40% 60%
3	C	10	50% 40% 10%
3	H	10	50% 40% 10%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	D	21	
4	I	21	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 10652 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 Uncharacterized protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	538	Total	C	N	O	S	0	0	0
			4383	2801	792	770	20			
1	F	538	Total	C	N	O	S	0	0	0
			4383	2801	792	770	20			

- Molecule 2 is a DNA chain called DNA (5'-D(P*AP*CP*CP*AP*GP*AP*CP*AP*CP*AP*CP*AP*TP*TP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	15	Total	C	N	O	P	0	0	0
			302	144	57	86	15			
2	G	15	Total	C	N	O	P	0	0	0
			302	144	57	86	15			

- Molecule 3 is a DNA chain called DNA (5'-D(P*GP*TP*TP*GP*GP*GP*AP*TP*TP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	10	Total	C	N	O	P	0	0	0
			211	100	38	63	10			
3	H	10	Total	C	N	O	P	0	0	0
			211	100	38	63	10			

- Molecule 4 is a DNA chain called DNA (5'-D(P*GP*AP*AP*TP*GP*TP*GP*TP*GP*TP*CP*TP*CP*AP*AP*TP*CP*CP*CP*AP*A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	21	Total	C	N	O	P	0	0	0
			429	205	77	126	21			
4	I	21	Total	C	N	O	P	0	0	0
			429	205	77	126	21			

- Molecule 5 is water.

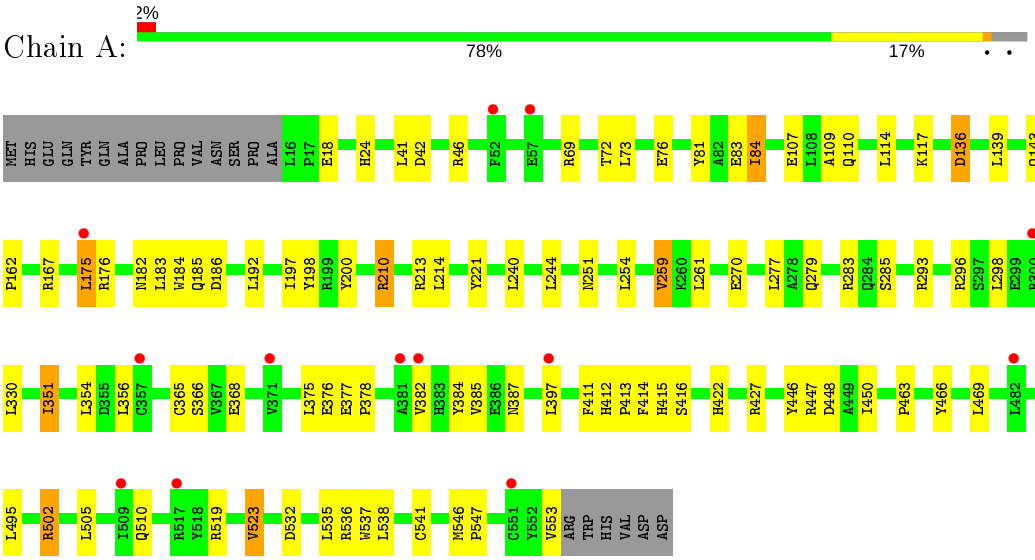
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total O 1 1	0	0
5	G	1	Total O 1 1	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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.

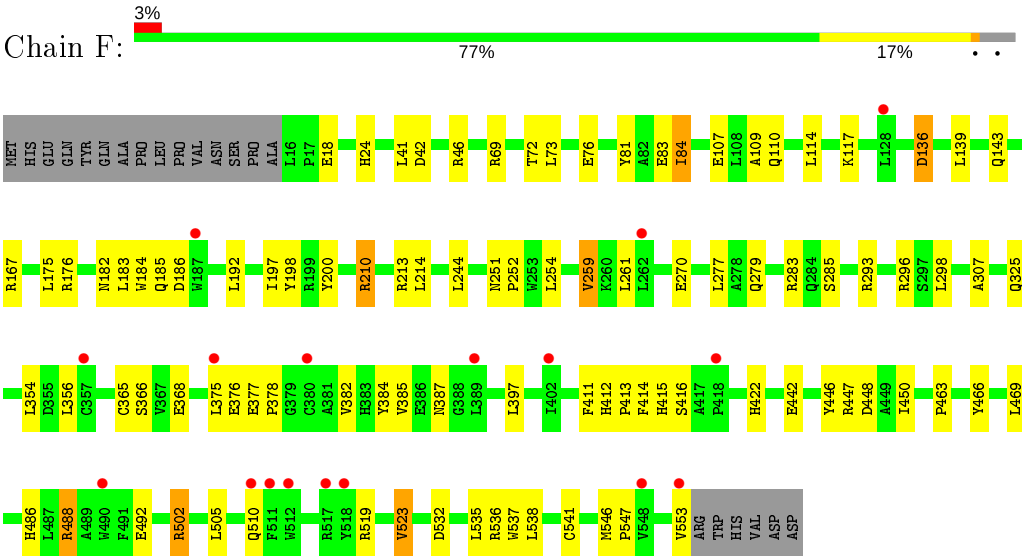
- Molecule 1: Uncharacterized protein

Chain A:



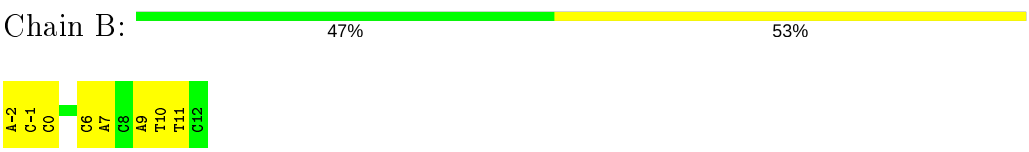
- Molecule 1: Uncharacterized protein

Chain F:



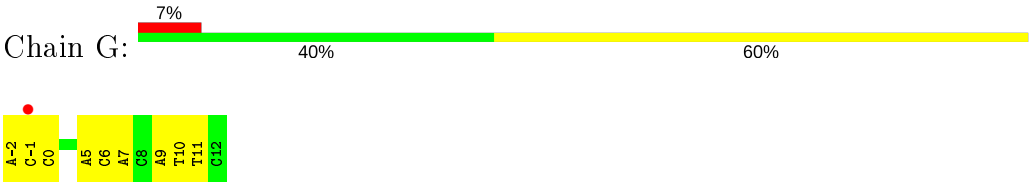
- Molecule 2: DNA (5'-D(P*AP*CP*CP*AP*GP*AP*CP*AP*CP*AP*CP*AP*TP*TP*C)-3')

Chain B:



• Molecule 2: DNA (5'-D(P*AP*CP*CP*AP*GP*AP*CP*AP*CP*AP*CP*AP*TP*TP*C)-3')

Chain G:



• Molecule 3: DNA (5'-D(P*GP*TP*TP*GP*GP*GP*AP*TP*TP*G)-3')

Chain C:

• Molecule 3: DNA (5'-D(P*GP*TP*TP*GP*GP*GP*AP*TP*TP*G)-3')

Chain H:

• Molecule 4: DNA (5'-D(P*GP*AP*AP*TP*GP*TP*GP*TP*GP*TP*CP*TP*CP*AP*AP*TP*CP*CP*CP*AP*A)-3')

Chain D:

• Molecule 4: DNA (5'-D(P*GP*AP*AP*TP*GP*TP*GP*TP*GP*TP*CP*TP*CP*AP*AP*TP*CP*CP*CP*AP*A)-3')

Chain I:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	76.58Å 106.66Å 142.18Å 90.00° 89.97° 90.00°	Depositor
Resolution (Å)	32.25 – 3.20 41.83 – 2.99	Depositor EDS
% Data completeness (in resolution range)	99.8 (32.25-3.20) 98.7 (41.83-2.99)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.58 (at 3.01Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, R_{free}	0.196 , 0.234 0.199 , 0.237	Depositor DCC
R_{free} test set	2314 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å^2)	98.3	Xtriage
Anisotropy	0.295	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 65.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.468 for h,-k,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	10652	wwPDB-VP
Average B, all atoms (Å^2)	118.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.87% 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	0.24	0/4497	0.42	0/6089
1	F	0.24	0/4497	0.42	0/6089
2	B	0.47	0/338	1.17	0/517
2	G	0.47	0/338	1.17	0/517
3	C	0.66	0/236	1.53	5/364 (1.4%)
3	H	0.67	0/236	1.54	6/364 (1.6%)
4	D	0.47	0/480	1.18	1/738 (0.1%)
4	I	0.47	0/480	1.18	1/738 (0.1%)
All	All	0.31	0/11102	0.69	13/15416 (0.1%)

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	C	8	DT	C6-C5-C7	-10.82	116.41	122.90
3	H	8	DT	C6-C5-C7	-10.36	116.68	122.90
3	C	8	DT	C4-C5-C7	8.16	123.90	119.00
3	H	8	DT	C4-C5-C7	7.43	123.46	119.00
3	H	8	DT	C3'-C2'-C1'	-7.21	93.84	102.50
3	C	8	DT	C3'-C2'-C1'	-7.06	94.03	102.50
3	H	8	DT	C1'-O4'-C4'	-7.02	103.08	110.10
3	C	8	DT	C1'-O4'-C4'	-6.89	103.21	110.10
4	I	1	DG	C3'-C2'-C1'	-6.36	94.87	102.50
4	D	1	DG	C3'-C2'-C1'	-6.35	94.88	102.50
3	H	8	DT	O4'-C1'-N1	6.18	112.33	108.00
3	C	8	DT	O4'-C1'-N1	6.09	112.26	108.00
3	H	8	DT	N3-C4-O4	5.02	122.91	119.90

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	A	4383	0	4293	63	0
1	F	4383	0	4293	64	0
2	B	302	0	168	13	0
2	G	302	0	168	12	0
3	C	211	0	115	6	0
3	H	211	0	115	6	0
4	D	429	0	238	8	0
4	I	429	0	238	10	0
5	B	1	0	0	0	0
5	G	1	0	0	1	0
All	All	10652	0	9628	151	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 (151) 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:412:HIS:ND1	1:A:413:PRO:O	2.16	0.78
1:F:412:HIS:ND1	1:F:413:PRO:O	2.16	0.77
1:A:329:ARG:NH2	1:A:532:ASP:OD1	2.18	0.75
1:F:329:ARG:NH2	1:F:532:ASP:OD1	2.18	0.74
1:F:183:LEU:HB2	2:G:0:DC:H42	1.53	0.73
1:A:107:GLU:H	1:A:110:GLN:HE21	1.34	0.72
1:F:107:GLU:H	1:F:110:GLN:HE21	1.34	0.72
1:A:183:LEU:HB2	2:B:0:DC:H42	1.53	0.72
1:A:351:ILE:HG21	1:A:538:LEU:HB3	1.74	0.68
1:F:351:ILE:HG21	1:F:538:LEU:HB3	1.74	0.68
1:A:279:GLN:HG3	1:A:298:LEU:HG	1.79	0.65
1:F:387:ASN:HD21	1:F:505:LEU:H	1.44	0.65
1:A:387:ASN:HD21	1:A:505:LEU:H	1.44	0.65
1:F:279:GLN:HG3	1:F:298:LEU:HG	1.79	0.65
1:A:109:ALA:HA	1:A:139:LEU:HD11	1.83	0.61
1:F:541:CYS:HB3	1:F:546:MET:HB2	1.83	0.61
1:A:541:CYS:HB3	1:A:546:MET:HB2	1.83	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:109:ALA:HA	1:F:139:LEU:HD11	1.83	0.60
1:A:411:PHE:HZ	2:B:-1:DC:H42	1.49	0.60
4:I:20:DA:H2"	4:I:21:DA:H5"	1.84	0.59
4:D:20:DA:H2"	4:D:21:DA:H5"	1.86	0.58
1:A:136:ASP:N	1:A:136:ASP:OD1	2.34	0.58
2:G:5:DA:OP1	5:G:101:HOH:O	2.17	0.58
1:F:365:CYS:SG	1:F:366:SER:N	2.77	0.58
1:F:385:VAL:HG12	1:F:469:LEU:HD21	1.86	0.57
1:A:385:VAL:HG12	1:A:469:LEU:HD21	1.86	0.57
1:A:365:CYS:SG	1:A:366:SER:N	2.77	0.57
1:A:412:HIS:HE1	2:B:-2:DA:H61	1.52	0.57
1:F:412:HIS:HE1	2:G:-2:DA:H61	1.51	0.57
1:F:411:PHE:HZ	2:G:-1:DC:H42	1.54	0.56
1:F:136:ASP:N	1:F:136:ASP:OD1	2.35	0.55
1:A:377:GLU:HG2	1:A:378:PRO:HD2	1.88	0.55
1:A:270:GLU:OE2	1:A:293:ARG:NH2	2.39	0.55
1:F:41:LEU:O	1:F:46:ARG:NH2	2.40	0.54
1:A:182:ASN:ND2	2:B:-1:DC:O2	2.40	0.54
1:A:41:LEU:O	1:A:46:ARG:NH2	2.40	0.54
1:F:182:ASN:ND2	2:G:-1:DC:O2	2.41	0.54
1:F:259:VAL:HG22	1:F:285:SER:HA	1.91	0.53
1:A:259:VAL:HG22	1:A:285:SER:HA	1.91	0.53
1:F:377:GLU:HG2	1:F:378:PRO:HD2	1.88	0.53
1:A:251:ASN:HD22	1:A:254:LEU:H	1.56	0.53
1:A:519:ARG:HA	1:A:547:PRO:HB2	1.91	0.53
2:G:11:DT:H3	4:I:2:DA:H62	1.57	0.52
1:F:251:ASN:HD22	1:F:254:LEU:H	1.57	0.52
1:F:356:LEU:HB2	1:F:553:VAL:HG22	1.92	0.52
1:F:519:ARG:HA	1:F:547:PRO:HB2	1.91	0.52
1:A:356:LEU:HB2	1:A:553:VAL:HG22	1.92	0.51
1:F:270:GLU:OE2	1:F:293:ARG:NH2	2.39	0.51
1:A:244:LEU:HD21	1:A:261:LEU:HD23	1.93	0.50
1:A:414:PHE:O	2:B:-2:DA:N6	2.44	0.50
1:A:69:ARG:NH2	3:C:8:DT:H5"	2.26	0.50
1:F:279:GLN:HE21	1:F:283:ARG:HE	1.59	0.50
1:A:279:GLN:HE21	1:A:283:ARG:HE	1.60	0.50
1:A:198:TYR:OH	4:D:13:DC:OP1	2.30	0.50
1:F:244:LEU:HD21	1:F:261:LEU:HD23	1.93	0.49
1:A:387:ASN:ND2	1:A:505:LEU:H	2.10	0.49
2:B:11:DT:H3	4:D:2:DA:H62	1.61	0.49
1:F:387:ASN:ND2	1:F:505:LEU:H	2.11	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:198:TYR:OH	4:I:13:DC:OP1	2.30	0.48
1:A:397:LEU:HB2	1:A:450:ILE:HD11	1.96	0.48
1:F:397:LEU:HB2	1:F:450:ILE:HD11	1.95	0.48
1:F:510:GLN:HG2	1:F:519:ARG:O	2.14	0.47
1:F:368:GLU:HG3	1:F:523:VAL:HG22	1.97	0.47
1:A:176:ARG:HD2	1:A:186:ASP:HA	1.96	0.47
1:A:81:TYR:HB2	1:A:84:ILE:HG12	1.96	0.47
1:F:412:HIS:CE1	2:G:-2:DA:H61	2.32	0.47
1:A:415:HIS:HA	2:B:-2:DA:N6	2.29	0.47
1:F:73:LEU:HB3	1:F:114:LEU:HD21	1.96	0.47
1:A:368:GLU:HG3	1:A:523:VAL:HG22	1.96	0.47
1:F:414:PHE:O	2:G:-2:DA:N6	2.48	0.47
1:F:81:TYR:HB2	1:F:84:ILE:HG12	1.97	0.47
1:A:73:LEU:HB3	1:A:114:LEU:HD21	1.96	0.46
1:A:510:GLN:HG2	1:A:519:ARG:O	2.14	0.46
1:A:446:TYR:O	1:A:450:ILE:HG12	2.16	0.46
1:F:210:ARG:HD2	1:F:213:ARG:HB2	1.97	0.46
1:A:192:LEU:HD13	1:A:198:TYR:HE2	1.80	0.46
1:A:210:ARG:HD2	1:A:213:ARG:HB2	1.97	0.46
1:F:69:ARG:NH2	3:H:8:DT:H5"	2.31	0.46
3:H:8:DT:H73	4:I:15:DA:N1	2.31	0.46
1:A:325:GLN:NE2	1:A:532:ASP:HB3	2.31	0.46
1:F:176:ARG:HD2	1:F:186:ASP:HA	1.97	0.46
1:F:192:LEU:HD13	1:F:198:TYR:HE2	1.81	0.45
1:F:416:SER:O	1:F:463:PRO:HD3	2.16	0.45
1:F:325:GLN:NE2	1:F:532:ASP:HB3	2.31	0.45
1:A:416:SER:O	1:A:463:PRO:HD3	2.16	0.45
1:F:192:LEU:HD23	1:F:197:ILE:HD12	1.99	0.45
1:F:446:TYR:O	1:F:450:ILE:HG12	2.16	0.45
3:H:9:DT:H2'	3:H:10:DG:C8	2.52	0.45
1:A:446:TYR:CZ	1:A:447:ARG:HG3	2.52	0.45
3:C:8:DT:H73	4:D:15:DA:N1	2.32	0.44
1:F:415:HIS:HA	2:G:-2:DA:N6	2.32	0.44
1:A:73:LEU:HD23	1:A:114:LEU:HD11	1.99	0.44
2:B:0:DC:H5"	2:B:0:DC:H6	1.82	0.44
2:G:6:DC:H2"	2:G:7:DA:H5'	1.99	0.44
2:B:6:DC:H2"	2:B:7:DA:H5'	1.99	0.44
1:A:412:HIS:CE1	2:B:-2:DA:H61	2.33	0.44
4:I:4:DT:H2'	4:I:5:DG:C8	2.53	0.44
1:F:446:TYR:CZ	1:F:447:ARG:HG3	2.52	0.44
3:C:9:DT:H2'	3:C:10:DG:C8	2.53	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:442:GLU:OE2	1:F:488:ARG:NH1	2.43	0.43
1:A:192:LEU:HD23	1:A:197:ILE:HD12	1.99	0.43
4:D:4:DT:H2'	4:D:5:DG:C8	2.53	0.43
1:F:18:GLU:HG2	1:F:24:HIS:CD2	2.54	0.43
1:A:546:MET:HA	1:A:547:PRO:HD3	1.85	0.43
1:A:375:LEU:HB3	1:A:382:VAL:HG21	2.01	0.43
2:G:0:DC:H6	2:G:0:DC:H5"	1.83	0.43
3:H:8:DT:H73	4:I:15:DA:C2	2.54	0.43
1:F:375:LEU:HB3	1:F:382:VAL:HG21	2.01	0.43
1:F:73:LEU:HD23	1:F:114:LEU:HD11	2.01	0.42
1:F:296:ARG:HG3	1:F:330:LEU:HD21	2.01	0.42
1:A:184:TRP:CZ3	1:A:185:GLN:HG2	2.55	0.42
1:A:329:ARG:HD3	4:D:4:DT:C5'	2.49	0.42
1:F:329:ARG:HD3	4:I:4:DT:C5'	2.49	0.42
1:A:18:GLU:HG2	1:A:24:HIS:CD2	2.54	0.42
1:A:296:ARG:HG3	1:A:330:LEU:HD21	2.01	0.42
1:A:192:LEU:HD13	1:A:198:TYR:CE2	2.55	0.42
1:A:466:TYR:OH	1:A:502:ARG:NH2	2.53	0.42
1:F:466:TYR:OH	1:F:502:ARG:NH2	2.53	0.42
3:C:8:DT:H73	4:D:15:DA:C2	2.54	0.42
1:F:251:ASN:HA	1:F:252:PRO:HD3	1.94	0.42
1:F:325:GLN:NE2	1:F:536:ARG:HE	2.18	0.42
1:A:240:LEU:HA	1:A:240:LEU:HD12	1.94	0.42
1:A:76:GLU:HB2	1:A:162:PRO:HG2	2.02	0.42
3:C:7:DA:H2"	3:C:8:DT:O2	2.20	0.41
1:F:76:GLU:HB2	1:F:162:PRO:HG2	2.02	0.41
2:G:9:DA:H2'	2:G:10:DT:C6	2.55	0.41
1:F:387:ASN:ND2	1:F:505:LEU:HB2	2.34	0.41
1:A:325:GLN:NE2	1:A:536:ARG:HE	2.18	0.41
1:A:486:HIS:CE1	1:A:546:MET:HG2	2.55	0.41
1:A:387:ASN:ND2	1:A:505:LEU:HB2	2.34	0.41
2:B:9:DA:H2'	2:B:10:DT:C6	2.55	0.41
1:F:486:HIS:CE1	1:F:546:MET:HG2	2.55	0.41
1:A:175:LEU:HA	1:A:175:LEU:HD12	1.89	0.41
1:A:221:TYR:HH	2:B:0:DC:H5	1.67	0.41
1:F:184:TRP:CZ3	1:F:185:GLN:HG2	2.55	0.41
1:F:192:LEU:HD13	1:F:198:TYR:CE2	2.56	0.41
3:H:6:DG:H2"	3:H:7:DA:C8	2.55	0.41
1:F:192:LEU:HB3	1:F:198:TYR:HD2	1.86	0.41
1:A:200:TYR:CD1	1:A:414:PHE:HA	2.56	0.41
3:C:6:DG:H2"	3:C:7:DA:C8	2.56	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:I:11:DC:H2'	4:I:11:DC:H6	1.74	0.41
1:A:183:LEU:HB2	2:B:0:DC:N4	2.30	0.40
1:A:117:LYS:N	4:D:20:DA:OP1	2.52	0.40
1:F:488:ARG:O	1:F:492:GLU:HG2	2.21	0.40
3:H:7:DA:H2"	3:H:8:DT:O2	2.20	0.40
1:A:427:ARG:HD2	1:A:495:LEU:HB3	2.04	0.40
1:F:200:TYR:CD1	1:F:414:PHE:HA	2.56	0.40
1:F:298:LEU:HB3	1:F:307:ALA:HB2	2.03	0.40
1:F:482:LEU:HA	1:F:483:PRO:HD3	1.94	0.40
1:F:117:LYS:N	4:I:20:DA:OP1	2.53	0.40
1:F:329:ARG:HD3	4:I:4:DT:H5'	2.04	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	536/559 (96%)	509 (95%)	27 (5%)	0	100	100
1	F	536/559 (96%)	509 (95%)	27 (5%)	0	100	100
All	All	1072/1118 (96%)	1018 (95%)	54 (5%)	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	441/460 (96%)	416 (94%)	25 (6%)	20 56
1	F	441/460 (96%)	416 (94%)	25 (6%)	20 56
All	All	882/920 (96%)	832 (94%)	50 (6%)	20 56

All (50) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	42	ASP
1	A	72	THR
1	A	83	GLU
1	A	84	ILE
1	A	136	ASP
1	A	143	GLN
1	A	151	ARG
1	A	152	LEU
1	A	167	ARG
1	A	175	LEU
1	A	210	ARG
1	A	214	LEU
1	A	259	VAL
1	A	277	LEU
1	A	351	ILE
1	A	354	LEU
1	A	376	GLU
1	A	384	TYR
1	A	422	HIS
1	A	448	ASP
1	A	488	ARG
1	A	502	ARG
1	A	523	VAL
1	A	535	LEU
1	A	537	TRP
1	F	42	ASP
1	F	72	THR
1	F	83	GLU
1	F	84	ILE
1	F	136	ASP
1	F	143	GLN
1	F	151	ARG
1	F	152	LEU
1	F	167	ARG
1	F	175	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	F	210	ARG
1	F	214	LEU
1	F	259	VAL
1	F	277	LEU
1	F	351	ILE
1	F	354	LEU
1	F	376	GLU
1	F	384	TYR
1	F	422	HIS
1	F	448	ASP
1	F	488	ARG
1	F	502	ARG
1	F	523	VAL
1	F	535	LEU
1	F	537	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	24	HIS
1	A	110	GLN
1	A	122	GLN
1	A	251	ASN
1	A	325	GLN
1	A	387	ASN
1	A	391	ASN
1	A	501	ASN
1	F	24	HIS
1	F	110	GLN
1	F	122	GLN
1	F	251	ASN
1	F	325	GLN
1	F	387	ASN
1	F	391	ASN
1	F	501	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

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, 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	538/559 (96%)	0.41	13 (2%) 59 44	72, 111, 155, 191	0
1	F	538/559 (96%)	0.42	18 (3%) 46 30	72, 111, 158, 196	0
2	B	15/15 (100%)	-0.11	0 100 100	118, 165, 208, 240	0
2	G	15/15 (100%)	0.04	1 (6%) 17 10	121, 162, 205, 251	0
3	C	10/10 (100%)	0.20	0 100 100	88, 98, 125, 133	0
3	H	10/10 (100%)	0.31	0 100 100	80, 99, 122, 132	0
4	D	21/21 (100%)	-0.24	0 100 100	93, 134, 185, 212	0
4	I	21/21 (100%)	-0.15	0 100 100	85, 128, 186, 203	0
All	All	1168/1210 (96%)	0.38	32 (2%) 54 39	72, 112, 163, 251	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	380	CYS	3.9
1	F	553	VAL	3.3
1	A	517	ARG	3.1
1	F	389	LEU	2.9
1	F	512	TRP	2.7
1	A	357	CYS	2.7
1	F	517	ARG	2.7
1	F	518	TYR	2.6
1	F	418	PRO	2.5
1	F	357	CYS	2.4
1	F	490	TRP	2.3
1	A	381	ALA	2.3
1	A	482	LEU	2.3
1	A	397	LEU	2.3
1	A	551	CYS	2.3
1	F	511	PHE	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	F	375	LEU	2.3
1	A	509	ILE	2.3
1	F	402	ILE	2.3
1	F	510	GLN	2.2
1	A	300	ARG	2.2
2	G	-1	DC	2.2
1	F	187	TRP	2.2
1	F	262	LEU	2.2
1	A	371	VAL	2.2
1	A	382	VAL	2.2
1	A	52	PHE	2.1
1	F	548	VAL	2.1
1	A	57	GLU	2.1
1	F	474	LEU	2.0
1	A	175	LEU	2.0
1	F	128	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 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.