



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 06:17 PM GMT

PDB ID : 1A02  
Title : STRUCTURE OF THE DNA BINDING DOMAINS OF NFAT, FOS AND JUN BOUND TO DNA  
Authors : Chen, L.; Glover, J.N.M.; Hogan, P.G.; Rao, A.; Harrison, S.C.  
Deposited on : 1997-12-08  
Resolution : 2.70 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

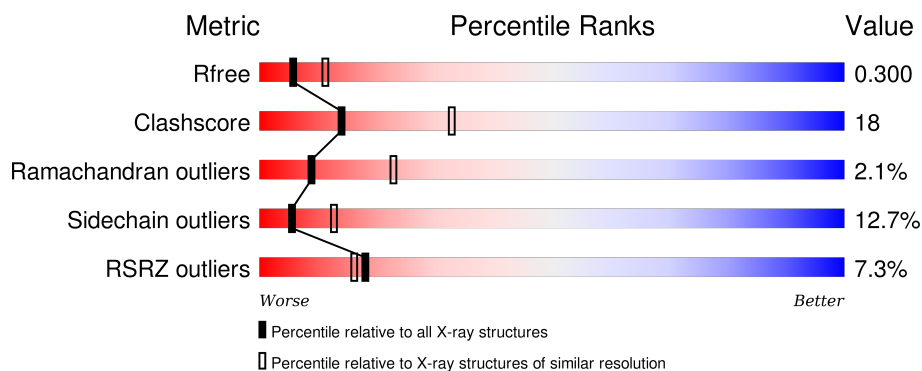
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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))
$R_{free}$	91344	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	20	<div> <div>40%</div> <div>60%</div> </div>
2	B	20	<div> <div>50%</div> <div>50%</div> </div>
3	N	301	<div> <div>9%</div> <div>47%</div> <div>40%</div> <div>6%</div> <div>7%</div> </div>
4	F	56	<div> <div>2%</div> <div>73%</div> <div>20%</div> <div>5%</div> </div>
5	J	56	<div> <div>7%</div> <div>68%</div> <div>23%</div> <div>7%</div> </div>

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 3974 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 DNA chain called DNA (5'-D(\*DTP\*DTP\*DGP\*DGP\*DAP\*DAP\*DAP\*DAP\*DTP\*DTP\*DTP\*DGP\*DTP\*DTP\*DTP\*DCP\*DAP\*DTP\*DAP\*DG)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	20	Total	C	N	O	P	0	0	0
			410	199	71	121	19			

- Molecule 2 is a DNA chain called DNA (5'-D(\*DAP\*DAP\*DCP\*DTP\*DAP\*DTP\*DGP\*DAP\*DAP\*DAP\*DCP\*DAP\*DAP\*DAP\*DTP\*DTP\*DTP\*DTP\*DCP\*DC)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	20	Total	C	N	O	P	0	0	0
			404	196	74	115	19			

- Molecule 3 is a protein called NUCLEAR FACTOR OF ACTIVATED T CELLS.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	N	280	Total	C	N	O	S	0	0	0
			2204	1383	404	408	9			

- Molecule 4 is a protein called AP-1 FRAGMENT FOS.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	F	53	Total	C	N	O	S	0	0	0
			442	262	92	87	1			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	138	MET	GLU	ENGINEERED	UNP P01100
F	154	SER	CYS	ENGINEERED	UNP P01100

- Molecule 5 is a protein called AP-1 FRAGMENT JUN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	J	52	Total 426	C 257	N 92	O 75	S 2	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	263	MET	ILE	ENGINEERED	UNP P05412
J	279	SER	CYS	ENGINEERED	UNP P05412

- Molecule 6 is water.

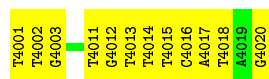
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	20	Total 20	O 20	0	0
6	B	18	Total 18	O 18	0	0
6	F	3	Total 3	O 3	0	0
6	J	1	Total 1	O 1	0	0
6	N	46	Total 46	O 46	0	0

### 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: DNA (5'-D(\*DTP\*DTP\*DGP\*DGP\*DAP\*DAP\*DAP\*DAP\*DTP\*DTP\*DTP\*DGP\*DTP\*DTP\*DTP\*DCP\*DAP\*DTP\*DAP\*DG)-3')

Chain A: 



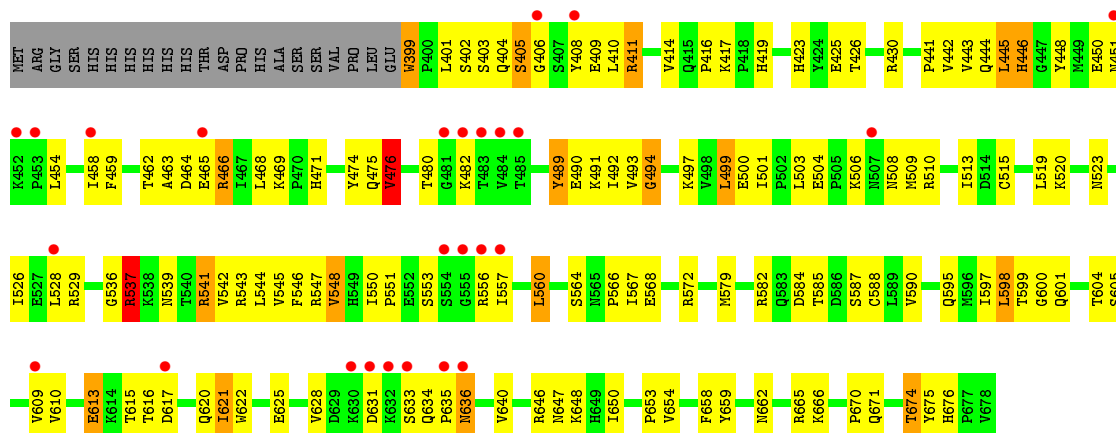
- Molecule 2: DNA (5'-D(\*DAP\*DAP\*DCP\*DTP\*DAP\*DTP\*DGP\*DAP\*DAP\*DAP\*DCP\*DAP\*DAP\*DAP\*DTP\*DTP\*DTP\*DTP\*DCP\*DC)-3')

Chain B: 



- Molecule 3: NUCLEAR FACTOR OF ACTIVATED T CELLS

Chain N: 

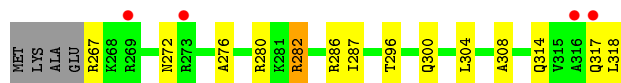


- Molecule 4: AP-1 FRAGMENT FOS

Chain F: 



- Molecule 5: AP-1 FRAGMENT JUN



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	64.66 Å   85.46 Å   83.37 Å 90.00°   112.03°   90.00°	Depositor
Resolution (Å)	10.00 – 2.70 19.49 – 2.69	Depositor EDS
% Data completeness (in resolution range)	90.1 (10.00-2.70) 94.4 (19.49-2.69)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.08	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.12 (at 2.71 Å)	Xtriage
Refinement program	X-PLOR 3.1	Depositor
R, $R_{free}$	0.246 , 0.303 0.254 , 0.300	Depositor DCC
$R_{free}$ test set	1642 reflections (7.59%)	DCC
Wilson B-factor (Å <sup>2</sup> )	49.2	Xtriage
Anisotropy	0.732	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 62.9	EDS
Estimated twinning fraction	0.037 for h,-k,-h-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 22079 reflections	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	3974	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.21% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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	0.86	0/459	1.09	1/708 (0.1%)
2	B	0.80	0/453	1.09	1/696 (0.1%)
3	N	0.52	0/2253	0.82	4/3050 (0.1%)
4	F	0.44	0/441	0.63	0/583
5	J	0.47	0/425	0.69	1/558 (0.2%)
All	All	0.59	0/4031	0.87	7/5595 (0.1%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	J	282	ARG	NE-CZ-NH2	7.23	123.92	120.30
3	N	411	ARG	NE-CZ-NH2	7.11	123.86	120.30
3	N	466	ARG	NE-CZ-NH2	6.53	123.56	120.30
2	B	5011	DC	N1-C1'-C2'	6.00	124.01	112.60
3	N	476	VAL	CB-CA-C	-5.50	100.94	111.40
1	A	4020	DG	N9-C1'-C2'	5.41	122.88	112.60
3	N	446	HIS	N-CA-C	5.21	125.06	111.00

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	410	0	231	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	404	0	228	14	0
3	N	2204	0	2168	107	0
4	F	442	0	461	10	0
5	J	426	0	472	8	0
6	A	20	0	0	1	0
6	B	18	0	0	0	0
6	F	3	0	0	0	0
6	J	1	0	0	0	0
6	N	46	0	0	2	0
All	All	3974	0	3560	136	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 18.

All (136) 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)
3:N:423:HIS:HB3	3:N:430:ARG:HG3	1.32	1.03
2:B:5003:DC:H2''	2:B:5004:DT:H71	1.42	1.02
1:A:4017:DA:H1'	1:A:4018:DT:H5'	1.40	1.01
3:N:613:GLU:HB2	3:N:622:TRP:HB3	1.42	0.99
3:N:474:TYR:CE1	3:N:520:LYS:HD3	2.09	0.88
2:B:5008:DA:H2'	5:J:280:ARG:HH22	1.39	0.88
3:N:399:TRP:HB3	3:N:547:ARG:HH22	1.39	0.87
3:N:584:ASP:HB2	3:N:597:ILE:H	1.40	0.87
3:N:490:GLU:HB3	3:N:500:GLU:HB3	1.56	0.86
3:N:410:LEU:HD22	3:N:548:VAL:HG22	1.56	0.84
3:N:600:GLY:O	3:N:636:ASN:HB2	1.79	0.82
3:N:401:LEU:HD22	4:F:180:GLN:HE22	1.45	0.81
1:A:4015:DT:H2''	1:A:4016:DC:H5'	1.63	0.79
3:N:406:GLY:HA3	3:N:560:LEU:HG	1.64	0.79
3:N:491:LYS:HE2	3:N:497:LYS:HD3	1.67	0.75
3:N:408:TYR:HB3	3:N:445:LEU:HD21	1.71	0.73
3:N:399:TRP:HB2	3:N:547:ARG:HH12	1.55	0.71
3:N:653:PRO:HB3	3:N:676:HIS:CD2	2.27	0.70
3:N:416:PRO:HG3	3:N:544:LEU:HD12	1.74	0.69
3:N:465:GLU:HG3	3:N:670:PRO:HG2	1.74	0.69
2:B:5008:DA:H2'	5:J:280:ARG:NH2	2.06	0.69
3:N:582:ARG:HB2	3:N:599:THR:HB	1.74	0.69
3:N:454:LEU:HB2	3:N:509:MET:HE1	1.73	0.69
3:N:526:ILE:O	3:N:529:ARG:HG2	1.93	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4017:DA:H2''	1:A:4018:DT:OP2	1.93	0.68
3:N:650:ILE:HD13	3:N:654:VAL:HG23	1.77	0.67
3:N:463:ALA:HA	3:N:543:ARG:HE	1.61	0.66
3:N:399:TRP:HB3	3:N:547:ARG:NH2	2.09	0.65
3:N:610:VAL:O	3:N:658:PHE:HA	1.95	0.65
3:N:441:PRO:HG2	3:N:513:ILE:HB	1.79	0.64
2:B:5003:DC:H2''	2:B:5004:DT:C7	2.23	0.63
3:N:408:TYR:CB	3:N:445:LEU:HD21	2.27	0.63
3:N:501:ILE:HG13	3:N:501:ILE:O	1.95	0.63
3:N:401:LEU:HD22	4:F:180:GLN:NE2	2.13	0.61
3:N:584:ASP:CB	3:N:597:ILE:H	2.12	0.61
1:A:4012:DG:H5''	3:N:665:ARG:HH22	1.65	0.60
3:N:425:GLU:HG3	3:N:519:LEU:HD11	1.85	0.59
3:N:408:TYR:HB3	3:N:445:LEU:CD2	2.31	0.59
3:N:416:PRO:HG2	3:N:567:ILE:HD11	1.83	0.59
1:A:4017:DA:C1'	1:A:4018:DT:H5'	2.23	0.59
3:N:613:GLU:HB2	3:N:622:TRP:CB	2.25	0.58
3:N:462:THR:O	3:N:543:ARG:HB2	2.03	0.58
2:B:5015:DT:H2''	2:B:5016:DT:OP2	2.04	0.58
4:F:162:THR:HG22	5:J:287:ILE:CG1	2.35	0.57
1:A:4011:DT:H4'	3:N:537:ARG:NH1	2.18	0.57
1:A:4001:DT:H2''	1:A:4002:DT:O5'	2.03	0.57
3:N:474:TYR:CZ	3:N:520:LYS:HD3	2.40	0.56
3:N:399:TRP:HB2	3:N:547:ARG:NH1	2.20	0.56
3:N:579:MET:O	3:N:600:GLY:HA3	2.04	0.56
3:N:419:HIS:HE1	3:N:601:GLN:HG3	1.70	0.56
5:J:300:GLN:O	5:J:304:LEU:HG	2.06	0.55
3:N:542:VAL:CG1	3:N:543:ARG:N	2.69	0.55
2:B:5015:DT:H2'	3:N:572:ARG:HH11	1.71	0.55
2:B:5008:DA:C2'	5:J:280:ARG:HH22	2.18	0.54
4:F:141:ARG:HH11	4:F:141:ARG:HG2	1.73	0.54
3:N:503:LEU:O	3:N:509:MET:SD	2.67	0.53
3:N:399:TRP:HE3	3:N:547:ARG:NH1	2.05	0.53
3:N:466:ARG:HB2	6:N:6086:HOH:O	2.08	0.53
2:B:5015:DT:H2'	3:N:572:ARG:NH1	2.23	0.53
3:N:408:TYR:CD2	3:N:550:ILE:HD12	2.44	0.53
3:N:584:ASP:HB2	3:N:597:ILE:N	2.18	0.53
2:B:5014:DA:H1'	2:B:5015:DT:H5'	1.90	0.52
3:N:476:VAL:HG23	3:N:497:LYS:HB3	1.91	0.52
3:N:560:LEU:HD12	3:N:560:LEU:N	2.24	0.52
3:N:542:VAL:O	3:N:566:PRO:HA	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:399:TRP:HE3	3:N:547:ARG:HH12	1.58	0.51
1:A:4014:DT:H3'	4:F:148:LYS:HE3	1.92	0.51
3:N:423:HIS:HB3	3:N:430:ARG:CG	2.23	0.51
3:N:404:GLN:HG2	3:N:405:SER:N	2.26	0.50
1:A:4017:DA:H1'	1:A:4018:DT:C5'	2.26	0.50
3:N:548:VAL:HG23	3:N:560:LEU:HD13	1.94	0.50
3:N:615:THR:HG23	3:N:621:ILE:HD12	1.94	0.50
2:B:5015:DT:H6	3:N:572:ARG:NH1	2.10	0.50
3:N:628:VAL:HG12	6:N:6005:HOH:O	2.11	0.49
3:N:419:HIS:CE1	3:N:601:GLN:HG3	2.46	0.49
3:N:401:LEU:CD2	4:F:180:GLN:HE22	2.21	0.49
2:B:5017:DT:H2''	2:B:5018:DT:H72	1.95	0.49
1:A:4002:DT:H2''	1:A:4003:DG:C8	2.48	0.49
4:F:165:LEU:O	4:F:169:THR:HG23	2.14	0.48
3:N:443:VAL:HG21	3:N:546:PHE:CD2	2.49	0.47
3:N:463:ALA:O	3:N:466:ARG:HG3	2.14	0.47
3:N:475:GLN:HB3	3:N:497:LYS:HE3	1.96	0.47
3:N:468:LEU:HD13	3:N:469:LYS:N	2.30	0.47
3:N:587:SER:HB2	3:N:674:THR:HG23	1.97	0.47
3:N:662:ASN:O	3:N:666:LYS:HB2	2.16	0.46
3:N:445:LEU:HD11	3:N:550:ILE:HD11	1.96	0.46
3:N:426:THR:HG22	3:N:426:THR:O	2.16	0.46
3:N:504:GLU:HB3	3:N:506:LYS:HD2	1.96	0.46
3:N:489:TYR:HB2	3:N:499:LEU:HD22	1.96	0.46
3:N:408:TYR:CZ	3:N:550:ILE:HG21	2.50	0.46
3:N:523:ASN:ND2	3:N:536:GLY:HA3	2.31	0.46
3:N:468:LEU:HD23	3:N:543:ARG:CZ	2.45	0.46
3:N:419:HIS:CD2	3:N:568:GLU:HB3	2.51	0.46
3:N:459:PHE:CZ	3:N:545:VAL:HG11	2.51	0.46
6:A:6020:HOH:O	5:J:276:ALA:HB2	2.16	0.45
3:N:406:GLY:CA	3:N:560:LEU:HG	2.41	0.45
3:N:458:ILE:N	3:N:499:LEU:O	2.50	0.45
3:N:493:VAL:HB	3:N:494:GLY:H	1.64	0.45
3:N:463:ALA:O	3:N:464:ASP:HB2	2.16	0.45
2:B:5001:DA:C8	2:B:5001:DA:O5'	2.69	0.45
3:N:414:VAL:HB	3:N:442:VAL:H	1.82	0.44
3:N:399:TRP:CB	3:N:547:ARG:HH12	2.26	0.44
3:N:653:PRO:HB3	3:N:676:HIS:HD2	1.79	0.44
3:N:444:GLN:HB2	3:N:510:ARG:HG3	1.99	0.44
3:N:551:PRO:HA	3:N:557:ILE:HD13	2.00	0.44
3:N:588:CYS:O	3:N:675:TYR:HA	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:548:VAL:HG23	3:N:560:LEU:HB2	2.00	0.44
3:N:646:ARG:HG3	3:N:647:ASN:H	1.81	0.43
1:A:4013:DT:H2"	1:A:4014:DT:H71	2.01	0.43
4:F:179:LEU:O	4:F:182:GLU:HB3	2.19	0.43
3:N:634:GLN:C	3:N:636:ASN:H	2.21	0.43
3:N:482:LYS:N	3:N:482:LYS:HD2	2.34	0.43
3:N:542:VAL:HG13	3:N:543:ARG:N	2.33	0.42
3:N:543:ARG:HG2	3:N:564:SER:O	2.18	0.42
4:F:176:LYS:O	4:F:180:GLN:HG3	2.20	0.42
2:B:5001:DA:O5'	2:B:5001:DA:H8	2.01	0.42
5:J:314:GLN:O	5:J:317:GLN:HG2	2.19	0.42
3:N:408:TYR:O	3:N:409:GLU:HB3	2.19	0.42
3:N:541:ARG:HB2	3:N:541:ARG:HE	1.61	0.42
3:N:503:LEU:HA	3:N:503:LEU:HD23	1.85	0.41
1:A:4002:DT:H2"	1:A:4003:DG:H8	1.85	0.41
3:N:598:LEU:HD22	3:N:640:VAL:HG21	2.01	0.41
4:F:182:GLU:OE2	5:J:308:ALA:HB1	2.21	0.41
3:N:414:VAL:HB	3:N:442:VAL:N	2.36	0.41
3:N:604:THR:OG1	3:N:605:SER:N	2.53	0.41
3:N:471:HIS:CE1	3:N:539:ASN:ND2	2.89	0.41
2:B:5014:DA:H2"	3:N:572:ARG:HH12	1.85	0.41
3:N:582:ARG:HG3	3:N:582:ARG:HH11	1.85	0.40
3:N:448:TYR:CE2	3:N:450:GLU:HB2	2.56	0.40
3:N:650:ILE:CD1	3:N:654:VAL:HG23	2.49	0.40
3:N:411:ARG:HE	3:N:446:HIS:HE1	1.70	0.40
3:N:409:GLU:O	3:N:409:GLU:CG	2.69	0.40
3:N:646:ARG:CG	3:N:647:ASN:H	2.34	0.40
3:N:609:VAL:HA	3:N:659:TYR:O	2.20	0.40
3:N:463:ALA:HA	3:N:543:ARG:NE	2.32	0.40
3:N:471:HIS:CE1	3:N:539:ASN:HD21	2.39	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	N	278/301 (92%)	242 (87%)	28 (10%)	8 (3%)	6	14
4	F	51/56 (91%)	51 (100%)	0	0	100	100
5	J	50/56 (89%)	50 (100%)	0	0	100	100
All	All	379/413 (92%)	343 (90%)	28 (7%)	8 (2%)	9	23

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	N	590	VAL
3	N	633	SER
3	N	480	THR
3	N	631	ASP
3	N	405	SER
3	N	494	GLY
3	N	537	ARG
3	N	635	PRO

### 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	N	238/269 (88%)	206 (87%)	32 (13%)	5	11
4	F	47/50 (94%)	43 (92%)	4 (8%)	13	30
5	J	45/48 (94%)	39 (87%)	6 (13%)	5	11
All	All	330/367 (90%)	288 (87%)	42 (13%)	5	13

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

Mol	Chain	Res	Type
3	N	399	TRP
3	N	402	SER

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Mol	Chain	Res	Type
3	N	403	SER
3	N	417	LYS
3	N	445	LEU
3	N	451	ASN
3	N	476	VAL
3	N	489	TYR
3	N	492	ILE
3	N	499	LEU
3	N	508	ASN
3	N	515	CYS
3	N	528	LEU
3	N	537	ARG
3	N	541	ARG
3	N	548	VAL
3	N	553	SER
3	N	556	ARG
3	N	560	LEU
3	N	585	THR
3	N	595	GLN
3	N	598	LEU
3	N	613	GLU
3	N	616	THR
3	N	617	ASP
3	N	620	GLN
3	N	621	ILE
3	N	625	GLU
3	N	636	ASN
3	N	648	LYS
3	N	671	GLN
3	N	674	THR
4	F	141	ARG
4	F	171	GLN
4	F	174	ASP
4	F	177	SER
5	J	267	ARG
5	J	272	ASN
5	J	282	ARG
5	J	286	ARG
5	J	296	THR
5	J	318	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
3	N	419	HIS
3	N	446	HIS
3	N	471	HIS
3	N	477	HIS
3	N	523	ASN
3	N	620	GLN
3	N	636	ASN
4	F	171	GLN
4	F	180	GLN
5	J	317	GLN

### 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 carbohydrates 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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	20/20 (100%)	-0.43	0 100 100	28, 36, 61, 64	0
2	B	20/20 (100%)	-0.40	0 100 100	22, 37, 51, 52	0
3	N	280/301 (93%)	0.61	26 (9%) 11 8	23, 53, 90, 99	0
4	F	53/56 (94%)	0.24	1 (1%) 70 70	28, 49, 73, 90	0
5	J	52/56 (92%)	0.33	4 (7%) 16 14	35, 50, 95, 99	0
All	All	425/453 (93%)	0.43	31 (7%) 18 16	22, 50, 89, 99	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	N	483	THR	12.5
3	N	484	VAL	10.3
3	N	481	GLY	9.1
3	N	631	ASP	8.3
3	N	485	THR	6.8
3	N	632	LYS	5.8
3	N	635	PRO	5.1
3	N	482	LYS	5.0
3	N	465	GLU	4.6
3	N	451	ASN	4.5
3	N	408	TYR	4.3
3	N	406	GLY	3.8
5	J	269	ARG	3.7
3	N	633	SER	3.4
3	N	528	LEU	3.3
3	N	630	LYS	3.3
3	N	554	SER	3.2
3	N	555	GLY	3.0
3	N	507	ASN	2.9
3	N	609	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
4	F	191	GLU	2.7
5	J	273	ARG	2.6
3	N	556	ARG	2.5
3	N	458	ILE	2.4
3	N	557	ILE	2.3
5	J	316	ALA	2.3
5	J	317	GLN	2.1
3	N	453	PRO	2.1
3	N	452	LYS	2.1
3	N	617	ASP	2.0
3	N	636	ASN	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.