



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 08:15 PM GMT

PDB ID : 1JFI
Title : Crystal Structure of the NC2-TBP-DNA Ternary Complex
Authors : Kamada, K.; Shu, F.; Chen, H.; Malik, S.; Stelzer, G.; Roeder, R.G.; Meisterernst, M.; Burley, S.K.; New York SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on : 2001-06-20
Resolution : 2.62 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

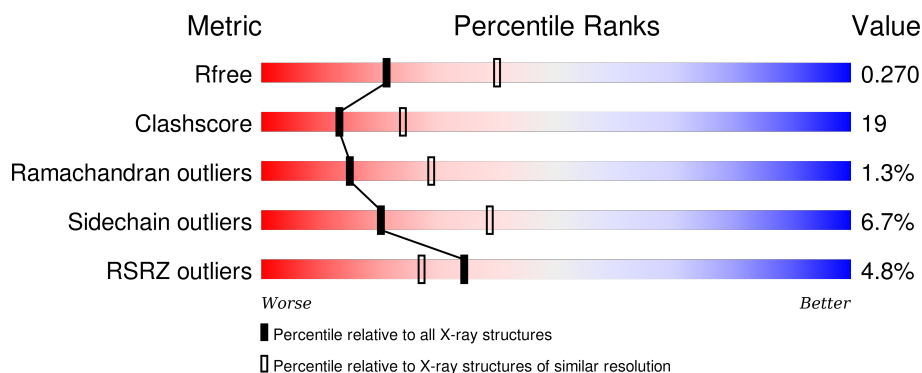
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.62 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	2700 (2.64-2.60)
Clashscore	102246	3065 (2.64-2.60)
Ramachandran outliers	100387	3015 (2.64-2.60)
Sidechain outliers	100360	3015 (2.64-2.60)
RSRZ outliers	91569	2706 (2.64-2.60)

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. 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	D	19	<div> <div>26%</div> <div>53%</div> <div>16%</div> <div>5%</div> </div>
2	E	19	<div>5%</div> <div>42%</div> <div>42%</div> <div>11%</div> <div>5%</div>
3	A	98	<div>3%</div> <div>37%</div> <div>22%</div> <div>5%</div> <div>36%</div>
4	B	179	<div>6%</div> <div>50%</div> <div>23%</div> <div>25%</div>
5	C	185	<div>3%</div> <div>67%</div> <div>28%</div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 3743 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 5'-D(*TP*TP*GP*GP*CP*TP*AP*TP*AP*AP*AP*A P*GP*GP*GP*CP*TP*CP*C)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	D	18	Total	C	N	O	P	0	0	0
			369	177	69	106	17			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	18	Total	C	N	O	P	0	0	0
			363	175	65	106	17			

- Molecule 3 is a protein called Transcription Regulator NC2 alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	63	Total	C	N	O	S	0	0	0
			490	311	87	88	4			

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	78	GLY	-	CLONING ARTIFACT	UNP Q14919
A	79	ASP	-	CLONING ARTIFACT	UNP Q14919
A	80	PRO	-	CLONING ARTIFACT	UNP Q14919
A	81	ALA	-	CLONING ARTIFACT	UNP Q14919
A	82	ALA	-	CLONING ARTIFACT	UNP Q14919
A	83	ASN	-	CLONING ARTIFACT	UNP Q14919
A	84	LYS	-	CLONING ARTIFACT	UNP Q14919
A	85	ALA	-	CLONING ARTIFACT	UNP Q14919
A	86	ARG	-	CLONING ARTIFACT	UNP Q14919
A	87	LYS	-	CLONING ARTIFACT	UNP Q14919
A	88	GLU	-	CLONING ARTIFACT	UNP Q14919
A	89	ALA	-	CLONING ARTIFACT	UNP Q14919

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Chain	Residue	Modelled	Actual	Comment	Reference
A	90	GLU	-	CLONING ARTIFACT	UNP Q14919
A	91	LEU	-	CLONING ARTIFACT	UNP Q14919
A	92	ALA	-	CLONING ARTIFACT	UNP Q14919
A	93	ALA	-	CLONING ARTIFACT	UNP Q14919
A	94	ALA	-	CLONING ARTIFACT	UNP Q14919
A	95	THR	-	CLONING ARTIFACT	UNP Q14919
A	96	ALA	-	CLONING ARTIFACT	UNP Q14919
A	97	GLU	-	CLONING ARTIFACT	UNP Q14919
A	98	GLN	-	CLONING ARTIFACT	UNP Q14919

- Molecule 4 is a protein called Transcription Regulator NC2 beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	B	135	Total	C	N	O	S	0	0	0
			1059	655	190	209	5			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	98	GLY	-	CLONING ARTIFACT	UNP Q01658
B	99	PRO	-	CLONING ARTIFACT	UNP Q01658
B	100	HIS	-	CLONING ARTIFACT	UNP Q01658

- Molecule 5 is a protein called TATA-BOX-BINDING PROTEIN (TBP).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	C	183	Total	C	N	O	S	0	0	0
			1453	941	257	247	8			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	355	GLY	-	CLONING ARTIFACT	UNP P20226
C	356	SER	-	CLONING ARTIFACT	UNP P20226
C	357	HIS	-	CLONING ARTIFACT	UNP P20226
C	358	MET	-	CLONING ARTIFACT	UNP P20226

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	O	0	0
			1	1		

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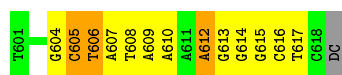
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total 1	O 1	0	0
6	C	6	Total 6	O 6	0	0
6	D	1	Total 1	O 1	0	0

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

Chain D:



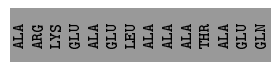
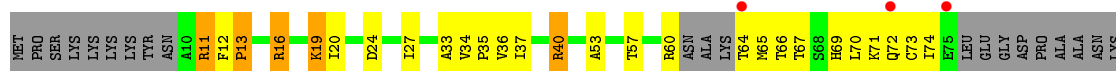
- Molecule 2: 5'-D(*G*GP*AP*GP*CP*CP*CP*TP*TP*TP*TP*AP*TP*AP*GP*CP*CP*AP*A)-3'

Chain E:



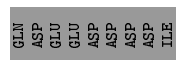
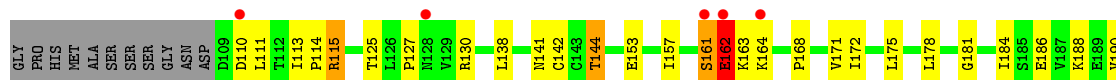
- Molecule 3: Transcription Regulator NC2 alpha chain

Chain A:

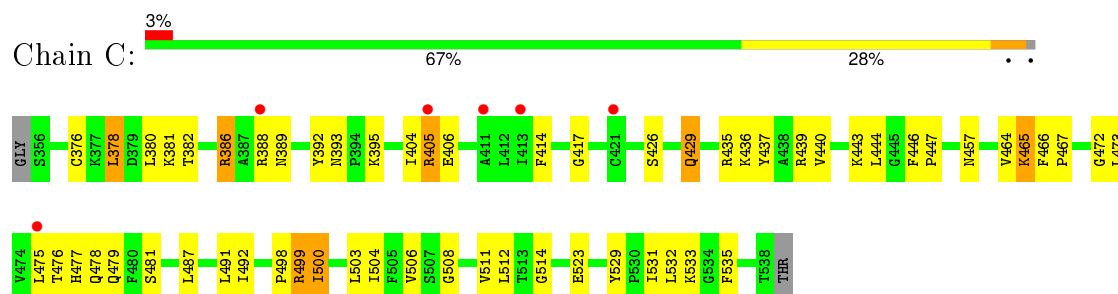


- Molecule 4: Transcription Regulator NC2 beta chain

Chain B:



● Molecule 5: TATA-BOX-BINDING PROTEIN (TBP)



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	76.68Å 119.08Å 155.08Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.84 – 2.62 19.84 – 2.62	Depositor EDS
% Data completeness (in resolution range)	97.4 (19.84-2.62) 98.8 (19.84-2.62)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.23 (at 2.63Å)	Xtriage
Refinement program	CNS 0.9	Depositor
R, R_{free}	0.233 , 0.277 0.230 , 0.270	Depositor DCC
R_{free} test set	1499 reflections (7.11%)	DCC
Wilson B-factor (Å ²)	60.6	Xtriage
Anisotropy	0.088	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 39.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 21381 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3743	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.50% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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 [i](#)

5.1 Standard geometry [i](#)

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	D	0.52	0/414	0.99	0/638
2	E	0.43	0/406	0.83	0/624
3	A	0.35	0/494	0.57	0/662
4	B	0.37	0/1068	0.55	0/1437
5	C	0.39	0/1480	0.63	0/1991
All	All	0.40	0/3862	0.68	0/5352

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	D	0	4
2	E	0	2
All	All	0	6

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	604	DG	Sidechain
1	D	605	DC	Sidechain
1	D	606	DT	Sidechain
1	D	612	DA	Sidechain
2	E	712	DA	Sidechain
2	E	713	DT	Sidechain

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	D	369	0	205	17	0
2	E	363	0	205	11	0
3	A	490	0	529	37	0
4	B	1059	0	1073	41	0
5	C	1453	0	1542	49	1
6	A	1	0	0	1	0
6	B	1	0	0	0	0
6	C	6	0	0	0	0
6	D	1	0	0	0	0
All	All	3743	0	3554	138	1

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 19.

All (138) 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:A:33:ALA:O	3:A:36:VAL:HG22	1.78	0.83
1:D:613:DG:H2"	1:D:614:DG:C8	2.14	0.82
3:A:36:VAL:HG21	4:B:194:CYS:SG	2.20	0.81
2:E:712:DA:H2"	2:E:713:DT:H5'	1.62	0.81
4:B:115:ARG:HG2	4:B:115:ARG:HH11	1.45	0.81
3:A:53:ALA:O	3:A:57:THR:HG23	1.85	0.77
3:A:24:ASP:HB3	3:A:27:ILE:HD13	1.67	0.77
1:D:615:DG:H2"	1:D:616:DC:H5"	1.66	0.76
5:C:378:LEU:HD22	5:C:417:GLY:HA2	1.67	0.76
5:C:473:LEU:HD12	5:C:491:LEU:HD11	1.67	0.75
4:B:201:ARG:HH21	4:B:202:ARG:HG3	1.51	0.74
5:C:499:ARG:HH11	5:C:499:ARG:HB2	1.53	0.73
4:B:172:ILE:HG23	4:B:184:ILE:HG23	1.69	0.73
5:C:500:ILE:HD11	5:C:512:LEU:HD23	1.72	0.70
3:A:57:THR:HG22	3:A:69:HIS:CD2	2.26	0.69
5:C:382:THR:O	5:C:386:ARG:HD3	1.93	0.69
5:C:476:THR:HB	5:C:477:HIS:HD2	1.58	0.67
5:C:382:THR:HG22	5:C:386:ARG:HE	1.56	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:615:DG:H2''	1:D:616:DC:C5'	2.24	0.67
1:D:615:DG:H5''	4:B:164:LYS:HD3	1.76	0.66
1:D:606:DT:H2''	1:D:607:DA:H5'	1.78	0.65
4:B:184:ILE:O	4:B:188:LYS:HG3	1.97	0.65
4:B:217:GLU:HG3	4:B:221:GLN:HE21	1.61	0.65
3:A:16:ARG:HB2	3:A:16:ARG:NH1	2.12	0.65
3:A:66:THR:H	3:A:69:HIS:HD2	1.43	0.64
1:D:613:DG:H2''	1:D:614:DG:N7	2.12	0.64
3:A:16:ARG:HB2	3:A:16:ARG:HH11	1.63	0.64
3:A:11:ARG:HH11	3:A:11:ARG:HB2	1.63	0.63
2:E:705:DC:H2''	2:E:706:DC:H5'	1.82	0.62
5:C:491:LEU:HD23	5:C:492:ILE:N	2.16	0.61
4:B:181:GLY:O	4:B:184:ILE:HG13	2.00	0.61
1:D:615:DG:C5'	4:B:164:LYS:HD3	2.30	0.61
5:C:382:THR:CG2	5:C:386:ARG:HE	2.14	0.61
5:C:529:TYR:CE2	5:C:533:LYS:HD2	2.36	0.61
3:A:34:VAL:O	3:A:37:ILE:HG12	2.01	0.60
4:B:115:ARG:CG	4:B:115:ARG:HH11	2.10	0.60
2:E:712:DA:H2''	2:E:713:DT:C5'	2.32	0.60
3:A:66:THR:H	3:A:69:HIS:CD2	2.19	0.60
4:B:219:LEU:O	4:B:223:GLN:HG3	2.02	0.60
5:C:457:ASN:HD21	5:C:514:GLY:H	1.47	0.59
4:B:193:GLU:O	4:B:197:VAL:HG23	2.02	0.59
4:B:236:LEU:O	4:B:236:LEU:HD23	2.03	0.59
5:C:436:LYS:O	5:C:440:VAL:HG23	2.03	0.59
3:A:53:ALA:HB1	3:A:70:LEU:HD12	1.84	0.59
5:C:382:THR:CG2	5:C:386:ARG:HH21	2.16	0.58
5:C:393:ASN:C	5:C:395:LYS:N	2.56	0.58
1:D:613:DG:H1	2:E:707:DC:H42	1.51	0.58
5:C:386:ARG:H	5:C:386:ARG:HD3	1.67	0.57
3:A:60:ARG:HG3	3:A:69:HIS:CE1	2.38	0.57
3:A:57:THR:HG22	3:A:69:HIS:CG	2.39	0.57
1:D:615:DG:C2'	1:D:616:DC:H5''	2.34	0.57
2:E:704:DG:H2''	2:E:705:DC:OP2	2.04	0.57
3:A:60:ARG:HG3	3:A:69:HIS:HE1	1.70	0.57
5:C:473:LEU:HD13	5:C:473:LEU:O	2.04	0.56
2:E:719:DA:H2'	4:B:115:ARG:HG3	1.87	0.55
3:A:34:VAL:HB	3:A:35:PRO:HD3	1.88	0.55
5:C:405:ARG:HD2	5:C:406:GLU:H	1.69	0.55
4:B:115:ARG:NH1	4:B:115:ARG:HG2	2.20	0.55
4:B:236:LEU:O	4:B:240:GLU:HG3	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:16:ARG:HH11	3:A:16:ARG:CB	2.19	0.55
5:C:393:ASN:C	5:C:395:LYS:H	2.09	0.55
2:E:707:DC:H2'	2:E:708:DT:H71	1.88	0.54
5:C:473:LEU:HD12	5:C:491:LEU:CD1	2.37	0.54
4:B:115:ARG:CG	4:B:115:ARG:NH1	2.66	0.53
2:E:719:DA:C2'	4:B:115:ARG:HG3	2.38	0.53
3:A:24:ASP:CB	3:A:27:ILE:HD13	2.36	0.52
4:B:125:THR:O	4:B:127:PRO:HD3	2.09	0.52
5:C:464:VAL:HG22	5:C:508:GLY:O	2.09	0.52
5:C:389:ASN:HD22	5:C:389:ASN:N	2.07	0.52
5:C:439:ARG:O	5:C:443:LYS:HG3	2.10	0.51
1:D:605:DC:H2'	1:D:606:DT:C7	2.40	0.51
1:D:607:DA:H2''	1:D:608:DT:H5'	1.92	0.51
4:B:190:VAL:O	4:B:193:GLU:HG2	2.11	0.50
5:C:440:VAL:O	5:C:444:LEU:HD13	2.12	0.50
5:C:405:ARG:HD2	5:C:405:ARG:N	2.27	0.50
5:C:389:ASN:ND2	5:C:389:ASN:N	2.59	0.50
3:A:19:LYS:HB3	4:B:111:LEU:HD13	1.93	0.50
5:C:467:PRO:HA	5:C:506:VAL:O	2.11	0.50
3:A:16:ARG:NH1	6:A:1001:HOH:O	2.45	0.50
5:C:386:ARG:N	5:C:386:ARG:HD3	2.27	0.49
2:E:703:DA:H2''	2:E:704:DG:O5'	2.12	0.49
3:A:74:ILE:HD11	4:B:142:CYS:SG	2.52	0.49
3:A:13:PRO:HB2	3:A:16:ARG:HB3	1.94	0.49
3:A:40:ARG:NH1	4:B:186:GLU:HB3	2.28	0.48
5:C:393:ASN:O	5:C:395:LYS:N	2.47	0.48
3:A:53:ALA:CB	3:A:70:LEU:HD12	2.44	0.48
4:B:231:GLN:O	4:B:234:ALA:HB3	2.13	0.48
3:A:65:MET:CE	3:A:70:LEU:HD11	2.43	0.48
4:B:226:PHE:HA	5:C:531:ILE:HD11	1.94	0.48
4:B:161:SER:C	4:B:162:GLU:HG3	2.34	0.47
4:B:125:THR:C	4:B:127:PRO:HD3	2.35	0.47
1:D:605:DC:H2'	1:D:606:DT:H72	1.97	0.47
3:A:16:ARG:O	3:A:20:ILE:HG13	2.14	0.47
4:B:184:ILE:HG22	4:B:188:LYS:HE3	1.97	0.47
5:C:376:CYS:O	5:C:378:LEU:HD13	2.14	0.47
4:B:141:ASN:O	4:B:144:THR:HG23	2.14	0.47
4:B:168:PRO:O	4:B:172:ILE:HG13	2.15	0.47
3:A:67:THR:OG1	3:A:71:LYS:HE3	2.14	0.47
4:B:192:GLN:OE1	4:B:192:GLN:HA	2.14	0.47
5:C:481:SER:HB3	5:C:491:LEU:HD21	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:404:ILE:HG23	5:C:437:TYR:CE1	2.51	0.45
3:A:71:LYS:C	3:A:73:CYS:H	2.19	0.45
4:B:161:SER:O	4:B:163:LYS:HG3	2.17	0.45
1:D:612:DA:H1'	5:C:414:PHE:CZ	2.51	0.45
1:D:615:DG:H5''	4:B:164:LYS:CD	2.43	0.45
3:A:37:ILE:HD11	4:B:171:VAL:HB	1.99	0.45
4:B:153:GLU:O	4:B:157:ILE:HG13	2.17	0.45
5:C:503:LEU:HB2	5:C:511:VAL:HB	2.00	0.44
5:C:473:LEU:C	5:C:473:LEU:HD13	2.39	0.43
5:C:381:LYS:HD2	5:C:392:TYR:HE2	1.84	0.43
5:C:472:GLY:O	5:C:475:LEU:HB2	2.18	0.43
5:C:386:ARG:N	5:C:386:ARG:CD	2.82	0.43
3:A:11:ARG:HH11	3:A:11:ARG:CB	2.30	0.43
5:C:498:PRO:HD3	5:C:523:GLU:CD	2.39	0.43
4:B:113:ILE:HG23	4:B:114:PRO:HD2	2.00	0.43
1:D:609:DA:H2''	1:D:610:DA:H5'	2.01	0.43
3:A:74:ILE:CD1	4:B:142:CYS:SG	3.07	0.42
5:C:405:ARG:HD2	5:C:405:ARG:H	1.83	0.42
3:A:19:LYS:HB3	4:B:111:LEU:CD1	2.48	0.42
3:A:70:LEU:HB3	4:B:138:LEU:HD23	2.00	0.42
2:E:711:DT:H6	2:E:711:DT:H2'	1.53	0.42
3:A:64:THR:HA	4:B:130:ARG:O	2.19	0.42
5:C:476:THR:OG1	5:C:535:PHE:HZ	2.02	0.41
5:C:435:ARG:O	5:C:439:ARG:HG2	2.19	0.41
4:B:199:LEU:HG	4:B:203:LYS:HE2	2.02	0.41
1:D:616:DC:C2'	1:D:617:DT:H71	2.49	0.41
2:E:706:DC:H2''	2:E:707:DC:C6	2.56	0.41
5:C:491:LEU:C	5:C:491:LEU:HD23	2.41	0.41
5:C:465:LYS:O	5:C:466:PHE:HB3	2.21	0.41
5:C:405:ARG:CD	5:C:405:ARG:H	2.33	0.41
3:A:12:PHE:HA	3:A:13:PRO:HD3	1.81	0.41
5:C:504:ILE:HD13	5:C:532:LEU:HD21	2.02	0.41
5:C:529:TYR:CZ	5:C:533:LYS:HD2	2.55	0.41
3:A:34:VAL:CB	3:A:35:PRO:HD3	2.50	0.40
5:C:426:SER:OG	5:C:429:GLN:HB2	2.21	0.40
1:D:605:DC:H2''	1:D:606:DT:O5'	2.21	0.40
3:A:11:ARG:HG3	3:A:12:PHE:N	2.37	0.40
5:C:446:PHE:HA	5:C:447:PRO:HD3	1.77	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:386:ARG:NH2	5:C:386:ARG:NH2[3_755]	1.88	0.32

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	
3	A	59/98 (60%)	56 (95%)	1 (2%)	2 (3%)	5	7
4	B	133/179 (74%)	123 (92%)	8 (6%)	2 (2%)	13	24
5	C	181/185 (98%)	170 (94%)	10 (6%)	1 (1%)	30	54
All	All	373/462 (81%)	349 (94%)	19 (5%)	5 (1%)	15	29

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	C	388	ARG
4	B	162	GLU
4	B	161	SER
3	A	72	GLN
3	A	13	PRO

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	
3	A	55/80 (69%)	51 (93%)	4 (7%)	17	34
4	B	117/151 (78%)	110 (94%)	7 (6%)	24	45

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	C	158/159 (99%)	147 (93%)	11 (7%)	19	36
All	All	330/390 (85%)	308 (93%)	22 (7%)	20	39

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	11	ARG
3	A	16	ARG
3	A	19	LYS
3	A	40	ARG
4	B	110	ASP
4	B	115	ARG
4	B	144	THR
4	B	162	GLU
4	B	175	LEU
4	B	178	LEU
4	B	233	GLN
5	C	378	LEU
5	C	380	LEU
5	C	386	ARG
5	C	405	ARG
5	C	429	GLN
5	C	465	LYS
5	C	478	GLN
5	C	479	GLN
5	C	487	LEU
5	C	499	ARG
5	C	500	ILE

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	69	HIS
4	B	141	ASN
4	B	159	ASN
4	B	173	GLN
4	B	223	GLN
4	B	239	GLN
5	C	366	GLN
5	C	389	ASN
5	C	457	ASN

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Mol	Chain	Res	Type
5	C	478	GLN
5	C	479	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, 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	D	18/19 (94%)	-0.28	0 100 100	37, 51, 100, 110	0
2	E	18/19 (94%)	0.01	1 (5%) 28 21	42, 53, 120, 139	0
3	A	63/98 (64%)	0.27	3 (4%) 34 27	39, 58, 109, 128	0
4	B	135/179 (75%)	0.17	10 (7%) 17 12	36, 60, 114, 132	0
5	C	183/185 (98%)	0.04	6 (3%) 50 43	30, 52, 76, 98	0
All	All	417/500 (83%)	0.10	20 (4%) 34 27	30, 56, 100, 139	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	B	240	GLU	4.2
4	B	241	TRP	4.0
5	C	388	ARG	4.0
3	A	75	GLU	3.9
4	B	238	GLN	3.7
3	A	72	GLN	3.5
5	C	421	CYS	3.3
4	B	235	GLU	3.3
4	B	164	LYS	3.2
4	B	110	ASP	3.0
2	E	702	DG	3.0
5	C	413	ILE	3.0
4	B	162	GLU	2.8
4	B	161	SER	2.7
4	B	128	ASN	2.6
4	B	242	LEU	2.6
3	A	64	THR	2.6
5	C	475	LEU	2.5
5	C	411	ALA	2.2
5	C	405	ARG	2.1

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.