

Full wwPDB X-ray Structure Validation Report (i)

Jan 27, 2024 - 06:41 PM EST

PDB ID	:	1CQT
Title	:	CRYSTAL STRUCTURE OF A TERNARY COMPLEX CONTAINING AN
		OCA-B PEPTIDE, THE OCT-1 POU DOMAIN, AND AN OCTAMER EL-
		EMENT
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Deposited on	:	1999-08-11
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 (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

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.



Motria	Whole archive	Similar resolution
wietric	$(\# { m Entries})$	$(\# { m Entries}, { m resolution} { m range}({ m \AA}))$
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (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 of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5%

Note EDS was not executed.

Mol	Chain	Length		Quality o	f chain		
1	М	15	27%		73%		
1	0	15		93%			7%
2	Ν	15		100%			
2	Р	15	7%	87%			7%
3	А	163	54%		25%	••	18%
3	В	163	41%		32%	6%	21%
4	Ι	44	36%	11% •		50%	
4	J	44	34%	18%		48%	



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 3649 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(*TP*GP*TP*AP*TP*GP*CP*AP*AP*AP* TP*AP*AP*GP*G)-3').

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	М	15	Total	С	Ν	0	Р	0	0	0
1	111	10	310	149	61	86	14	0	0	0
1	0	14	Total	С	Ν	0	Р	0	0	0
1	0	14	293	139	59	81	14	0	0	0

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
2	Ν	15	Total	С	Ν	Ο	Р	0	0	0
	11	10	299	146	49	90	14	0		
0	D	14	Total	С	Ν	Ο	Р	0	0	0
		14	281	136	44	87	14	0		

• Molecule 3 is a protein called POU DOMAIN, CLASS 2, TRANSCRIPTION FACTOR 1.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
2	Δ	124	Total	С	Ν	0	S	0	0	0
5	А	104	1061	672	187	196	6	0	0	0
2	P	120	Total	С	Ν	0	S	0	0	0
5	Б	129	1042	653	187	196	6	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	-2	GLY	PRO	conflict	UNP P14859
A	0	ARG	LEU	conflict	UNP P14859
В	498	GLY	PRO	conflict	UNP P14859
В	500	ARG	LEU	conflict	UNP P14859

• Molecule 4 is a protein called POU DOMAIN, CLASS 2, ASSOCIATING FACTOR 1.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace	
4	T	99	Total	С	Ν	0	0	0	Ο
-1	1	22	179	113	38	28	0	0	0
4	T	<u> </u>	Total	С	Ν	Ο	0	0	0
<u>+</u>	J	20	184	116	39	29	0	0	0



3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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.

Note EDS was not executed.

• Molecule 1: DN)	JA (5'-D(*TP*GP	*TP*AP*TP*	GP*CP*AP*A	AP*AP*TP*A	P*AP*GP*G)-3'
Chain M:	27%	7	3%		
1201 7203 7203 7204 7205 7205 7205 7205 7211 7211 7211 7211 7211 7211 7211 721					
• Molecule 1: DN)	JA (5'-D(*TP*GP	*TP*AP*TP*	GP*CP*AP*A	AP*AP*TP*A	P*AP*GP*G)-3'
Chain O:		93%		7%	
DT 7703 7703 7705 7705 7705 7705 7705 7705	G715 G715				
• Molecule 2: DN)	VA (5'-D(*AP*CP	*CP*TP*TP*	AP*TP*TP*T	TP*GP*CP*A	.P*TP*AP*C)-3'
Chain N:		100%			
A216 C217 C218 T219 T220 A221 T224 T224 C226 C226 C226 C226	A229 C230				
• Molecule 2: DN)	NA (5'-D(*AP*CP	*CP*TP*TP*	АР*ТР*ТР*Т	TP*GP*CP*A	.P*TP*AP*C)-3'
Chain P: 7%		87%		7%	
DA C717 C718 T719 T720 T720 T723 T724 G726 G726 C726 C726 C726 T728	A729 C730				
• Molecule 3: PO	U DOMAIN, CLA	SS 2, TRANSC	CRIPTION FA	CTOR 1	
Chain A:	54%		25% • •	18%	
GLY SER ARG GLU GLU CL LO LO ELO ELO	A13 F16 F26 T26 T26 T27 V30 M34 M34 M34 M34 M34 M34 M34 M34 M34 M34	L37 N40 843 147 L55 NKG	K64 K64 F65 L67 L67 E68 K69 K70 K71	A74 E75 A275 A275 A275 A275 SER A27 SER SER	SER



• Molecule 4: POU DOMAIN, CLASS 2, ASSOCIATING FACTOR 1

Chain J:	34%	18%	48%
MET LEU TRP GLN GLN PRO PRO GLU GLU	ALA PRO ALA PRO A800 A800 4803 V805 V805	R807 V808 V808 V812 V812 L815 L815 L815 L815 ALA ALA ALA ALA	



4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants	93.72Å 93.72Å 152.65Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 - 3.20	Depositor
% Data completeness	99.5 (30.00-3.20)	Depositor
(in resolution range)		Depositor
R_{merge}	0.08	Depositor
R _{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.264 , 0.326	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3649	wwPDB-VP
Average B, all atoms $(Å^2)$	65.0	wwPDB-VP



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	Bond lengths		angles
	Ullaili	RMSZ	# Z > 5	RMSZ	# Z > 5
1	М	0.32	0/349	0.77	0/538
1	0	0.26	0/330	0.75	0/508
2	N	0.35	0/333	0.84	0/511
2	Р	0.26	0/312	0.68	0/478
3	А	0.34	0/1076	0.56	0/1445
3	В	0.35	0/1052	0.62	0/1405
4	Ι	0.52	0/181	0.75	0/240
4	J	0.35	0/186	0.64	0/247
All	All	0.34	0/3819	0.67	0/5372

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (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	М	310	0	171	37	0
1	0	293	0	158	48	0
2	N	299	0	173	36	0
2	Р	281	0	161	57	0
3	А	1061	0	1046	35	0
3	В	1042	0	1019	53	0
4	Ι	179	0	195	12	0
4	J	184	0	197	8	0



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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	3649	0	3120	256	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 38.

All (256) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom 1	Atom 2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:M:209:DA:H2"	1:M:210:DA:H5'	1.21	1.12
1:M:204:DA:H2"	1:M:205:DT:H5'	1.22	1.09
1:M:204:DA:H2"	1:M:205:DT:C5'	1.82	1.08
2:N:223:DT:H2"	2:N:224:DT:H5"	1.08	1.06
2:N:219:DT:H2'	2:N:220:DT:H72	1.36	1.06
2:P:728:DT:H2"	2:P:729:DA:C8	1.92	1.05
1:O:702:DG:H2"	1:O:703:DT:C5'	1.85	1.05
2:P:727:DA:H1'	2:P:728:DT:H5"	1.39	1.03
2:N:226:DC:H2"	2:N:227:DA:H5'	1.04	1.03
2:N:223:DT:C2'	2:N:224:DT:H5"	1.90	1.01
1:M:202:DG:H5'	3:A:26:THR:HG21	1.39	1.00
1:O:702:DG:H2"	1:O:703:DT:H5"	1.43	0.98
2:N:226:DC:H2"	2:N:227:DA:C5'	1.93	0.98
1:M:214:DG:H2"	1:M:215:DG:H5"	1.49	0.92
1:M:214:DG:C2'	1:M:215:DG:H5"	1.99	0.92
1:M:214:DG:H2"	1:M:215:DG:C5'	2.01	0.91
2:N:226:DC:C2'	2:N:227:DA:H5'	1.97	0.90
1:M:202:DG:H2"	1:M:203:DT:H5'	1.52	0.90
1:M:209:DA:H2"	1:M:210:DA:C5'	2.03	0.89
1:M:215:DG:H5'	1:M:215:DG:H8	1.39	0.87
1:M:202:DG:H2"	1:M:203:DT:C5'	2.03	0.87
2:N:221:DA:H1'	2:N:222:DT:H5"	1.55	0.87
2:P:726:DC:H2"	2:P:727:DA:C8	2.09	0.86
2:N:218:DC:H2'	2:N:219:DT:H72	1.57	0.85
2:P:727:DA:C1'	2:P:728:DT:H5"	2.06	0.85
1:M:214:DG:H1'	1:M:215:DG:H5"	1.58	0.85
1:O:702:DG:H2"	1:O:703:DT:H5'	1.57	0.84
2:N:219:DT:H2'	2:N:220:DT:C7	2.11	0.81
1:M:214:DG:C1'	1:M:215:DG:H5"	2.11	0.81
2:P:721:DA:H1'	2:P:722:DT:H5"	1.64	0.79
1:O:703:DT:H2"	1:O:704:DA:H8	1.47	0.78
3:B:641:GLU:HB3	3:B:644:VAL:HG12	1.64	0.78
1:M:204:DA:C2'	1:M:205:DT:H5'	2.10	0.78



	At a	Interatomic	Clash
Atom-1	Atom-2	distance (\AA)	overlap (Å)
1:O:714:DG:H2"	1:O:715:DG:H5'	1.66	0.77
2:P:728:DT:H2"	2:P:729:DA:H8	1.49	0.77
1:O:703:DT:H3'	3:B:527:GLN:HE22	1.46	0.77
2:N:223:DT:H2"	2:N:224:DT:C5'	2.03	0.77
1:M:215:DG:H5'	1:M:215:DG:C8	2.19	0.76
2:P:722:DT:N1	2:P:723:DT:H72	2.00	0.76
2:P:727:DA:C2'	2:P:728:DT:H5"	2.17	0.75
2:N:218:DC:H2'	2:N:219:DT:C7	2.17	0.74
2:P:723:DT:H2"	2:P:724:DT:H5'	1.69	0.74
2:N:216:DA:H2"	2:N:217:DC:OP2	1.86	0.74
2:P:722:DT:C6	2:P:723:DT:H72	2.23	0.73
1:O:702:DG:C2'	1:O:703:DT:H5"	2.18	0.73
1:O:703:DT:H3'	3:B:527:GLN:NE2	2.03	0.72
2:P:722:DT:C2'	2:P:723:DT:C7	2.68	0.71
2:P:722:DT:C2'	2:P:723:DT:H73	2.20	0.71
2:P:727:DA:H1'	2:P:728:DT:C5'	2.20	0.70
3:B:659:ILE:HD11	4:J:804:GLN:HA	1.73	0.70
2:N:228:DT:H1'	2:N:229:DA:C8	2.27	0.69
4:J:803:TYR:HB3	4:J:807:ARG:HH21	1.58	0.69
1:O:703:DT:H2"	1:O:704:DA:C8	2.27	0.68
1:O:712:DA:H2"	1:O:713:DA:C8	2.29	0.68
1:M:210:DA:H2"	1:M:211:DT:H5'	1.76	0.68
1:M:202:DG:H5'	3:A:26:THR:CG2	2.22	0.67
1:M:203:DT:H2"	1:M:204:DA:O5'	1.94	0.67
4:I:303:TYR:HD2	4:I:307:ARG:NH2	1.92	0.67
1:M:204:DA:H2"	1:M:205:DT:H5"	1.73	0.67
1:M:209:DA:C2'	1:M:210:DA:H5'	2.14	0.66
3:A:143:GLU:O	3:A:147:VAL:HG23	1.96	0.66
2:P:726:DC:C2'	2:P:727:DA:C8	2.78	0.66
2:N:221:DA:H1'	2:N:222:DT:C5'	2.26	0.66
2:P:725:DG:N7	3:B:545:THR:HG21	2.10	0.66
2:P:728:DT:C2'	2:P:729:DA:C8	2.75	0.64
4:I:303:TYR:HD2	4:I:307:ARG:HH21	1.45	0.64
3:A:155:LYS:HE3	4:I:304:GLN:HB3	1.80	0.64
2:P:727:DA:H2"	2:P:728:DT:C5'	2.28	0.63
2:P:722:DT:H2'	2:P:723:DT:C7	2.29	0.63
2:P:725:DG:H4'	2:P:726:DC:OP1	1.99	0.63
2:P:726:DC:H2"	2:P:727:DA:H8	1.61	0.63
1:O:705:DT:H2"	1:O:706:DG:C8	2.34	0.63
1:O:708:DA:C2	1:O:709:DA:C6	2.86	0.62
2:P:719:DT:H2'	2:P:720:DT:H72	1.79	0.62



	A L O	Interatomic	Clash	
Atom-1	Atom-2	distance (\AA)	overlap (Å)	
1:0:711:DT:OP1	3:B:603:LYS:HB3	1.99	0.62	
1:M:204:DA:C2'	1:M:205:DT:C5'	2.69	0.62	
2:P:722:DT:H2"	2:P:723:DT:H73	1.82	0.62	
4:I:303:TYR:CD2	4:I:307:ARG:NH2	2.68	0.61	
3:B:619:SER:O	3:B:622:GLU:HB3	2.01	0.61	
3:A:55:LEU:HD22	3:A:59:ASN:OD1	2.00	0.61	
1:O:706:DG:H2"	1:O:707:DC:H6	1.65	0.60	
2:P:722:DT:C2	2:P:723:DT:C5	2.89	0.60	
2:P:729:DA:C8	2:P:730:DC:C5	2.90	0.60	
3:B:650:CYS:HA	3:B:653:ARG:NH1	2.16	0.60	
1:M:208:DA:H1'	1:M:209:DA:C8	2.37	0.59	
1:O:710:DA:H1'	1:O:711:DT:H5"	1.84	0.59	
3:B:523:LEU:HB3	3:B:525:PHE:CE1	2.38	0.58	
2:P:722:DT:H2'	2:P:723:DT:H73	1.84	0.58	
2:N:218:DC:H2"	2:N:219:DT:O5'	2.03	0.58	
1:O:709:DA:H2"	1:O:710:DA:O5'	2.03	0.58	
1:O:702:DG:C2'	1:O:703:DT:C5'	2.74	0.57	
1:O:713:DA:H2"	1:0:714:DG:OP2	2.05	0.57	
1:O:708:DA:C2	1:O:709:DA:N1	2.72	0.57	
2:P:728:DT:H5'	2:P:728:DT:H6	1.69	0.57	
4:I:303:TYR:C	4:I:303:TYR:CD1	2.79	0.57	
1:M:203:DT:OP2	3:A:27:GLN:HG2	2.04	0.57	
1:O:710:DA:C5'	3:B:605:ARG:HA	2.35	0.56	
3:A:55:LEU:O	4:I:312:VAL:HG23	2.06	0.56	
3:B:633:MET:O	3:B:637:GLN:HB2	2.04	0.56	
1:M:210:DA:H1'	1:M:211:DT:C5'	2.36	0.56	
3:B:554:ASN:HD22	3:B:554:ASN:N	2.02	0.56	
1:M:202:DG:H2"	1:M:203:DT:H5"	1.85	0.56	
3:B:643:GLU:HG3	3:B:644:VAL:N	2.20	0.56	
1:O:712:DA:H1'	1:O:713:DA:C8	2.40	0.55	
2:P:725:DG:C8	3:B:545:THR:HG21	2.40	0.55	
1:O:703:DT:OP2	3:B:527:GLN:HG3	2.07	0.55	
1:O:712:DA:C2	2:P:721:DA:C2	2.94	0.55	
2:P:719:DT:C2'	2:P:720:DT:H72	2.36	0.55	
1:M:204:DA:H2'	1:M:205:DT:H71	1.88	0.55	
3:A:64:LYS:N	3:A:65:PRO:HD2	2.21	0.55	
4:J:811:PRO:O	4:J:815:LEU:HD22	2.07	0.54	
4:I:303:TYR:C	4:I:303:TYR:HD1	2.10	0.54	
2:P:727:DA:H2"	2:P:728:DT:H5"	1.87	0.53	
3:A:6:LEU:HD11	4:I:316:LEU:CD2	2.38	0.53	
1:O:711:DT:H2"	1:O:712:DA:O5'	2.09	0.53	



	A L O	Interatomic	Clash	
Atom-1	Atom-2	distance (\AA)	overlap (Å)	
2:N:229:DA:H2"	2:N:230:DC:O5'	2.08	0.53	
2:P:728:DT:C2	2:P:729:DA:C5	2.97	0.53	
4:I:303:TYR:CD1	4:I:303:TYR:O	2.62	0.52	
2:N:220:DT:H1'	2:N:221:DA:H5'	1.91	0.52	
3:A:37:LEU:HD22	3:A:70:TRP:HD1	1.75	0.52	
2:N:221:DA:C1'	2:N:222:DT:H5"	2.34	0.52	
2:P:718:DC:H2"	2:P:719:DT:O5'	2.09	0.52	
3:A:26:THR:O	3:A:30:VAL:HG23	2.10	0.52	
3:B:516:PHE:CE1	3:B:567:LEU:HB3	2.44	0.52	
1:O:708:DA:C2	1:O:709:DA:C2	2.97	0.52	
2:P:723:DT:H1'	2:P:724:DT:H5"	1.92	0.52	
3:B:555:LEU:O	4:J:812:VAL:HG23	2.10	0.51	
2:P:721:DA:C2	2:P:722:DT:C2	2.99	0.51	
2:N:218:DC:C6	2:N:219:DT:H72	2.46	0.51	
1:O:705:DT:O2	1:O:706:DG:C5	2.63	0.51	
1:O:710:DA:H5"	3:B:605:ARG:HA	1.93	0.51	
3:A:34:MET:HA	3:A:37:LEU:HB3	1.92	0.51	
3:B:641:GLU:HB3	3:B:644:VAL:CG1	2.39	0.51	
1:O:705:DT:H2"	1:O:706:DG:N7	2.26	0.50	
3:B:553:LEU:HA	3:B:560:MET:CE	2.41	0.50	
1:M:204:DA:C2	2:N:229:DA:C2	2.98	0.50	
2:N:217:DC:H2"	2:N:218:DC:OP2	2.11	0.50	
1:O:703:DT:C2'	1:O:704:DA:C8	2.94	0.50	
1:0:714:DG:O6	2:P:718:DC:N4	2.45	0.50	
1:M:210:DA:H1'	1:M:211:DT:H5"	1.93	0.50	
2:P:729:DA:C5	2:P:730:DC:C4	2.99	0.50	
3:A:68:GLU:O	3:A:72:ASN:HB2	2.11	0.50	
2:N:221:DA:H2"	2:N:222:DT:H5'	1.94	0.50	
2:N:219:DT:H2"	2:N:220:DT:C6	2.47	0.49	
3:B:559:ASN:O	3:B:563:LEU:HD13	2.13	0.49	
3:A:159:ILE:HD11	4:I:304:GLN:HA	1.94	0.49	
2:P:722:DT:C2'	2:P:723:DT:H72	2.42	0.49	
3:A:33:ALA:HB1	3:A:70:TRP:NE1	2.27	0.49	
2:P:719:DT:C6	2:P:720:DT:H72	2.48	0.49	
2:P:720:DT:C2	2:P:721:DA:C8	3.00	0.49	
3:B:538:TYR:CE1	3:B:566:LEU:HA	2.47	0.49	
1:O:704:DA:H2"	1:O:705:DT:H5'	1.95	0.49	
1:O:708:DA:H4'	3:B:605:ARG:NH2	2.28	0.48	
3:A:6:LEU:HD11	4:I:316:LEU:HD21	1.95	0.48	
2:N:225:DG:H1'	2:N:226:DC:C5	2.48	0.48	
3:B:523:LEU:HB3	3:B:525:PHE:HE1	1.77	0.48	



			Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:O:706:DG:C8	1:O:707:DC:C5	3.01	0.48
2:P:719:DT:H2"	2:P:720:DT:C6	2.49	0.48
3:B:613:ARG:HH21	3:B:652:ARG:NH2	2.12	0.48
2:P:722:DT:H2'	2:P:723:DT:H72	1.96	0.48
3:A:27:GLN:O	3:A:47:ILE:HG21	2.14	0.48
1:0:710:DA:OP2	3:B:644:VAL:HG23	2.13	0.48
3:A:35:GLY:HA2	3:A:40:ASN:O	2.13	0.48
2:N:223:DT:C3'	2:N:224:DT:H5"	2.41	0.48
3:A:43:SER:O	3:A:47:ILE:HG22	2.14	0.48
1:M:201:DT:H2"	1:M:202:DG:OP2	2.14	0.47
2:P:721:DA:C4	2:P:722:DT:C5	3.01	0.47
3:B:538:TYR:HE1	3:B:566:LEU:O	1.97	0.47
1:O:706:DG:C4	1:O:707:DC:C5	3.02	0.47
2:P:723:DT:H2"	2:P:724:DT:C5'	2.42	0.47
2:N:223:DT:OP1	3:A:59:ASN:HB2	2.15	0.47
1:O:712:DA:H2"	1:O:713:DA:N7	2.29	0.47
1:O:712:DA:C4	1:O:713:DA:C5	3.03	0.47
2:P:720:DT:H2"	2:P:721:DA:OP2	2.15	0.47
1:M:210:DA:C2'	1:M:211:DT:H5'	2.44	0.47
2:P:721:DA:N3	2:P:722:DT:C6	2.82	0.47
2:P:729:DA:C4	2:P:730:DC:C6	3.02	0.47
2:P:719:DT:C2'	2:P:720:DT:C7	2.93	0.46
3:B:635:ALA:HB1	3:B:641:GLU:O	2.16	0.46
3:B:648:TRP:O	3:B:652:ARG:HB2	2.15	0.46
3:B:638:LEU:HB3	3:B:640:MET:HG2	1.97	0.46
2:N:224:DT:H2"	2:N:225:DG:O5'	2.16	0.46
2:N:226:DC:C2'	2:N:227:DA:C5'	2.76	0.46
2:P:718:DC:H6	2:P:719:DT:H71	1.80	0.46
3:A:5:ASP:O	3:A:9:LEU:HD23	2.16	0.45
1:M:210:DA:H1'	1:M:211:DT:H5'	1.98	0.45
2:P:729:DA:C5	2:P:730:DC:C5	3.04	0.45
1:O:710:DA:H5'	3:B:605:ARG:HA	1.98	0.45
3:A:130:GLU:O	3:A:134:ILE:HG13	2.16	0.45
3:A:34:MET:HE1	3:A:67:LEU:HD13	1.98	0.45
1:O:708:DA:H2	1:O:709:DA:C2	2.33	0.45
3:A:131:ILE:HD13	3:A:146:ARG:HA	1.99	0.45
1:M:202:DG:C2'	1:M:203:DT:H5"	2.46	0.44
3:B:512:PHE:CZ	3:B:568:GLU:HG3	2.52	0.44
1:O:712:DA:C2'	1:O:713:DA:C8	2.98	0.44
3:B:553:LEU:HA	3:B:560:MET:HE1	2.00	0.44
1:M:202:DG:C2'	1:M:203:DT:C5'	2.88	0.44



		Interatomic	Clash
Atom-1	Atom-1 Atom-2		overlap (Å)
3:B:556:SER:OG	3:B:559:ASN:HB2	2.18	0.44
1:O:705:DT:H1'	1:O:706:DG:C8	2.52	0.44
1:O:706:DG:C5	1:O:707:DC:C4	3.05	0.44
3:B:511:GLN:O	3:B:514:LYS:HB3	2.18	0.44
4:I:312:VAL:HA	4:I:315:LEU:HB2	2.00	0.44
1:O:704:DA:H1'	1:O:705:DT:H5"	1.99	0.43
3:A:135:ALA:HB1	3:A:140:MET:O	2.18	0.43
3:B:650:CYS:HA	3:B:653:ARG:HH12	1.80	0.43
1:M:202:DG:H3'	3:A:26:THR:HB	2.00	0.43
3:B:614:VAL:HG23	3:B:615:ALA:N	2.34	0.43
1:O:709:DA:H1'	3:B:605:ARG:HG3	2.01	0.43
3:A:4:SER:OG	3:A:64:LYS:HE2	2.19	0.43
3:A:120:PHE:CD2	3:A:124:GLN:HA	2.54	0.43
3:A:155:LYS:HA	3:A:158:ARG:CZ	2.48	0.43
3:B:655:LYS:HE3	4:J:804:GLN:HB3	2.00	0.43
3:A:33:ALA:HB1	3:A:70:TRP:HE1	1.83	0.43
3:B:537:LEU:HD12	3:B:537:LEU:HA	1.88	0.43
3:B:658:ARG:NE	4:J:805:GLY:O	2.51	0.43
1:O:708:DA:C4'	3:B:605:ARG:NH2	2.82	0.43
2:P:718:DC:H6	2:P:719:DT:C7	2.32	0.43
2:P:722:DT:C2	2:P:723:DT:H72	2.54	0.42
1:M:215:DG:C5'	1:M:215:DG:C8	2.99	0.42
3:B:569:LYS:O	3:B:573:ASP:HB2	2.18	0.42
2:P:722:DT:H2"	2:P:723:DT:C7	2.44	0.42
3:A:10:GLU:O	3:A:13:ALA:HB3	2.19	0.42
3:B:507:GLU:C	3:B:509:LEU:H	2.22	0.42
3:B:638:LEU:O	3:B:639:ASN:HB2	2.18	0.42
2:N:217:DC:H6	2:N:217:DC:H2'	1.70	0.42
2:N:222:DT:C2'	2:N:223:DT:H72	2.48	0.42
4:J:808:VAL:O	4:J:811:PRO:HD3	2.20	0.42
3:A:117:GLU:O	3:A:121:LEU:HD23	2.19	0.42
3:B:627:THR:HG22	3:B:628:SER:N	2.35	0.42
1:M:208:DA:H1'	1:M:209:DA:N7	2.35	0.42
2:N:218:DC:C2'	2:N:219:DT:C7	2.93	0.42
3:B:643:GLU:HB2	3:B:646:ARG:NH1	2.35	0.42
1:M:210:DA:C2	1:M:211:DT:C2	3.08	0.41
3:B:520:ARG:HG3	3:B:520:ARG:HH11	1.84	0.41
4:J:804:GLN:H	4:J:804:GLN:CD	2.23	0.41
2:N:226:DC:H1'	2:N:227:DA:H5"	2.02	0.41
2:N:219:DT:C6	2:N:220:DT:H72	2.55	0.41
3:B:517:LYS:O	3:B:521:ILE:HG13	2.21	0.41



Atom 1	Atom 2	Interatomic	Clash
Atom-1	Atom-2	distance (\AA)	overlap (Å)
2:N:219:DT:C2'	2:N:220:DT:C7	2.93	0.41
2:P:719:DT:H2"	2:P:720:DT:C7	2.50	0.41
1:O:713:DA:H1'	1:O:714:DG:H5'	2.03	0.41
2:N:216:DA:C6	2:N:217:DC:C4	3.09	0.41
1:O:706:DG:H2"	1:O:707:DC:C6	2.51	0.41
1:O:706:DG:H2"	1:O:707:DC:O5'	2.20	0.41
3:A:16:PHE:CE1	3:A:67:LEU:HB3	2.56	0.41
3:B:520:ARG:HG3	3:B:520:ARG:NH1	2.36	0.41
2:N:221:DA:H2"	2:N:222:DT:OP2	2.20	0.40
2:P:720:DT:O2	2:P:721:DA:C8	2.75	0.40
2:P:722:DT:O2	2:P:723:DT:C6	2.74	0.40
3:A:160:ASN:HA	3:A:161:PRO:HD2	1.78	0.40
2:P:725:DG:H2"	2:P:726:DC:C5	2.56	0.40
3:A:34:MET:HE2	3:A:67:LEU:HA	2.03	0.40
3:B:627:THR:HG22	3:B:628:SER:H	1.87	0.40
2:P:720:DT:C2	2:P:721:DA:N7	2.89	0.40
3:B:507:GLU:C	3:B:509:LEU:N	2.72	0.40
3:B:511:GLN:HE21	3:B:515:THR:HG23	1.86	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
3	А	130/163~(80%)	114 (88%)	12 (9%)	4(3%)	4 26
3	В	121/163~(74%)	108 (89%)	8 (7%)	5(4%)	3 21
4	Ι	20/44~(46%)	$17 \ (85\%)$	2(10%)	1 (5%)	2 16
4	J	21/44~(48%)	15 (71%)	6(29%)	0	100 100
All	All	292/414 (70%)	254 (87%)	28 (10%)	10 (3%)	3 24

All (10) Ramachandran outliers are listed below:



Mol	Chain	Res	Type
3	В	574	ALA
3	В	631	ILE
3	В	526	THR
4	Ι	303	TYR
3	А	72	ASN
3	В	603	LYS
3	А	74	ALA
3	А	159	ILE
3	В	545	THR
3	А	43	SER

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 side chain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Perce	entiles
3	А	111/148~(75%)	104 (94%)	7~(6%)	18	52
3	В	110/148~(74%)	97~(88%)	13 (12%)	5	23
4	Ι	18/34~(53%)	17 (94%)	1 (6%)	21	57
4	J	18/34~(53%)	18 (100%)	0	100	100
All	All	257/364 (71%)	236 (92%)	21 (8%)	11	41

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	А	10	GLU
3	А	25	PHE
3	А	59	ASN
3	А	67	LEU
3	А	72	ASN
3	А	129	GLU
3	А	137	GLN
3	В	537	LEU
3	В	538	TYR
3	В	554	ASN
3	В	559	ASN
3	В	566	LEU



Continuca from prettous paye				
Mol	Chain	Res	Type	
3	В	573	ASP	
3	В	575	GLU	
3	В	602	ARG	
3	В	610	THR	
3	В	617	GLU	
3	В	643	GLU	
3	В	646	ARG	
3	В	649	PHE	
4	Ι	303	TYR	

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
3	А	59	ASN
3	А	111	ASN
3	А	160	ASN
3	В	511	GLN
3	В	518	GLN
3	В	554	ASN
4	J	804	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

