Full wwPDB X-ray Structure Validation Report ⓘ

Sep 13, 2023 – 05:05 AM EDT

PDB ID	:	4PSO
Title	:	Crystal structure of apeThermo-DBP-RP2 bound to ssDNA dT10
Authors	:	Gahlei, H.; von Moeller, H.; Eppers, D.; Loll, B.; Wahl, M.C.
Deposited on	:	2014-03-07
Resolution	:	2.90 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 types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

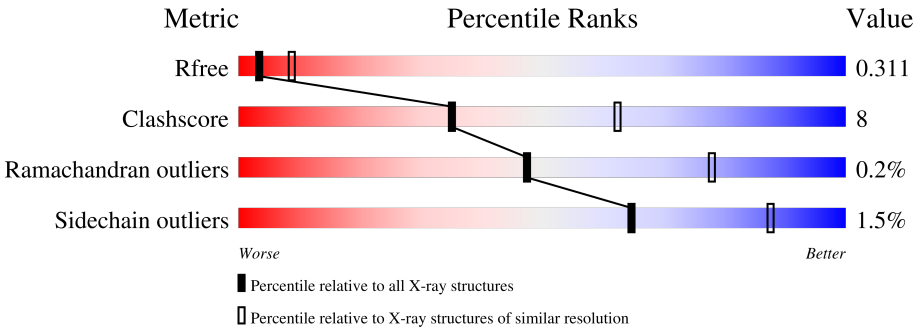
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 2.90 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	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)

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%

Mol	Chain	Length	Quality of chain
1	A	237	72% 19% • 8%
1	B	237	74% 18% 7%
1	C	237	72% 20% • 7%
1	D	237	70% 21% • 8%
1	F	237	75% 17% 8%
1	G	237	72% 19% • 8%
1	H	237	78% 14% • 7%

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Mol	Chain	Length	Quality of chain
1	I	237	78% 15% 7%
2	E	10	20% 40% 10% 30%
2	L	10	20% 40% 40%
2	X	10	20% 20% 60%
2	Z	10	20% 20% 60%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 14476 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 ssDNA binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	218	Total	C	N	O	S	0	0	0
			1734	1097	310	324	3			
1	B	220	Total	C	N	O	S	0	0	0
			1748	1106	313	326	3			
1	C	220	Total	C	N	O	S	0	0	0
			1748	1106	313	326	3			
1	D	219	Total	C	N	O	S	0	0	0
			1739	1100	311	325	3			
1	F	219	Total	C	N	O	S	0	0	0
			1741	1102	312	324	3			
1	G	217	Total	C	N	O	S	0	0	0
			1723	1091	306	323	3			
1	H	220	Total	C	N	O	S	0	0	0
			1748	1106	313	326	3			
1	I	221	Total	C	N	O	S	0	0	0
			1752	1108	314	327	3			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP Q9YAS7
A	-1	ALA	-	expression tag	UNP Q9YAS7
A	1	LEU	-	expression tag	UNP Q9YAS7
B	-2	GLY	-	expression tag	UNP Q9YAS7
B	-1	ALA	-	expression tag	UNP Q9YAS7
B	1	LEU	-	expression tag	UNP Q9YAS7
C	-2	GLY	-	expression tag	UNP Q9YAS7
C	-1	ALA	-	expression tag	UNP Q9YAS7
C	1	LEU	-	expression tag	UNP Q9YAS7
D	-2	GLY	-	expression tag	UNP Q9YAS7
D	-1	ALA	-	expression tag	UNP Q9YAS7
D	1	LEU	-	expression tag	UNP Q9YAS7
F	-2	GLY	-	expression tag	UNP Q9YAS7

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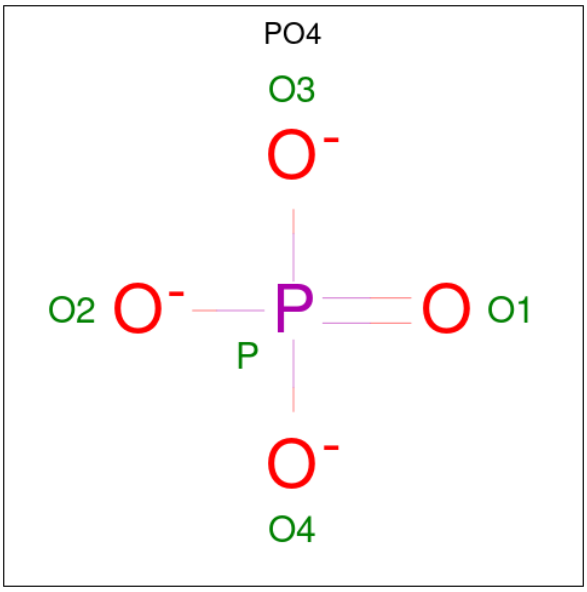
Chain	Residue	Modelled	Actual	Comment	Reference
F	-1	ALA	-	expression tag	UNP Q9YAS7
F	1	LEU	-	expression tag	UNP Q9YAS7
G	-2	GLY	-	expression tag	UNP Q9YAS7
G	-1	ALA	-	expression tag	UNP Q9YAS7
G	1	LEU	-	expression tag	UNP Q9YAS7
H	-2	GLY	-	expression tag	UNP Q9YAS7
H	-1	ALA	-	expression tag	UNP Q9YAS7
H	1	LEU	-	expression tag	UNP Q9YAS7
I	-2	GLY	-	expression tag	UNP Q9YAS7
I	-1	ALA	-	expression tag	UNP Q9YAS7
I	1	LEU	-	expression tag	UNP Q9YAS7

- Molecule 2 is a DNA chain called polydeoxyribonucleotide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	10	Total	C	N	O	P	0	0	0
			200	100	20	70	10			
2	E	7	Total	C	N	O	P	0	0	0
			140	70	14	49	7			
2	X	4	Total	C	N	O	P	0	0	0
			80	40	8	28	4			
2	Z	4	Total	C	N	O	P	0	0	0
			80	40	8	28	4			

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total O P 5 4 1	0	0

- Molecule 4 is water.

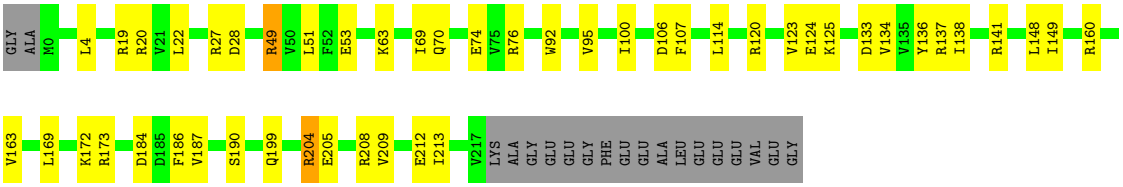
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	8	Total O 8 8	0	0
4	B	6	Total O 6 6	0	0
4	C	6	Total O 6 6	0	0
4	D	5	Total O 5 5	0	0
4	F	3	Total O 3 3	0	0
4	G	4	Total O 4 4	0	0
4	H	1	Total O 1 1	0	0
4	I	3	Total O 3 3	0	0
4	E	1	Total O 1 1	0	0
4	X	1	Total O 1 1	0	0

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.

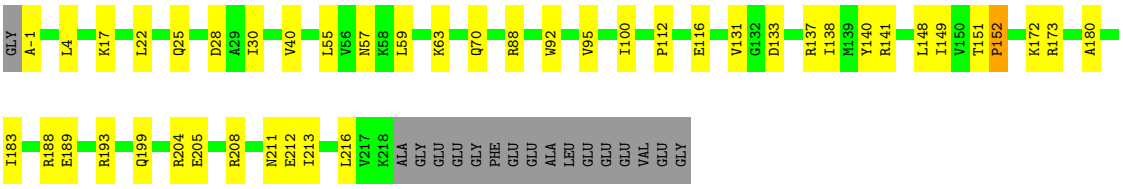
• Molecule 1: ssDNA binding protein

Chain A:



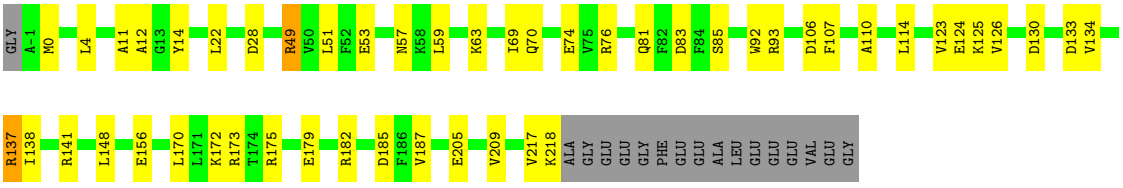
• Molecule 1: ssDNA binding protein

Chain B:



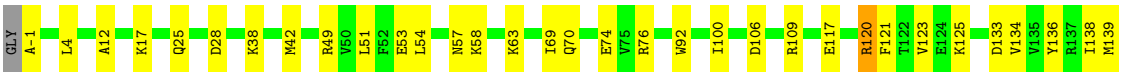
• Molecule 1: ssDNA binding protein

Chain C:



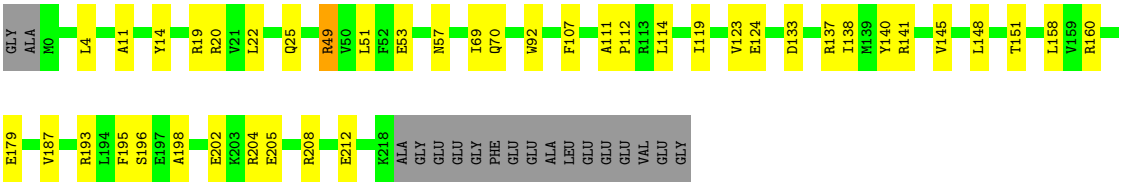
• Molecule 1: ssDNA binding protein

Chain D:



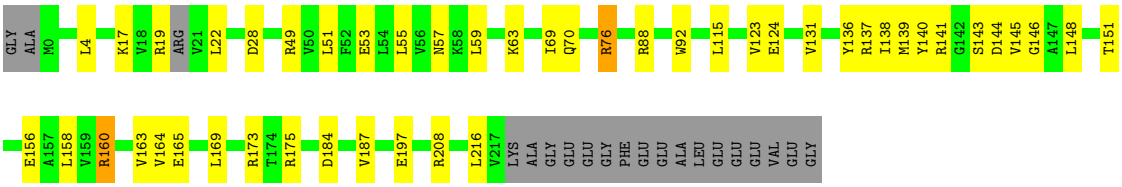
• Molecule 1: ssDNA binding protein

Chain F:



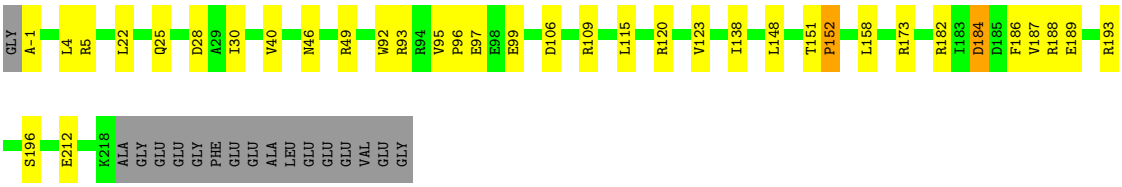
• Molecule 1: ssDNA binding protein

Chain G:



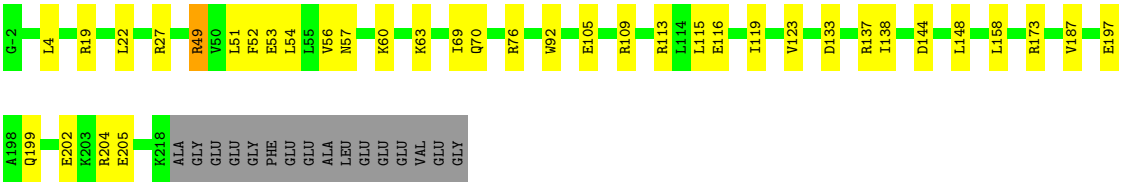
• Molecule 1: ssDNA binding protein

Chain H:



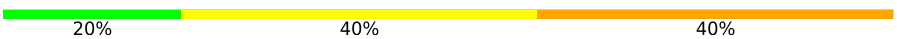
• Molecule 1: ssDNA binding protein

Chain I:



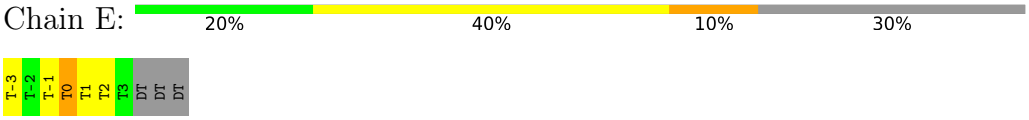
• Molecule 2: polydeoxyribonucleotide

Chain L:



• Molecule 2: polydeoxyribonucleotide

Chain E:



• Molecule 2: polydeoxyribonucleotide

Chain X:

• Molecule 2: polydeoxyribonucleotide

Chain Z:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	120.49Å 190.28Å 89.79Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.93 – 2.90 48.38 – 2.32	Depositor EDS
% Data completeness (in resolution range)	99.9 (29.93-2.90) 90.9 (48.38-2.32)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.19 (at 2.32Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1389)	Depositor
R, R_{free}	0.267 , 0.309 0.268 , 0.311	Depositor DCC
R_{free} test set	4084 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	32.9	Xtriage
Anisotropy	0.097	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 57.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.87	EDS
Total number of atoms	14476	wwPDB-VP
Average B, all atoms (Å^2)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.63% 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

Bond lengths and bond angles in the following residue types are not validated in this section: PO4

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	0.25	0/1754	0.47	0/2373
1	B	0.25	0/1768	0.48	0/2391
1	C	0.26	0/1768	0.49	0/2391
1	D	0.26	0/1759	0.51	0/2380
1	F	0.25	0/1761	0.46	0/2381
1	G	0.25	0/1742	0.47	0/2356
1	H	0.24	0/1768	0.43	0/2391
1	I	0.24	0/1772	0.45	0/2396
2	E	0.51	0/153	1.69	3/234 (1.3%)
2	L	0.52	0/219	1.72	7/336 (2.1%)
2	X	0.56	0/87	1.55	1/132 (0.8%)
2	Z	0.58	0/87	1.55	0/132
All	All	0.27	0/14638	0.57	11/19893 (0.1%)

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	L	5	DT	O4'-C1'-N1	7.78	113.44	108.00
2	E	2	DT	O4'-C1'-N1	7.34	113.14	108.00
2	X	7	DT	O4'-C1'-N1	6.02	112.22	108.00
2	L	3	DT	C6-C5-C7	-5.85	119.39	122.90
2	L	5	DT	O4'-C4'-C3'	-5.63	102.25	104.50
2	L	1	DT	O4'-C1'-C2'	-5.59	101.43	105.90
2	E	0	DT	C5-C4-O4	-5.48	121.06	124.90
2	E	0	DT	N3-C4-O4	5.39	123.13	119.90
2	L	8	DT	N3-C4-O4	5.16	123.00	119.90
2	L	1	DT	N1-C1'-C2'	5.01	122.13	112.60
2	L	3	DT	C4-C5-C7	5.00	122.00	119.00

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	1734	0	1800	39	0
1	B	1748	0	1818	41	0
1	C	1748	0	1818	37	0
1	D	1739	0	1805	44	0
1	F	1741	0	1808	37	1
1	G	1723	0	1786	41	1
1	H	1748	0	1818	29	0
1	I	1752	0	1821	31	0
2	E	140	0	85	3	0
2	L	200	0	121	12	0
2	X	80	0	49	2	0
2	Z	80	0	49	2	0
3	B	5	0	0	1	0
4	A	8	0	0	1	0
4	B	6	0	0	1	0
4	C	6	0	0	0	0
4	D	5	0	0	2	0
4	E	1	0	0	0	0
4	F	3	0	0	0	0
4	G	4	0	0	0	0
4	H	1	0	0	0	0
4	I	3	0	0	2	0
4	X	1	0	0	0	0
All	All	14476	0	14778	239	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 8.

All (239) 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:G:137:ARG:NH2	1:G:146:GLY:O	2.03	0.92
1:H:5:ARG:HD3	1:I:27:ARG:HH12	1.41	0.83
1:C:63:LYS:HD3	2:L:3:DT:H5'	1.64	0.78
1:G:137:ARG:NH2	1:G:138:ILE:O	2.19	0.76
1:D:138:ILE:HD11	1:D:148:LEU:HB2	1.69	0.75
1:F:70:GLN:NE2	1:G:28:ASP:OD2	2.17	0.74
1:B:133:ASP:OD2	1:D:173:ARG:NH1	2.20	0.74
1:F:138:ILE:HD11	1:F:148:LEU:HB2	1.71	0.72
1:A:70:GLN:NE2	1:B:28:ASP:OD1	2.15	0.71
1:G:138:ILE:HD11	1:G:148:LEU:HB2	1.72	0.71
1:B:193:ARG:HD2	1:H:93:ARG:HD3	1.74	0.69
1:A:173:ARG:NH1	1:C:133:ASP:OD2	2.26	0.69
1:H:184:ASP:O	1:H:188:ARG:NH2	2.26	0.68
1:A:136:TYR:OH	1:A:184:ASP:OD1	2.11	0.68
1:G:123:VAL:HG21	1:G:187:VAL:HG12	1.75	0.68
1:G:137:ARG:HH11	1:G:144:ASP:HB3	1.59	0.68
1:H:138:ILE:HD11	1:H:148:LEU:HB2	1.75	0.67
1:B:17:LYS:HZ2	2:L:9:DT:H3	1.43	0.66
1:C:53:GLU:OE1	1:C:57:ASN:ND2	2.29	0.66
1:G:53:GLU:OE1	1:G:57:ASN:ND2	2.29	0.66
1:C:4:LEU:HD12	1:C:22:LEU:HD13	1.77	0.65
1:G:137:ARG:NH1	1:G:144:ASP:HB3	2.11	0.65
1:B:173:ARG:NH2	1:D:133:ASP:OD2	2.20	0.65
1:I:4:LEU:HD12	1:I:22:LEU:HD13	1.79	0.64
1:A:125:LYS:HE3	1:A:134:VAL:HG13	1.80	0.64
1:D:53:GLU:OE1	1:D:57:ASN:ND2	2.31	0.63
1:A:106:ASP:OD1	1:A:107:PHE:N	2.31	0.63
1:C:81:GLN:HE22	1:G:124:GLU:HB2	1.62	0.63
1:D:106:ASP:OD1	1:D:109:ARG:NH2	2.30	0.63
1:G:156:GLU:OE2	1:G:175:ARG:NH1	2.31	0.63
1:B:92:TRP:HB3	1:C:92:TRP:HB3	1.80	0.62
1:G:4:LEU:HD12	1:G:22:LEU:HD13	1.80	0.62
1:I:138:ILE:HD11	1:I:148:LEU:HB2	1.81	0.62
1:C:106:ASP:OD1	1:C:107:PHE:N	2.33	0.62
1:B:208:ARG:NH2	1:D:199:GLN:OE1	2.32	0.62
1:F:53:GLU:OE1	1:F:57:ASN:ND2	2.32	0.62
1:G:131:VAL:HG21	1:I:158:LEU:HD11	1.83	0.61
1:I:76:ARG:NH2	4:I:303:HOH:O	2.28	0.61
1:A:114:LEU:HD21	1:D:53:GLU:HG3	1.81	0.61
1:D:160:ARG:HH21	1:D:160:ARG:HB3	1.65	0.61
1:D:123:VAL:HG21	1:D:187:VAL:HG12	1.83	0.61
1:G:136:TYR:OH	1:G:184:ASP:OD1	2.17	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:92:TRP:HB3	1:D:92:TRP:HB3	1.82	0.60
1:G:160:ARG:HG3	1:G:173:ARG:HA	1.84	0.60
1:D:25:GLN:NE2	4:D:305:HOH:O	2.35	0.60
1:I:53:GLU:OE1	1:I:57:ASN:ND2	2.33	0.60
1:B:4:LEU:HD12	1:B:22:LEU:HD13	1.84	0.59
1:A:123:VAL:HG21	1:A:187:VAL:HG12	1.85	0.59
1:B:189:GLU:HG2	1:H:95:VAL:HG13	1.83	0.59
1:B:193:ARG:CD	1:H:93:ARG:HD3	2.33	0.59
1:F:4:LEU:HD12	1:F:22:LEU:HD13	1.84	0.59
1:H:25:GLN:HE21	2:Z:12:DT:H3	1.51	0.59
1:A:133:ASP:OD2	1:C:173:ARG:NH1	2.36	0.58
1:A:28:ASP:OD2	1:B:70:GLN:NE2	2.29	0.58
1:A:53:GLU:OE1	1:D:141:ARG:NH2	2.36	0.58
1:A:204:ARG:NH1	1:C:205:GLU:OE1	2.35	0.58
1:C:130:ASP:OD1	1:C:218:LYS:HD3	2.03	0.58
1:G:173:ARG:NH1	1:I:133:ASP:OD2	2.34	0.58
1:F:160:ARG:NH2	1:H:212:GLU:OE1	2.35	0.57
1:D:58:LYS:NZ	4:D:303:HOH:O	2.37	0.57
1:I:123:VAL:HG21	1:I:187:VAL:HG12	1.86	0.57
1:C:126:VAL:HG12	1:C:217:VAL:HG11	1.85	0.57
1:F:123:VAL:HG21	1:F:187:VAL:HG12	1.86	0.56
1:D:125:LYS:HE3	1:D:134:VAL:HG13	1.87	0.56
1:F:20:ARG:NH1	2:Z:14:DT:O3'	2.30	0.56
1:G:145:VAL:HG12	1:G:165:GLU:HB2	1.87	0.56
1:C:28:ASP:OD2	1:D:70:GLN:NE2	2.25	0.56
1:B:172:LYS:HD2	1:B:199:GLN:NE2	2.21	0.56
1:C:123:VAL:HG21	1:C:187:VAL:HG12	1.88	0.56
1:D:74:GLU:OE2	1:D:76:ARG:NE	2.37	0.56
1:C:12:ALA:HB3	2:L:4:DT:H1'	1.89	0.55
1:H:-1:ALA:N	4:I:303:HOH:O	2.38	0.55
1:G:115:LEU:HG	1:H:46:ASN:HB3	1.87	0.55
1:H:123:VAL:HG21	1:H:187:VAL:HG12	1.88	0.55
1:A:205:GLU:HG2	1:C:205:GLU:HG2	1.89	0.55
1:F:25:GLN:HE21	2:X:8:DT:H3	1.53	0.55
1:B:55:LEU:HD23	1:B:59:LEU:HD12	1.88	0.55
1:C:125:LYS:HE3	1:C:134:VAL:HG13	1.89	0.55
1:F:107:PHE:CE2	1:I:54:LEU:HB2	2.41	0.55
1:F:107:PHE:CD2	1:I:54:LEU:HB2	2.42	0.55
1:C:138:ILE:HD11	1:C:148:LEU:HB2	1.89	0.55
1:F:151:THR:HB	1:F:158:LEU:HB2	1.89	0.55
1:G:140:TYR:OH	1:G:141:ARG:NH2	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4:LEU:HD12	1:A:22:LEU:HD13	1.88	0.55
1:B:17:LYS:NZ	2:L:9:DT:H3	2.04	0.55
1:F:20:ARG:HH22	1:I:204:ARG:CZ	2.19	0.54
1:H:158:LEU:HD13	1:H:173:ARG:HE	1.72	0.54
1:A:49:ARG:NH1	1:D:117:GLU:O	2.40	0.54
1:D:160:ARG:HB3	1:D:160:ARG:NH2	2.23	0.54
1:F:119:ILE:HG12	1:I:49:ARG:NH1	2.23	0.54
1:B:112:PRO:HB2	1:G:144:ASP:OD2	2.08	0.54
1:D:178:VAL:HG13	1:D:182:ARG:HB2	1.89	0.54
1:G:92:TRP:HB3	1:H:92:TRP:HB3	1.90	0.54
1:B:211:ASN:ND2	2:L:1:DT:C2	2.76	0.53
1:D:121:PHE:N	1:D:192:SER:OG	2.34	0.53
1:C:81:GLN:NE2	1:G:124:GLU:HB2	2.23	0.53
1:G:208:ARG:NH1	1:I:199:GLN:OE1	2.40	0.53
2:E:-3:DT:H6	2:E:-3:DT:H5'	1.73	0.53
1:H:4:LEU:HD12	1:H:22:LEU:HD13	1.89	0.53
1:A:120:ARG:HB2	1:A:120:ARG:CZ	2.38	0.53
1:A:141:ARG:NH2	1:D:53:GLU:OE1	2.41	0.52
1:D:120:ARG:HA	1:D:192:SER:HB3	1.92	0.52
1:H:182:ARG:O	1:H:186:PHE:N	2.36	0.52
1:H:186:PHE:O	1:H:189:GLU:HG2	2.09	0.52
1:B:216:LEU:HD11	1:D:173:ARG:HD3	1.91	0.52
1:B:193:ARG:HD2	1:H:93:ARG:HH11	1.74	0.52
1:F:202:GLU:HG2	1:I:19:ARG:HD3	1.91	0.52
1:G:124:GLU:HB3	1:G:137:ARG:HB3	1.91	0.52
1:H:106:ASP:HA	1:H:109:ARG:HH11	1.75	0.52
1:C:12:ALA:HB2	1:C:63:LYS:HB2	1.92	0.51
1:F:140:TYR:OH	1:F:141:ARG:NH2	2.44	0.51
1:B:141:ARG:NH2	1:C:53:GLU:OE2	2.38	0.51
1:B:188:ARG:HB3	1:H:99:GLU:OE1	2.10	0.51
2:E:-1:DT:H4'	2:E:0:DT:OP1	2.10	0.51
1:C:81:GLN:NE2	1:G:139:MET:SD	2.83	0.51
1:D:38:LYS:O	1:D:42:MET:HB2	2.10	0.51
1:B:57:ASN:OD1	1:C:141:ARG:NH2	2.44	0.51
1:G:163:VAL:HG22	1:G:169:LEU:HB2	1.92	0.51
1:A:51:LEU:HD13	1:A:69:ILE:HD13	1.93	0.50
1:H:106:ASP:OD1	1:H:109:ARG:NH1	2.45	0.50
1:G:145:VAL:O	1:G:164:VAL:N	2.37	0.50
1:A:76:ARG:CZ	1:B:-1:ALA:HB2	2.42	0.50
1:D:172:LYS:HD2	1:D:199:GLN:NE2	2.27	0.50
1:F:92:TRP:HB3	1:I:92:TRP:HB3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:124:GLU:OE2	1:F:137:ARG:HD2	2.12	0.50
1:G:51:LEU:HD13	1:G:69:ILE:HD13	1.93	0.50
2:L:3:DT:H2"	2:L:4:DT:H5"	1.93	0.49
1:I:113:ARG:O	1:I:116:GLU:HB3	2.13	0.49
1:D:17:LYS:HZ2	2:E:1:DT:H3	1.59	0.49
1:I:137:ARG:HD3	1:I:144:ASP:OD1	2.12	0.49
1:I:51:LEU:HD13	1:I:69:ILE:HD13	1.93	0.49
1:A:172:LYS:HE3	1:A:199:GLN:OE1	2.13	0.49
1:B:131:VAL:HB	1:D:153:LEU:HD13	1.95	0.49
1:F:124:GLU:OE2	1:F:137:ARG:NH1	2.46	0.49
1:F:140:TYR:CZ	1:F:141:ARG:NH2	2.81	0.48
1:F:114:LEU:HD21	1:I:53:GLU:HG3	1.93	0.48
1:A:163:VAL:HG22	1:A:169:LEU:HB2	1.96	0.48
1:F:205:GLU:HA	1:F:208:ARG:NH1	2.28	0.48
1:D:12:ALA:HB2	1:D:63:LYS:HB2	1.95	0.48
2:L:8:DT:O5'	2:L:9:DT:H72	2.14	0.48
1:C:156:GLU:OE2	1:C:175:ARG:NH1	2.47	0.48
1:G:137:ARG:HH21	1:G:138:ILE:N	2.11	0.48
1:G:216:LEU:HD13	1:I:173:ARG:HH21	1.79	0.48
1:G:197:GLU:HG2	1:G:197:GLU:O	2.14	0.47
1:C:74:GLU:HG2	1:C:76:ARG:HG2	1.95	0.47
1:F:160:ARG:HH21	1:H:212:GLU:CD	2.18	0.47
1:F:193:ARG:O	1:F:196:SER:OG	2.22	0.47
1:A:4:LEU:O	1:A:70:GLN:HA	2.14	0.47
1:A:208:ARG:HG3	1:A:209:VAL:N	2.28	0.47
1:B:172:LYS:HD2	1:B:199:GLN:HE21	1.79	0.47
1:D:139:MET:HA	1:D:145:VAL:HG22	1.97	0.47
1:F:4:LEU:O	1:F:70:GLN:HA	2.15	0.47
1:B:30:ILE:HD11	1:B:40:VAL:HG21	1.97	0.47
1:A:138:ILE:HD11	1:A:148:LEU:HB2	1.96	0.46
1:B:116:GLU:OE2	1:G:143:SER:OG	2.28	0.46
1:F:205:GLU:HA	1:F:208:ARG:HH12	1.80	0.46
1:H:115:LEU:HD23	1:H:115:LEU:HA	1.76	0.46
1:B:149:ILE:HB	1:B:213:ILE:HG23	1.96	0.46
1:F:51:LEU:HD13	1:F:69:ILE:HD13	1.98	0.46
2:L:6:DT:H3'	2:L:7:DT:H5"	1.96	0.46
1:H:30:ILE:HD11	1:H:40:VAL:HG21	1.97	0.46
1:B:140:TYR:OH	1:C:49:ARG:NH1	2.48	0.46
1:B:131:VAL:HG21	1:D:158:LEU:HD11	1.98	0.46
1:F:20:ARG:HH22	1:I:204:ARG:NH2	2.13	0.46
1:A:74:GLU:OE2	1:A:76:ARG:NE	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:158:LEU:HD13	1:G:173:ARG:HE	1.80	0.45
1:A:95:VAL:HG11	1:A:100:ILE:HD11	1.98	0.45
1:A:124:GLU:OE2	1:A:137:ARG:HD2	2.16	0.45
1:F:140:TYR:HB3	1:F:145:VAL:HG11	1.99	0.45
1:C:182:ARG:NH1	1:C:185:ASP:OD2	2.49	0.45
1:F:204:ARG:NH2	1:G:19:ARG:HH22	2.15	0.45
1:I:197:GLU:O	1:I:197:GLU:HG2	2.17	0.45
1:A:20:ARG:HG2	2:L:6:DT:H2"	1.99	0.45
1:G:88:ARG:NE	1:H:97:GLU:OE1	2.50	0.45
1:A:28:ASP:CG	1:B:88:ARG:HH22	2.20	0.45
1:C:11:ALA:O	1:C:14:TYR:HD2	2.00	0.45
1:F:208:ARG:O	1:F:212:GLU:HG3	2.17	0.45
4:A:308:HOH:O	1:D:100:ILE:HG21	2.17	0.44
1:A:212:GLU:OE1	1:C:172:LYS:HE2	2.17	0.44
1:F:19:ARG:HD3	1:I:202:GLU:HG2	1.99	0.44
1:I:56:VAL:O	1:I:60:LYS:HD3	2.17	0.44
2:L:5:DT:H2'	2:L:6:DT:C6	2.53	0.44
1:H:96:PRO:HB2	1:H:99:GLU:HG2	1.99	0.44
1:A:186:PHE:O	1:A:190:SER:OG	2.21	0.44
1:D:4:LEU:O	1:D:70:GLN:HA	2.18	0.44
1:C:63:LYS:HE2	1:C:63:LYS:HB3	1.70	0.44
1:B:205:GLU:OE2	1:D:208:ARG:NE	2.48	0.44
1:C:76:ARG:HH21	1:D:-1:ALA:HB2	1.83	0.44
1:G:137:ARG:HH21	1:G:138:ILE:H	1.66	0.43
1:H:28:ASP:OD2	1:I:70:GLN:NE2	2.44	0.43
1:C:51:LEU:HD13	1:C:69:ILE:HD13	2.00	0.43
1:B:95:VAL:HG11	1:B:100:ILE:HD11	2.00	0.43
1:C:83:ASP:OD1	1:C:85:SER:OG	2.27	0.43
1:I:105:GLU:HG2	1:I:109:ARG:NH1	2.34	0.43
1:I:115:LEU:HD23	1:I:115:LEU:HA	1.79	0.43
1:D:53:GLU:O	1:D:57:ASN:HB2	2.18	0.43
1:F:49:ARG:CZ	1:I:119:ILE:HG12	2.49	0.43
1:G:17:LYS:NZ	2:X:8:DT:OP1	2.47	0.43
1:I:105:GLU:HG2	1:I:109:ARG:HH12	1.83	0.43
1:A:141:ARG:HH22	1:D:57:ASN:ND2	2.16	0.43
1:F:195:PHE:HA	1:F:198:ALA:HB2	2.00	0.43
1:B:216:LEU:HD13	1:D:173:ARG:NH2	2.34	0.42
1:G:55:LEU:HD23	1:G:59:LEU:HD12	2.01	0.42
1:G:63:LYS:HB3	1:G:63:LYS:HE2	1.83	0.42
1:B:25:GLN:NE2	4:B:406:HOH:O	2.52	0.42
1:G:4:LEU:O	1:G:70:GLN:HA	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:107:PHE:CD1	1:D:54:LEU:HB2	2.54	0.42
1:A:28:ASP:OD1	1:B:88:ARG:NH2	2.46	0.42
1:B:151:THR:HA	1:B:152:PRO:HD3	1.87	0.42
1:C:59:LEU:O	1:C:93:ARG:NH2	2.52	0.42
1:D:136:TYR:CE1	1:D:187:VAL:HG21	2.55	0.42
1:H:151:THR:HA	1:H:152:PRO:HD3	1.91	0.42
1:C:110:ALA:O	1:C:114:LEU:HG	2.20	0.42
1:F:179:GLU:OE1	1:F:179:GLU:N	2.53	0.42
1:B:180:ALA:HA	1:B:183:ILE:HG13	2.02	0.42
1:B:212:GLU:O	1:B:216:LEU:HG	2.20	0.42
1:B:138:ILE:HD11	1:B:148:LEU:HB2	2.01	0.42
1:C:124:GLU:CD	1:C:137:ARG:HH21	2.23	0.42
1:I:52:PHE:CE1	1:I:56:VAL:HG21	2.55	0.42
1:A:149:ILE:HB	1:A:213:ILE:HG23	2.02	0.41
1:G:151:THR:HB	1:G:158:LEU:HB2	2.01	0.41
2:L:4:DT:H2'	2:L:5:DT:O4'	2.20	0.41
1:C:70:GLN:NE2	1:D:28:ASP:OD2	2.33	0.41
1:D:51:LEU:HD13	1:D:69:ILE:HD13	2.02	0.41
1:B:137:ARG:HD2	1:B:137:ARG:HA	1.75	0.41
1:H:193:ARG:O	1:H:196:SER:OG	2.30	0.41
1:I:4:LEU:O	1:I:70:GLN:HA	2.20	0.41
1:F:11:ALA:O	1:F:14:TYR:HD2	2.04	0.41
1:C:170:LEU:HD11	1:C:209:VAL:HG21	2.03	0.41
1:D:163:VAL:HG22	1:D:169:LEU:HB2	2.01	0.41
1:G:146:GLY:HA3	1:G:163:VAL:HA	2.03	0.41
1:A:19:ARG:NH1	3:B:301:PO4:O4	2.53	0.41
1:F:111:ALA:HB3	1:F:112:PRO:HD3	2.03	0.41
1:B:4:LEU:O	1:B:70:GLN:HA	2.21	0.41
1:A:27:ARG:NH2	2:L:5:DT:O3'	2.54	0.40
1:A:107:PHE:CE1	1:D:54:LEU:HB2	2.57	0.40
1:A:63:LYS:HE2	1:A:63:LYS:HB3	1.80	0.40
1:D:181:ASP:OD1	1:D:182:ARG:HG2	2.21	0.40
1:F:133:ASP:OD2	1:H:173:ARG:NH1	2.55	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)
1:F:179:GLU:OE1	1:G:76:ARG:NH1[2_855]	2.18	0.02

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	216/237 (91%)	211 (98%)	5 (2%)	0	100	100
1	B	218/237 (92%)	213 (98%)	5 (2%)	0	100	100
1	C	218/237 (92%)	213 (98%)	4 (2%)	1 (0%)	29	61
1	D	217/237 (92%)	210 (97%)	5 (2%)	2 (1%)	17	48
1	F	217/237 (92%)	212 (98%)	5 (2%)	0	100	100
1	G	213/237 (90%)	208 (98%)	5 (2%)	0	100	100
1	H	218/237 (92%)	213 (98%)	5 (2%)	0	100	100
1	I	219/237 (92%)	214 (98%)	5 (2%)	0	100	100
All	All	1736/1896 (92%)	1694 (98%)	39 (2%)	3 (0%)	47	78

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	154	ASN
1	C	0	MET
1	D	120	ARG

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	189/201 (94%)	186 (98%)	3 (2%)	62	86
1	B	190/201 (94%)	187 (98%)	3 (2%)	62	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	C	190/201 (94%)	187 (98%)	3 (2%)	62 86
1	D	189/201 (94%)	186 (98%)	3 (2%)	62 86
1	F	189/201 (94%)	188 (100%)	1 (0%)	88 96
1	G	188/201 (94%)	185 (98%)	3 (2%)	62 86
1	H	190/201 (94%)	186 (98%)	4 (2%)	53 81
1	I	190/201 (94%)	187 (98%)	3 (2%)	62 86
All	All	1515/1608 (94%)	1492 (98%)	23 (2%)	65 87

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	49	ARG
1	A	160	ARG
1	A	204	ARG
1	B	63	LYS
1	B	152	PRO
1	B	204	ARG
1	C	49	ARG
1	C	137	ARG
1	C	179	GLU
1	D	49	ARG
1	D	160	ARG
1	D	197	GLU
1	F	49	ARG
1	G	49	ARG
1	G	76	ARG
1	G	160	ARG
1	H	49	ARG
1	H	120	ARG
1	H	152	PRO
1	H	184	ASP
1	I	49	ARG
1	I	63	LYS
1	I	205	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	81	GLN

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Mol	Chain	Res	Type
1	D	57	ASN
1	I	79	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)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	PO4	B	301	-	4,4,4	0.92	0	6,6,6	0.41	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	301	PO4	1	0

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.