



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 07:43 AM EDT

PDB ID : 2IT0 / pdb_00002it0
Title : Crystal structure of a two-domain IdeR-DNA complex crystal form II
Authors : Wisedchaisri, G.; Chou, C.J.; Wu, M.; Roach, C.; Rice, A.E.; Holmes, R.K.;
Beeson, C.; Hol, W.G.
Deposited on : 2006-10-18
Resolution : 2.60 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 : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

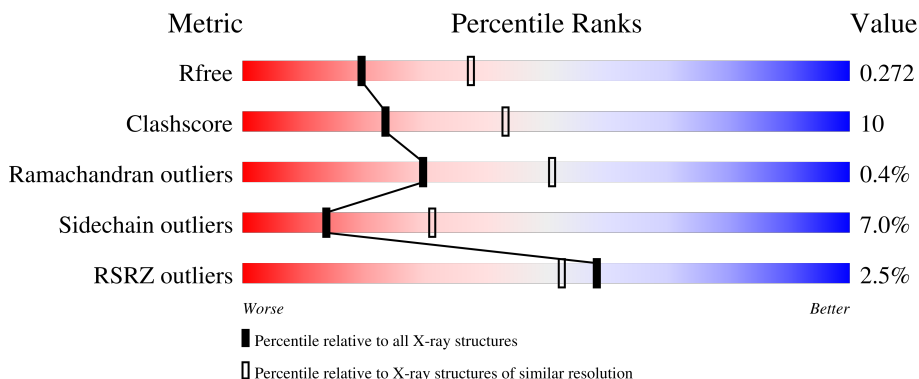
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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}	180053	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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 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 $\leq 5\%$. 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	E	33	
2	F	33	
3	A	157	
3	B	157	
3	C	157	

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Mol	Chain	Length	Quality of chain
3	D	157	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into three segments: a green segment on the left labeled '64%', a yellow segment in the middle labeled '22%', and a grey segment on the right labeled '13%'. A small red square is at the beginning of the bar, and a small black dot is at the end of the grey segment. A '%' symbol is positioned above the bar.</p>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 5916 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 mbtA/mbtB operator strand 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
1	E	33	670	321	117	200	32	0	0	0

- Molecule 2 is a DNA chain called mbtA/mbtB operator strand 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	F	33	677	322	131	192	32	0	0	0

- Molecule 3 is a protein called Iron-dependent repressor ideR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	A	145	1151	720	209	217	5	0	0	0
3	B	145	1155	722	209	219	5	0	0	0
3	C	137	1089	678	200	206	5	0	0	0
3	D	137	1089	678	200	206	5	0	0	0

There are 68 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	141	ALA	-	expression tag	UNP P0A672
A	142	SER	-	expression tag	UNP P0A672
A	143	GLU	-	expression tag	UNP P0A672
A	144	ASN	-	expression tag	UNP P0A672
A	145	LEU	-	expression tag	UNP P0A672
A	146	TYR	-	expression tag	UNP P0A672
A	147	PHE	-	expression tag	UNP P0A672
A	148	GLN	-	expression tag	UNP P0A672

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Chain	Residue	Modelled	Actual	Comment	Reference
A	149	GLY	-	expression tag	UNP P0A672
A	150	GLY	-	expression tag	UNP P0A672
A	151	GLY	-	expression tag	UNP P0A672
A	152	HIS	-	expression tag	UNP P0A672
A	153	HIS	-	expression tag	UNP P0A672
A	154	HIS	-	expression tag	UNP P0A672
A	155	HIS	-	expression tag	UNP P0A672
A	156	HIS	-	expression tag	UNP P0A672
A	157	HIS	-	expression tag	UNP P0A672
B	141	ALA	-	expression tag	UNP P0A672
B	142	SER	-	expression tag	UNP P0A672
B	143	GLU	-	expression tag	UNP P0A672
B	144	ASN	-	expression tag	UNP P0A672
B	145	LEU	-	expression tag	UNP P0A672
B	146	TYR	-	expression tag	UNP P0A672
B	147	PHE	-	expression tag	UNP P0A672
B	148	GLN	-	expression tag	UNP P0A672
B	149	GLY	-	expression tag	UNP P0A672
B	150	GLY	-	expression tag	UNP P0A672
B	151	GLY	-	expression tag	UNP P0A672
B	152	HIS	-	expression tag	UNP P0A672
B	153	HIS	-	expression tag	UNP P0A672
B	154	HIS	-	expression tag	UNP P0A672
B	155	HIS	-	expression tag	UNP P0A672
B	156	HIS	-	expression tag	UNP P0A672
B	157	HIS	-	expression tag	UNP P0A672
C	141	ALA	-	expression tag	UNP P0A672
C	142	SER	-	expression tag	UNP P0A672
C	143	GLU	-	expression tag	UNP P0A672
C	144	ASN	-	expression tag	UNP P0A672
C	145	LEU	-	expression tag	UNP P0A672
C	146	TYR	-	expression tag	UNP P0A672
C	147	PHE	-	expression tag	UNP P0A672
C	148	GLN	-	expression tag	UNP P0A672
C	149	GLY	-	expression tag	UNP P0A672
C	150	GLY	-	expression tag	UNP P0A672
C	151	GLY	-	expression tag	UNP P0A672
C	152	HIS	-	expression tag	UNP P0A672
C	153	HIS	-	expression tag	UNP P0A672
C	154	HIS	-	expression tag	UNP P0A672
C	155	HIS	-	expression tag	UNP P0A672
C	156	HIS	-	expression tag	UNP P0A672

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Chain	Residue	Modelled	Actual	Comment	Reference
C	157	HIS	-	expression tag	UNP P0A672
D	141	ALA	-	expression tag	UNP P0A672
D	142	SER	-	expression tag	UNP P0A672
D	143	GLU	-	expression tag	UNP P0A672
D	144	ASN	-	expression tag	UNP P0A672
D	145	LEU	-	expression tag	UNP P0A672
D	146	TYR	-	expression tag	UNP P0A672
D	147	PHE	-	expression tag	UNP P0A672
D	148	GLN	-	expression tag	UNP P0A672
D	149	GLY	-	expression tag	UNP P0A672
D	150	GLY	-	expression tag	UNP P0A672
D	151	GLY	-	expression tag	UNP P0A672
D	152	HIS	-	expression tag	UNP P0A672
D	153	HIS	-	expression tag	UNP P0A672
D	154	HIS	-	expression tag	UNP P0A672
D	155	HIS	-	expression tag	UNP P0A672
D	156	HIS	-	expression tag	UNP P0A672
D	157	HIS	-	expression tag	UNP P0A672

- Molecule 4 is NICKEL (II) ION (CCD ID: NI) (formula: Ni).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	3	Total Ni 3 3	0	0
4	B	3	Total Ni 3 3	0	0
4	C	3	Total Ni 3 3	0	0
4	D	3	Total Ni 3 3	0	0

- Molecule 5 is ACETATE ION (CCD ID: ACT) (formula: C₂H₃O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0
5	C	1	Total C O 4 2 2	0	0
5	C	1	Total C O 4 2 2	0	0
5	C	1	Total C O 4 2 2	0	0
5	D	1	Total C O 4 2 2	0	0
5	D	1	Total C O 4 2 2	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	E	4	Total O 4 4	0	0
6	F	4	Total O 4 4	0	0

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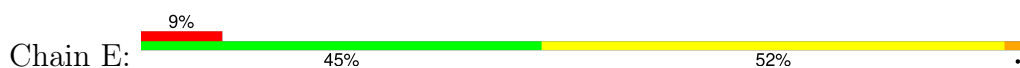
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	6	Total O 6 6	0	0
6	B	10	Total O 10 10	0	0
6	C	4	Total O 4 4	0	0
6	D	5	Total O 5 5	0	0

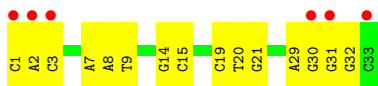
3 Residue-property plots [i](#)

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 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.

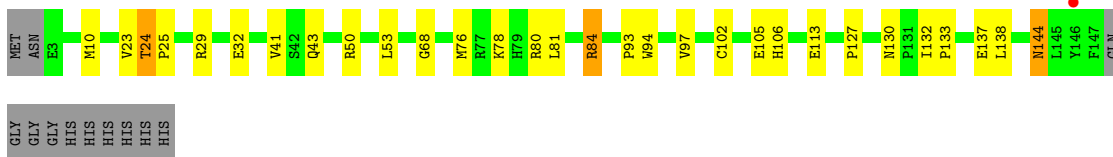
- Molecule 1: mbtA/mbtB operator strand 1



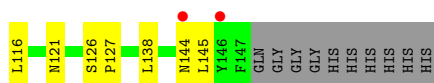
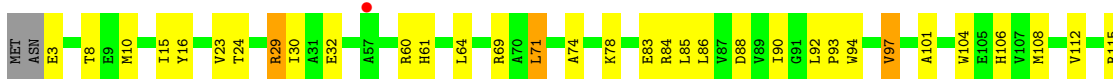
- Molecule 2: mbtA/mbtB operator strand 2



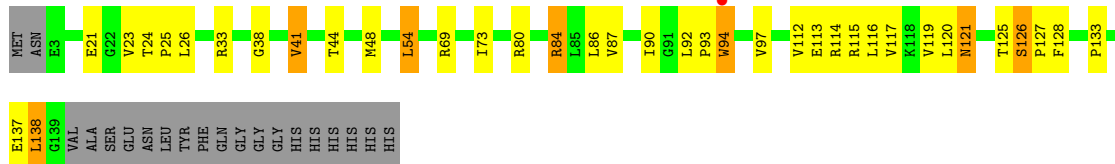
- Molecule 3: Iron-dependent repressor ideR



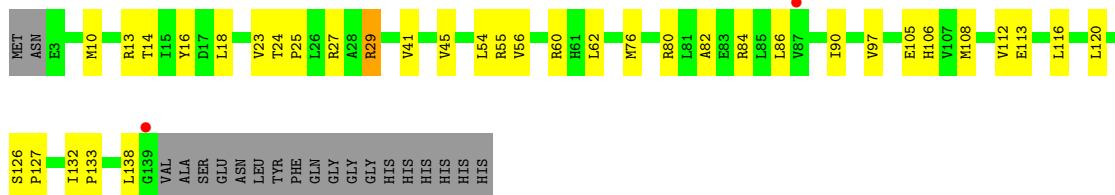
- Molecule 3: Iron-dependent repressor ideR



- Molecule 3: Iron-dependent repressor ideR



• Molecule 3: Iron-dependent repressor ideR



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	54.01Å 70.36Å 79.57Å 108.95° 103.08° 94.84°	Depositor
Resolution (Å)	50.00 – 2.60 50.00 – 2.60	Depositor EDS
% Data completeness (in resolution range)	96.3 (50.00-2.60) 96.3 (50.00-2.60)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	0.13	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.03 (at 2.61Å)	Xtrriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.226 , 0.273 0.227 , 0.272	Depositor DCC
R_{free} test set	1596 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å ²)	29.7	Xtrriage
Anisotropy	0.132	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 39.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	5916	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.04% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	E	0.32	0/749	1.04	2/1154 (0.2%)
2	F	0.31	0/761	0.93	0/1173
3	A	0.50	0/1170	0.81	0/1587
3	B	0.50	0/1174	0.82	0/1592
3	C	0.47	0/1106	0.81	0/1499
3	D	0.47	0/1106	0.78	0/1499
All	All	0.45	0/6066	0.86	2/8504 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	27	DT	C1'-O4'-C4'	-6.05	100.62	109.70
1	E	27	DT	N1-C1'-C2'	5.39	121.58	113.50

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	E	670	0	375	14	0
2	F	677	0	371	17	0
3	A	1151	0	1157	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	1155	0	1161	27	0
3	C	1089	0	1101	24	0
3	D	1089	0	1101	21	0
4	A	3	0	0	0	0
4	B	3	0	0	0	0
4	C	3	0	0	0	0
4	D	3	0	0	0	0
5	A	12	0	9	0	0
5	B	8	0	6	1	0
5	C	12	0	9	0	0
5	D	8	0	6	0	0
6	A	6	0	0	1	0
6	B	10	0	0	3	0
6	C	4	0	0	0	0
6	D	5	0	0	0	0
6	E	4	0	0	0	0
6	F	4	0	0	0	0
All	All	5916	0	5296	113	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 10.

All (113) 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:C:80:ARG:HG2	3:C:126:SER:HB2	1.45	0.96
3:D:16:TYR:HD1	3:D:76:MET:HE2	1.39	0.87
3:D:16:TYR:CD1	3:D:76:MET:HE2	2.10	0.84
3:C:92:LEU:HD12	3:C:93:PRO:HD2	1.67	0.75
3:C:114:ARG:HG3	3:C:138:LEU:HD22	1.69	0.75
2:F:14:DG:H2''	2:F:15:DC:H5'	1.68	0.74
3:A:78:LYS:NZ	3:A:113:GLU:OE2	2.20	0.72
1:E:29:DA:H2''	1:E:30:DG:OP2	1.89	0.71
3:C:94:TRP:O	3:C:97:VAL:HG22	1.89	0.71
1:E:5:DG:H2'	1:E:6:DT:H71	1.73	0.69
1:E:11:DA:H2''	1:E:12:DC:H5'	1.74	0.68
3:C:120:LEU:O	3:C:121:ASN:HB2	1.98	0.63
2:F:30:DG:H2''	2:F:31:DG:OP2	1.99	0.62
3:B:61:HIS:CE1	5:B:2002:ACT:O	2.51	0.62
3:A:137:GLU:OE1	3:A:137:GLU:N	2.29	0.62
1:E:33:DG:OP2	1:E:33:DG:H8	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:73:ILE:HG23	3:C:133:PRO:HB2	1.83	0.60
3:C:21:GLU:OE1	3:C:33:ARG:NH2	2.31	0.60
3:A:29:ARG:HH11	3:A:32:GLU:CD	2.10	0.60
2:F:7:DA:H4'	3:B:60:ARG:HH22	1.67	0.59
1:E:30:DG:H2''	1:E:31:DT:H72	1.84	0.59
3:B:74:ALA:O	3:B:78:LYS:HG3	2.03	0.58
3:B:3:GLU:HB3	6:B:2007:HOH:O	2.04	0.57
3:D:76:MET:HG2	3:D:133:PRO:HG3	1.87	0.56
2:F:2:DA:H2''	2:F:3:DC:OP2	2.06	0.55
3:D:86:LEU:HD23	3:D:90:ILE:HD12	1.89	0.55
3:C:87:VAL:HG22	3:C:97:VAL:HG11	1.88	0.55
2:F:2:DA:H1'	2:F:3:DC:O5'	2.07	0.55
3:A:43:GLN:NE2	6:A:2004:HOH:O	2.40	0.54
2:F:29:DA:H2'	2:F:29:DA:OP2	2.08	0.54
3:D:82:ALA:O	3:D:86:LEU:HG	2.08	0.54
3:D:84:ARG:HB3	3:D:120:LEU:HD13	1.90	0.54
3:B:94:TRP:CH2	3:B:127:PRO:HB2	2.43	0.53
3:C:113:GLU:O	3:C:117:VAL:HG23	2.07	0.53
1:E:32:DG:H2''	1:E:33:DG:OP2	2.09	0.53
3:B:104:TRP:O	3:B:108:MET:HG3	2.08	0.52
2:F:2:DA:H2'	2:F:2:DA:OP2	2.08	0.52
3:C:54:LEU:HD12	3:C:54:LEU:C	2.35	0.52
2:F:7:DA:OP1	3:B:29:ARG:NH2	2.44	0.51
3:A:93:PRO:HD3	3:B:115:ARG:CZ	2.40	0.51
2:F:31:DG:H2''	2:F:32:DG:OP2	2.11	0.50
3:D:27:ARG:HG3	3:D:62:LEU:HD11	1.94	0.50
3:D:80:ARG:HG2	3:D:126:SER:HB3	1.94	0.49
3:B:60:ARG:NE	6:B:2006:HOH:O	2.45	0.48
3:B:86:LEU:HA	3:B:90:ILE:HB	1.96	0.48
3:C:80:ARG:HG2	3:C:126:SER:CB	2.32	0.48
1:E:16:DC:H2'	1:E:17:DT:C6	2.49	0.48
2:F:7:DA:H1'	2:F:8:DA:H5'	1.95	0.48
2:F:19:DC:H2''	2:F:20:DT:H5'	1.95	0.47
3:B:8:THR:HB	6:B:2005:HOH:O	2.13	0.47
3:C:115:ARG:O	3:C:119:VAL:HG23	2.13	0.47
3:B:94:TRP:CZ3	3:B:127:PRO:HB2	2.48	0.47
3:C:112:VAL:O	3:C:116:LEU:HG	2.14	0.47
3:A:93:PRO:HD3	3:B:115:ARG:NE	2.30	0.47
3:A:76:MET:CG	3:A:133:PRO:HG3	2.45	0.47
3:A:76:MET:HG2	3:A:133:PRO:HG3	1.96	0.47
3:A:80:ARG:NH1	3:A:130:ASN:HB3	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:8:DA:H2''	2:F:9:DT:H71	1.96	0.47
3:D:108:MET:HE2	3:D:108:MET:HB3	1.79	0.47
3:C:114:ARG:HG3	3:C:138:LEU:CD2	2.44	0.46
3:C:69:ARG:O	3:C:73:ILE:HG13	2.15	0.46
2:F:1:DC:H2''	2:F:2:DA:OP2	2.14	0.46
2:F:8:DA:H5''	3:B:60:ARG:HD2	1.98	0.46
2:F:7:DA:H4'	3:B:60:ARG:NH2	2.29	0.46
3:C:87:VAL:CG2	3:C:97:VAL:HG11	2.44	0.46
3:D:14:THR:O	3:D:18:LEU:HG	2.16	0.45
3:D:108:MET:HE3	3:D:112:VAL:HG12	1.98	0.45
1:E:21:DC:H2'	1:E:22:DT:C6	2.51	0.45
3:D:80:ARG:HB3	3:D:132:ILE:HG12	1.97	0.45
3:A:105:GLU:HG3	3:A:106:HIS:CE1	2.51	0.45
3:B:92:LEU:HD12	3:B:93:PRO:HD2	1.98	0.45
3:D:108:MET:HE2	3:D:113:GLU:HG3	1.98	0.45
3:B:16:TYR:HE2	3:B:69:ARG:HH12	1.63	0.45
3:B:94:TRP:HA	3:B:97:VAL:HG13	1.98	0.45
3:B:83:GLU:HG3	3:B:101:ALA:CB	2.48	0.44
3:A:144:ASN:ND2	3:A:144:ASN:C	2.75	0.44
3:D:112:VAL:O	3:D:116:LEU:HG	2.18	0.44
1:E:10:DC:H2'	1:E:11:DA:C8	2.51	0.44
3:C:84:ARG:HA	3:C:127:PRO:HG3	1.99	0.44
2:F:14:DG:C2'	2:F:15:DC:H5'	2.43	0.44
3:B:15:ILE:HG21	3:B:64:LEU:HD21	1.99	0.44
3:B:29:ARG:NH1	3:B:32:GLU:OE1	2.51	0.44
3:B:84:ARG:NE	3:B:88:ASP:OD2	2.45	0.44
3:C:24:THR:HA	3:C:25:PRO:HD3	1.83	0.43
3:A:10:MET:HE1	3:A:102:CYS:SG	2.58	0.43
3:A:29:ARG:NE	3:A:29:ARG:HA	2.34	0.43
3:C:126:SER:C	3:C:128:PHE:H	2.26	0.43
3:D:24:THR:HA	3:D:25:PRO:HD3	1.77	0.43
1:E:26:DT:H2''	1:E:27:DT:H6	1.84	0.43
3:A:81:LEU:HD23	3:A:132:ILE:HD13	2.01	0.42
3:B:85:LEU:HD13	3:B:116:LEU:CD2	2.49	0.42
3:A:53:LEU:O	3:A:68:GLY:HA3	2.19	0.42
3:B:10:MET:SD	3:B:106:HIS:CE1	3.11	0.42
1:E:31:DT:H2''	1:E:32:DG:OP2	2.18	0.42
3:D:56:VAL:HG12	3:D:60:ARG:HA	2.01	0.42
3:A:24:THR:HA	3:A:25:PRO:HD3	1.76	0.42
3:C:120:LEU:O	3:C:121:ASN:CB	2.67	0.42
3:C:38:GLY:O	3:C:41:VAL:HG22	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:84:ARG:HG2	3:A:127:PRO:HD3	2.01	0.41
1:E:13:DA:C2	2:F:21:DG:C2	3.08	0.41
3:C:24:THR:HG22	3:C:26:LEU:HG	2.01	0.41
3:C:86:LEU:HD23	3:C:90:ILE:HD12	2.02	0.41
3:D:13:ARG:HD3	3:D:105:GLU:OE1	2.20	0.41
3:D:84:ARG:HG2	3:D:127:PRO:HD3	2.03	0.41
3:C:44:THR:O	3:C:48:MET:HG3	2.20	0.41
1:E:4:DT:OP1	3:D:29:ARG:NH2	2.53	0.41
1:E:5:DG:H2'	1:E:6:DT:C6	2.56	0.41
3:A:50:ARG:O	3:A:50:ARG:HG2	2.19	0.41
3:B:71:LEU:HD23	3:B:71:LEU:HA	1.95	0.40
3:B:29:ARG:NH1	3:B:32:GLU:CD	2.79	0.40
3:B:83:GLU:HG3	3:B:101:ALA:HB2	2.03	0.40
3:D:45:VAL:HG13	3:D:54:LEU:HD11	2.04	0.40
3:D:10:MET:SD	3:D:106:HIS:CE1	3.14	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	A	143/157 (91%)	139 (97%)	4 (3%)	0	100	100
3	B	143/157 (91%)	140 (98%)	3 (2%)	0	100	100
3	C	135/157 (86%)	125 (93%)	8 (6%)	2 (2%)	8	18
3	D	135/157 (86%)	123 (91%)	12 (9%)	0	100	100
All	All	556/628 (88%)	527 (95%)	27 (5%)	2 (0%)	30	51

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	94	TRP
3	C	121	ASN

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	125/135 (93%)	117 (94%)	8 (6%)	16	35
3	B	126/135 (93%)	114 (90%)	12 (10%)	8	18
3	C	119/135 (88%)	111 (93%)	8 (7%)	15	33
3	D	119/135 (88%)	113 (95%)	6 (5%)	22	46
All	All	489/540 (91%)	455 (93%)	34 (7%)	14	31

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	23	VAL
3	A	24	THR
3	A	41	VAL
3	A	84	ARG
3	A	94	TRP
3	A	97	VAL
3	A	138	LEU
3	A	144	ASN
3	B	23	VAL
3	B	24	THR
3	B	29	ARG
3	B	30	ILE
3	B	71	LEU
3	B	97	VAL
3	B	112	VAL
3	B	121	ASN
3	B	126	SER
3	B	138	LEU
3	B	144	ASN
3	B	145	LEU

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Mol	Chain	Res	Type
3	C	23	VAL
3	C	41	VAL
3	C	54	LEU
3	C	84	ARG
3	C	125	THR
3	C	126	SER
3	C	137	GLU
3	C	138	LEU
3	D	23	VAL
3	D	29	ARG
3	D	41	VAL
3	D	55	ARG
3	D	97	VAL
3	D	138	LEU

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

Mol	Chain	Res	Type
3	A	43	GLN
3	A	130	ASN
3	A	144	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 22 ligands modelled in this entry, 12 are monoatomic - leaving 10 for Mogul analysis.

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
5	ACT	C	2003	4	3,3,3	0.74	0	3,3,3	1.59	0
5	ACT	A	2003	4	3,3,3	0.89	0	3,3,3	1.11	0
5	ACT	B	2002	4	3,3,3	0.85	0	3,3,3	1.66	1 (33%)
5	ACT	A	2002	4	3,3,3	0.85	0	3,3,3	1.34	0
5	ACT	C	2002	4	3,3,3	0.89	0	3,3,3	1.33	0
5	ACT	B	2001	4	3,3,3	0.82	0	3,3,3	1.42	0
5	ACT	D	2001	4	3,3,3	0.83	0	3,3,3	1.50	0
5	ACT	A	2001	4	3,3,3	0.75	0	3,3,3	1.55	1 (33%)
5	ACT	D	2002	4	3,3,3	0.93	0	3,3,3	1.35	0
5	ACT	C	2001	4	3,3,3	0.79	0	3,3,3	1.48	0

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	2002	ACT	OXT-C-O	-2.18	113.92	122.03
5	A	2001	ACT	OXT-C-CH3	2.04	123.60	115.05

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
5	B	2002	ACT	1	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	E	33/33 (100%)	0.26	3 (9%) 15 11	10, 27, 62, 65	0
2	F	33/33 (100%)	0.35	6 (18%) 3 3	12, 24, 66, 71	0
3	A	145/157 (92%)	-0.03	1 (0%) 84 82	10, 21, 32, 39	0
3	B	145/157 (92%)	0.09	3 (2%) 63 58	10, 22, 37, 41	0
3	C	137/157 (87%)	0.02	1 (0%) 84 82	12, 24, 34, 43	0
3	D	137/157 (87%)	0.15	2 (1%) 72 68	17, 24, 35, 39	0
All	All	630/694 (90%)	0.08	16 (2%) 58 52	10, 23, 38, 71	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	1	DC	3.3
1	E	33	DG	3.2
1	E	32	DG	3.1
2	F	33	DC	2.6
2	F	30	DG	2.6
3	C	94	TRP	2.5
3	D	139	GLY	2.5
2	F	2	DA	2.4
1	E	31	DT	2.4
2	F	31	DG	2.3
3	A	146	TYR	2.3
3	B	144	ASN	2.2
3	B	57	ALA	2.1
3	D	87	VAL	2.1
2	F	3	DC	2.0
3	B	146	TYR	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	ACT	A	2001	4/4	0.73	0.23	24,25,26,27	0
5	ACT	D	2002	4/4	0.73	0.19	26,27,28,29	0
5	ACT	C	2002	4/4	0.78	0.17	21,22,22,23	0
5	ACT	C	2001	4/4	0.79	0.27	38,39,39,40	0
5	ACT	D	2001	4/4	0.80	0.19	28,28,29,30	0
5	ACT	A	2002	4/4	0.80	0.28	40,40,41,41	0
5	ACT	B	2001	4/4	0.83	0.18	16,16,18,18	0
5	ACT	C	2003	4/4	0.83	0.20	19,19,20,21	0
5	ACT	A	2003	4/4	0.86	0.14	19,20,20,21	0
4	NI	B	1003	1/1	0.93	0.08	42,42,42,42	0
5	ACT	B	2002	4/4	0.96	0.11	8,11,11,12	0
4	NI	C	1003	1/1	0.96	0.07	23,23,23,23	0
4	NI	D	1003	1/1	0.97	0.08	37,37,37,37	0
4	NI	A	1003	1/1	0.98	0.05	29,29,29,29	0
4	NI	D	1002	1/1	0.99	0.04	19,19,19,19	0
4	NI	B	1002	1/1	0.99	0.03	16,16,16,16	0
4	NI	A	1002	1/1	0.99	0.02	15,15,15,15	0
4	NI	C	1001	1/1	0.99	0.02	27,27,27,27	0
4	NI	A	1001	1/1	0.99	0.03	20,20,20,20	0
4	NI	D	1001	1/1	0.99	0.04	25,25,25,25	0
4	NI	B	1001	1/1	1.00	0.03	16,16,16,16	0
4	NI	C	1002	1/1	1.00	0.02	19,19,19,19	0

6.5 Other polymers [i](#)

There are no such residues in this entry.