



# Full wwPDB X-ray Structure Validation Report ⓘ

May 18, 2020 – 06:07 pm BST

PDB ID : 4HUH  
Title : Structure of the bacteriophage T4 tail terminator protein, gp15 (C-terminal truncation mutant 1-261).  
Authors : Fokine, A.; Zhang, Z.; Kanamaru, S.; Bowman, V.D.; Aksyuk, A.; Arisaka, F.; Rao, V.B.; Rossmann, M.G.  
Deposited on : 2012-11-02  
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](mailto: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.

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

MolProbity : 4.02b-467  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
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) : 2.11

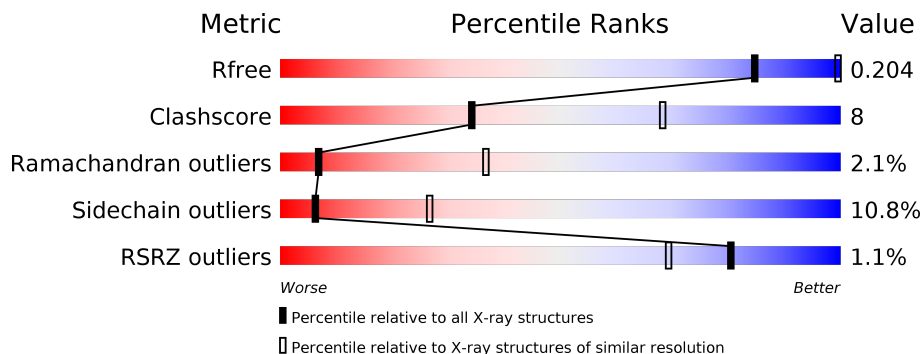
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 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.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	A	261	
1	B	261	
1	C	261	
1	D	261	
1	E	261	
1	F	261	

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 10145 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.

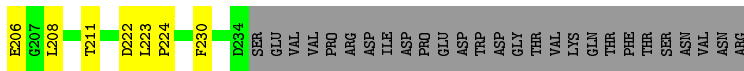
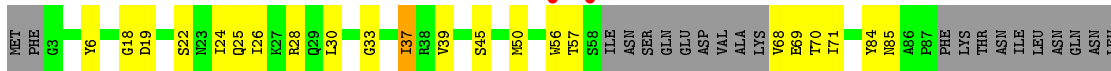
- Molecule 1 is a protein called Tail connector protein Gp15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	211	Total 1742	C 1123	N 283	O 328	S 8	0	0	0
1	B	202	Total 1673	C 1082	N 271	O 312	S 8	0	0	0
1	C	202	Total 1674	C 1083	N 271	O 312	S 8	0	0	0
1	D	202	Total 1673	C 1082	N 271	O 312	S 8	0	0	0
1	E	206	Total 1702	C 1102	N 276	O 316	S 8	0	0	0
1	F	203	Total 1681	C 1088	N 272	O 313	S 8	0	0	0

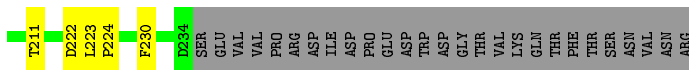
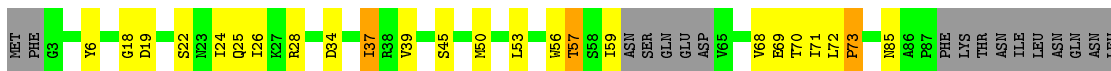




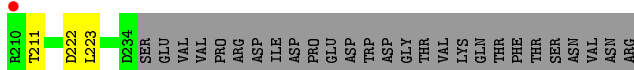
- Molecule 1: Tail connector protein Gp15



- Molecule 1: Tail connector protein Gp15



- Molecule 1: Tail connector protein Gp15



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	65.87Å 76.31Å 93.89Å 109.04° 104.62° 89.30°	Depositor
Resolution (Å)	45.91 – 3.20 49.64 – 3.20	Depositor EDS
% Data completeness (in resolution range)	91.7 (45.91-3.20) 91.8 (49.64-3.20)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.86 (at 3.19Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, $R_{free}$	0.171 , 0.202 0.176 , 0.204	Depositor DCC
$R_{free}$ test set	1277 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	61.0	Xtrriage
Anisotropy	0.819	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 62.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	10145	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	62.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.06% of the height of the origin peak. No significant pseudotranslation is detected.*

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

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 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	A	0.45	0/1787	0.60	0/2421
1	B	0.45	0/1717	0.60	0/2325
1	C	0.45	0/1718	0.61	0/2326
1	D	0.47	0/1717	0.61	0/2325
1	E	0.45	0/1746	0.63	1/2364 (0.0%)
1	F	0.46	0/1725	0.60	0/2336
All	All	0.45	0/10410	0.61	1/14097 (0.0%)

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	E	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	E	73	PRO	N-CA-C	-5.38	98.12	112.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	E	72	LEU	Peptide

## 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	1742	0	1673	30	0
1	B	1673	0	1605	29	0
1	C	1674	0	1607	33	0
1	D	1673	0	1605	28	0
1	E	1702	0	1643	26	0
1	F	1681	0	1616	24	0
All	All	10145	0	9749	168	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 8.

All (168) 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:C:109:TYR:HB3	1:C:161:ARG:HH22	1.41	0.86
1:B:108:GLN:HB3	1:B:200:PRO:HD2	1.63	0.80
1:F:109:TYR:HB3	1:F:161:ARG:HH22	1.46	0.79
1:B:109:TYR:HB3	1:B:161:ARG:HH22	1.48	0.79
1:A:109:TYR:HB3	1:A:161:ARG:HH22	1.47	0.78
1:F:106:VAL:HG22	1:F:107:SER:H	1.48	0.78
1:D:109:TYR:HB3	1:D:161:ARG:HH22	1.49	0.78
1:E:109:TYR:HB3	1:E:161:ARG:HH22	1.49	0.76
1:C:106:VAL:HG22	1:C:107:SER:H	1.49	0.75
1:F:151:GLU:OE2	1:F:161:ARG:NH1	2.22	0.72
1:C:108:GLN:HB3	1:C:200:PRO:HD2	1.75	0.69
1:A:108:GLN:HB3	1:A:200:PRO:HD2	1.73	0.69
1:A:151:GLU:OE2	1:A:161:ARG:NH1	2.23	0.69
1:E:108:GLN:HB3	1:E:200:PRO:HD2	1.73	0.69
1:E:151:GLU:OE2	1:E:161:ARG:NH1	2.24	0.68
1:B:151:GLU:OE2	1:B:161:ARG:NH1	2.24	0.67
1:D:108:GLN:HB3	1:D:200:PRO:HD2	1.77	0.65
1:D:151:GLU:OE2	1:D:161:ARG:NH1	2.25	0.64
1:D:19:ASP:HA	1:D:22:SER:HB2	1.80	0.64
1:F:19:ASP:HA	1:F:22:SER:HB2	1.80	0.64
1:A:19:ASP:HA	1:A:22:SER:HB2	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:106:VAL:HG12	1:B:107:SER:H	1.62	0.63
1:C:151:GLU:OE2	1:C:161:ARG:NH1	2.26	0.63
1:E:19:ASP:HA	1:E:22:SER:HB2	1.81	0.62
1:E:106:VAL:HG12	1:E:107:SER:H	1.65	0.62
1:B:19:ASP:HA	1:B:22:SER:HB2	1.81	0.62
1:C:19:ASP:HA	1:C:22:SER:HB2	1.83	0.59
1:D:85:ASN:OD1	1:D:115:LYS:HE3	2.03	0.58
1:F:85:ASN:OD1	1:F:115:LYS:HE3	2.04	0.58
1:E:85:ASN:OD1	1:E:115:LYS:HE3	2.05	0.57
1:E:124:THR:HG21	1:E:130:MET:HG2	1.87	0.57
1:B:85:ASN:OD1	1:B:115:LYS:HE3	2.04	0.57
1:D:69:GLU:OE2	1:D:126:TYR:OH	2.19	0.56
1:C:85:ASN:OD1	1:C:115:LYS:HE3	2.05	0.56
1:D:26:ILE:HD11	1:D:37:ILE:HD11	1.88	0.56
1:F:108:GLN:HB3	1:F:200:PRO:HD2	1.86	0.56
1:A:85:ASN:OD1	1:A:115:LYS:HE3	2.06	0.55
1:E:69:GLU:OE2	1:E:126:TYR:OH	2.18	0.55
1:B:114:ILE:HG12	1:B:115:LYS:H	1.72	0.54
1:A:149:MET:HE2	1:A:163:ILE:HG13	1.88	0.54
1:D:149:MET:HE2	1:D:163:ILE:HG13	1.90	0.54
1:C:149:MET:HE2	1:C:163:ILE:HG13	1.89	0.54
1:B:149:MET:HE2	1:B:163:ILE:HG13	1.89	0.53
1:B:124:THR:HG21	1:B:130:MET:HG2	1.90	0.53
1:B:114:ILE:HG12	1:B:115:LYS:N	2.24	0.52
1:C:26:ILE:HD11	1:C:37:ILE:HD11	1.91	0.52
1:E:149:MET:HE2	1:E:163:ILE:HG13	1.91	0.51
1:A:114:ILE:HG12	1:A:115:LYS:N	2.26	0.51
1:C:114:ILE:HG12	1:C:115:LYS:N	2.26	0.50
1:A:124:THR:HG21	1:A:130:MET:HG2	1.93	0.50
1:C:6:TYR:CD2	1:C:208:LEU:HG	2.46	0.50
1:D:222:ASP:N	1:D:222:ASP:OD1	2.44	0.50
1:C:114:ILE:HG12	1:C:115:LYS:H	1.76	0.50
1:A:64:ASP:O	1:A:67:LYS:N	2.45	0.50
1:D:168:MET:HB2	1:D:191:THR:HG22	1.93	0.50
1:D:56:TRP:HB3	1:D:71:ILE:HD13	1.94	0.50
1:C:222:ASP:N	1:C:222:ASP:OD1	2.45	0.49
1:A:222:ASP:N	1:A:222:ASP:OD1	2.44	0.49
1:A:114:ILE:HG12	1:A:115:LYS:H	1.77	0.49
1:D:6:TYR:CD2	1:D:208:LEU:HG	2.47	0.49
1:F:124:THR:HG21	1:F:130:MET:HG2	1.95	0.49
1:C:69:GLU:OE2	1:C:126:TYR:OH	2.25	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:108:GLN:CB	1:B:199:TYR:HB2	2.43	0.49
1:E:147:THR:HG23	1:E:163:ILE:HB	1.94	0.49
1:D:124:THR:HG21	1:D:130:MET:HG2	1.95	0.49
1:C:168:MET:HB2	1:C:191:THR:HG22	1.95	0.48
1:C:124:THR:HG21	1:C:130:MET:HG2	1.95	0.48
1:F:222:ASP:N	1:F:222:ASP:OD1	2.44	0.48
1:F:109:TYR:HB3	1:F:161:ARG:NH2	2.23	0.48
1:A:147:THR:HG23	1:A:163:ILE:HB	1.95	0.48
1:A:30:LEU:HB2	1:A:33:GLY:O	2.14	0.48
1:E:26:ILE:HD11	1:E:37:ILE:HD11	1.94	0.48
1:F:30:LEU:HB2	1:F:33:GLY:O	2.14	0.48
1:C:53:LEU:O	1:C:57:THR:HB	2.14	0.47
1:F:149:MET:HE2	1:F:163:ILE:HG13	1.96	0.47
1:B:26:ILE:HD11	1:B:37:ILE:HD11	1.95	0.47
1:E:168:MET:HB2	1:E:191:THR:HG22	1.96	0.47
1:F:26:ILE:HD11	1:F:37:ILE:HD11	1.96	0.47
1:F:6:TYR:CD2	1:F:208:LEU:HG	2.49	0.47
1:B:56:TRP:HB3	1:B:71:ILE:HD13	1.96	0.47
1:C:106:VAL:HG22	1:C:107:SER:N	2.22	0.47
1:C:106:VAL:CG2	1:C:107:SER:H	2.22	0.47
1:F:108:GLN:HB3	1:F:199:TYR:HB2	1.95	0.47
1:D:114:ILE:HG12	1:D:115:LYS:N	2.30	0.47
1:E:223:LEU:HA	1:E:224:PRO:HD3	1.80	0.46
1:A:26:ILE:HD11	1:A:37:ILE:HD11	1.95	0.46
1:D:114:ILE:HG12	1:D:115:LYS:H	1.80	0.46
1:F:56:TRP:HB3	1:F:71:ILE:HD13	1.96	0.46
1:A:12:ARG:NH2	1:A:199:TYR:OH	2.49	0.46
1:B:222:ASP:OD1	1:B:222:ASP:N	2.47	0.46
1:C:12:ARG:NH2	1:C:199:TYR:OH	2.49	0.46
1:F:147:THR:HG23	1:F:163:ILE:HB	1.96	0.46
1:A:61:SER:O	1:A:64:ASP:HB2	2.16	0.46
1:A:67:LYS:O	1:A:68:VAL:HG23	2.15	0.46
1:D:24:ILE:O	1:D:39:VAL:HG23	2.16	0.46
1:E:114:ILE:HG12	1:E:115:LYS:H	1.80	0.46
1:E:56:TRP:HB3	1:E:71:ILE:HD13	1.97	0.46
1:E:108:GLN:CB	1:E:199:TYR:HB2	2.46	0.45
1:A:114:ILE:HD12	1:A:198:MET:HE3	1.98	0.45
1:E:203:ASP:OD1	1:E:204:ASP:N	2.49	0.45
1:A:109:TYR:HB3	1:A:161:ARG:NH2	2.25	0.45
1:C:56:TRP:HB3	1:C:71:ILE:HD13	1.97	0.45
1:E:114:ILE:HG12	1:E:115:LYS:N	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:203:ASP:OD1	1:A:204:ASP:N	2.49	0.45
1:E:6:TYR:CD2	1:E:208:LEU:HG	2.51	0.45
1:F:106:VAL:CG2	1:F:107:SER:H	2.26	0.45
1:F:114:ILE:HG12	1:F:115:LYS:N	2.31	0.45
1:A:106:VAL:HG12	1:A:107:SER:H	1.82	0.45
1:A:56:TRP:HB3	1:A:71:ILE:HD13	1.99	0.45
1:C:24:ILE:O	1:C:39:VAL:HG23	2.17	0.45
1:F:114:ILE:HG12	1:F:115:LYS:H	1.81	0.45
1:C:108:GLN:CB	1:C:199:TYR:HB2	2.47	0.45
1:F:203:ASP:OD1	1:F:204:ASP:N	2.50	0.45
1:D:30:LEU:HB2	1:D:33:GLY:O	2.17	0.44
1:F:168:MET:HB2	1:F:191:THR:HG22	2.00	0.44
1:D:211:THR:HB	1:D:223:LEU:HB3	2.00	0.44
1:A:108:GLN:CB	1:A:199:TYR:HB2	2.47	0.44
1:B:114:ILE:HD12	1:B:198:MET:HE3	2.00	0.44
1:B:53:LEU:O	1:B:57:THR:HB	2.18	0.44
1:B:147:THR:HG23	1:B:163:ILE:HB	2.00	0.44
1:D:114:ILE:HD12	1:D:198:MET:HE3	1.99	0.44
1:B:6:TYR:CD2	1:B:208:LEU:HG	2.53	0.43
1:D:147:THR:HG23	1:D:163:ILE:HB	1.99	0.43
1:E:124:THR:CB	1:E:130:MET:HG2	2.49	0.43
1:D:223:LEU:HA	1:D:224:PRO:HD3	1.80	0.43
1:C:223:LEU:HA	1:C:224:PRO:HD3	1.82	0.43
1:D:110:ASN:HA	1:D:111:PRO:HD3	1.73	0.43
1:E:222:ASP:OD1	1:E:222:ASP:N	2.48	0.43
1:B:136:GLN:HG3	1:C:201:PRO:HG2	2.01	0.43
1:D:124:THR:CB	1:D:130:MET:HG2	2.49	0.43
1:C:203:ASP:OD1	1:C:204:ASP:N	2.52	0.43
1:E:53:LEU:O	1:E:57:THR:HB	2.19	0.43
1:A:6:TYR:CD2	1:A:208:LEU:HG	2.54	0.42
1:D:106:VAL:HG12	1:D:107:SER:H	1.83	0.42
1:E:110:ASN:HA	1:E:111:PRO:HD3	1.76	0.42
1:C:147:THR:HG23	1:C:163:ILE:HB	2.01	0.42
1:C:108:GLN:HB3	1:C:199:TYR:HB2	2.01	0.42
1:C:109:TYR:HB3	1:C:161:ARG:NH2	2.22	0.42
1:A:110:ASN:HA	1:A:111:PRO:HD3	1.75	0.42
1:B:124:THR:CB	1:B:130:MET:HG2	2.50	0.42
1:B:24:ILE:O	1:B:39:VAL:HG23	2.19	0.42
1:B:69:GLU:OE2	1:B:126:TYR:OH	2.20	0.42
1:D:203:ASP:OD1	1:D:204:ASP:N	2.52	0.42
1:A:59:ILE:HG13	1:A:59:ILE:H	1.51	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:203:ASP:OD1	1:B:204:ASP:N	2.53	0.42
1:E:18:GLY:HA3	1:E:230:PHE:CZ	2.55	0.42
1:A:168:MET:HB2	1:A:191:THR:HG22	2.02	0.42
1:C:211:THR:HB	1:C:223:LEU:HB3	2.00	0.42
1:F:24:ILE:O	1:F:39:VAL:HG23	2.19	0.42
1:D:18:GLY:HA3	1:D:230:PHE:CZ	2.55	0.42
1:B:109:TYR:HB3	1:B:161:ARG:NH2	2.24	0.41
1:B:151:GLU:OE2	1:B:161:ARG:HD2	2.20	0.41
1:A:18:GLY:HA3	1:A:230:PHE:CZ	2.54	0.41
1:A:108:GLN:HB3	1:A:199:TYR:HB2	2.02	0.41
1:B:211:THR:HB	1:B:223:LEU:HB3	2.01	0.41
1:E:211:THR:HB	1:E:223:LEU:HB3	2.03	0.41
1:B:168:MET:HB2	1:B:191:THR:HG22	2.02	0.41
1:B:18:GLY:HA3	1:B:230:PHE:CZ	2.56	0.41
1:C:114:ILE:HD12	1:C:198:MET:HE3	2.03	0.41
1:C:142:GLN:HB3	1:D:84:TYR:CE1	2.55	0.41
1:A:211:THR:HB	1:A:223:LEU:HB3	2.03	0.41
1:B:12:ARG:NH2	1:B:199:TYR:OH	2.54	0.41
1:F:110:ASN:HA	1:F:111:PRO:HD3	1.70	0.41
1:F:211:THR:HB	1:F:223:LEU:HB3	2.04	0.40
1:C:18:GLY:HA3	1:C:230:PHE:CZ	2.57	0.40
1:C:130:MET:HE2	1:C:130:MET:HB3	1.94	0.40
1:D:108:GLN:CB	1:D:199:TYR:HB2	2.51	0.40
1:E:24:ILE:O	1:E:39:VAL:HG23	2.21	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
1	A	205/261 (78%)	181 (88%)	17 (8%)	7 (3%)	<b>3</b>   <b>24</b>

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	194/261 (74%)	175 (90%)	14 (7%)	5 (3%)	5	31
1	C	194/261 (74%)	176 (91%)	15 (8%)	3 (2%)	10	44
1	D	194/261 (74%)	176 (91%)	14 (7%)	4 (2%)	7	37
1	E	198/261 (76%)	178 (90%)	16 (8%)	4 (2%)	7	38
1	F	195/261 (75%)	177 (91%)	16 (8%)	2 (1%)	15	54
All	All	1180/1566 (75%)	1063 (90%)	92 (8%)	25 (2%)	7	37

All (25) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	65	VAL
1	B	108	GLN
1	D	108	GLN
1	E	108	GLN
1	A	67	LYS
1	A	108	GLN
1	C	108	GLN
1	D	106	VAL
1	A	68	VAL
1	D	111	PRO
1	A	106	VAL
1	B	109	TYR
1	E	73	PRO
1	A	111	PRO
1	C	111	PRO
1	E	106	VAL
1	E	111	PRO
1	B	106	VAL
1	B	111	PRO
1	C	154	GLY
1	F	111	PRO
1	A	154	GLY
1	B	154	GLY
1	D	154	GLY
1	F	154	GLY

### 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	192/240 (80%)	168 (88%)	24 (12%)	4	21
1	B	184/240 (77%)	165 (90%)	19 (10%)	7	29
1	C	184/240 (77%)	167 (91%)	17 (9%)	9	33
1	D	184/240 (77%)	164 (89%)	20 (11%)	6	26
1	E	187/240 (78%)	166 (89%)	21 (11%)	6	25
1	F	185/240 (77%)	165 (89%)	20 (11%)	6	27
All	All	1116/1440 (78%)	995 (89%)	121 (11%)	6	27

All (121) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	25	GLN
1	A	28	ARG
1	A	34	ASP
1	A	37	ILE
1	A	45	SER
1	A	50	MET
1	A	57	THR
1	A	59	ILE
1	A	62	GLN
1	A	64	ASP
1	A	67	LYS
1	A	68	VAL
1	A	70	THR
1	A	106	VAL
1	A	110	ASN
1	A	114	ILE
1	A	124	THR
1	A	125	ARG
1	A	127	GLU
1	A	138	LEU
1	A	161	ARG
1	A	184	ARG
1	A	190	LEU
1	A	206	GLU
1	B	25	GLN
1	B	28	ARG

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	B	34	ASP
1	B	37	ILE
1	B	45	SER
1	B	50	MET
1	B	57	THR
1	B	68	VAL
1	B	70	THR
1	B	110	ASN
1	B	114	ILE
1	B	124	THR
1	B	125	ARG
1	B	127	GLU
1	B	138	LEU
1	B	161	ARG
1	B	184	ARG
1	B	190	LEU
1	B	206	GLU
1	C	25	GLN
1	C	28	ARG
1	C	37	ILE
1	C	45	SER
1	C	50	MET
1	C	57	THR
1	C	70	THR
1	C	109	TYR
1	C	110	ASN
1	C	114	ILE
1	C	124	THR
1	C	125	ARG
1	C	138	LEU
1	C	161	ARG
1	C	184	ARG
1	C	190	LEU
1	C	206	GLU
1	D	25	GLN
1	D	28	ARG
1	D	37	ILE
1	D	45	SER
1	D	50	MET
1	D	57	THR
1	D	68	VAL
1	D	70	THR

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	D	106	VAL
1	D	109	TYR
1	D	110	ASN
1	D	114	ILE
1	D	124	THR
1	D	125	ARG
1	D	127	GLU
1	D	138	LEU
1	D	161	ARG
1	D	184	ARG
1	D	190	LEU
1	D	206	GLU
1	E	25	GLN
1	E	28	ARG
1	E	34	ASP
1	E	37	ILE
1	E	45	SER
1	E	50	MET
1	E	57	THR
1	E	59	ILE
1	E	68	VAL
1	E	70	THR
1	E	109	TYR
1	E	110	ASN
1	E	114	ILE
1	E	124	THR
1	E	125	ARG
1	E	127	GLU
1	E	138	LEU
1	E	161	ARG
1	E	184	ARG
1	E	190	LEU
1	E	206	GLU
1	F	25	GLN
1	F	28	ARG
1	F	30	LEU
1	F	37	ILE
1	F	45	SER
1	F	50	MET
1	F	57	THR
1	F	59	ILE
1	F	70	THR

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Mol	Chain	Res	Type
1	F	109	TYR
1	F	110	ASN
1	F	114	ILE
1	F	124	THR
1	F	125	ARG
1	F	127	GLU
1	F	138	LEU
1	F	161	ARG
1	F	184	ARG
1	F	190	LEU
1	F	206	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled '#RSRZ > 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q < 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2	OWAB(Å <sup>2</sup> )	Q < 0.9
1	A	211/261 (80%)	-0.05	1 (0%) 91 86	20, 56, 113, 151	0
1	B	202/261 (77%)	-0.05	1 (0%) 91 86	20, 54, 112, 145	0
1	C	202/261 (77%)	-0.03	2 (0%) 82 72	20, 55, 115, 145	0
1	D	202/261 (77%)	0.00	4 (1%) 65 51	20, 55, 115, 145	0
1	E	206/261 (78%)	-0.09	2 (0%) 82 72	20, 57, 126, 154	0
1	F	203/261 (77%)	0.02	3 (1%) 73 61	20, 57, 119, 160	0
All	All	1226/1566 (78%)	-0.03	13 (1%) 80 69	20, 56, 119, 160	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	183	ARG	7.1
1	C	183	ARG	5.7
1	F	183	ARG	5.3
1	A	183	ARG	5.1
1	D	177	ASP	3.1
1	E	183	ARG	2.8
1	C	56	TRP	2.8
1	F	210	ARG	2.8
1	F	105	VAL	2.7
1	D	56	TRP	2.4
1	B	177	ASP	2.2
1	E	177	ASP	2.2
1	D	58	SER	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.