



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 15, 2020 – 10:47 pm BST

PDB ID : 2DNS
Title : The crystal structure of D-amino acid amidase from Ochrobactrum anthropi SV3 complexed with D-Phenylalanine
Authors : Okazaki, S.; Suzuki, A.; Komeda, H.; Asano, Y.; Yamane, T.
Deposited on : 2006-04-26
Resolution : 2.40 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 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

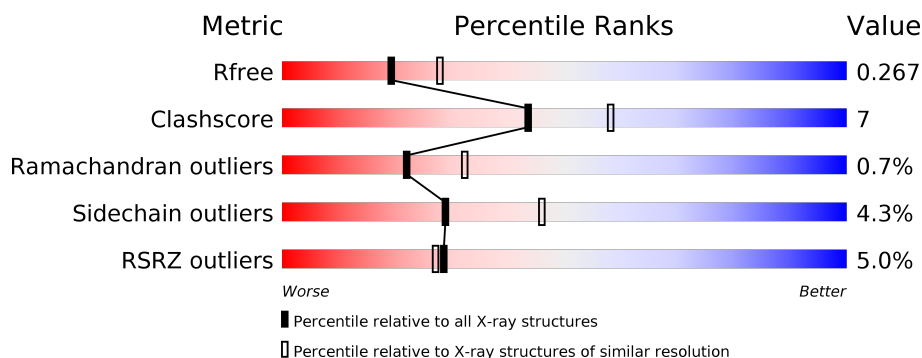
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria 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	363	<div> <div>%</div> <div> <div></div> <div>84%</div> <div>14%</div> <div>•</div> </div> </div>
1	B	363	<div> <div>3%</div> <div> <div></div> <div>88%</div> <div>10%</div> <div>•</div> </div> </div>
1	C	363	<div> <div>2%</div> <div> <div></div> <div>87%</div> <div>11%</div> <div>••</div> </div> </div>
1	D	363	<div> <div>%</div> <div> <div></div> <div>88%</div> <div>10%</div> <div>•</div> </div> </div>
1	E	363	<div> <div>4%</div> <div> <div></div> <div>75%</div> <div>18%</div> <div>••</div> </div> </div>
1	F	363	<div> <div>18%</div> <div> <div></div> <div>60%</div> <div>21%</div> <div>•</div> <div>17%</div> </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 17094 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.

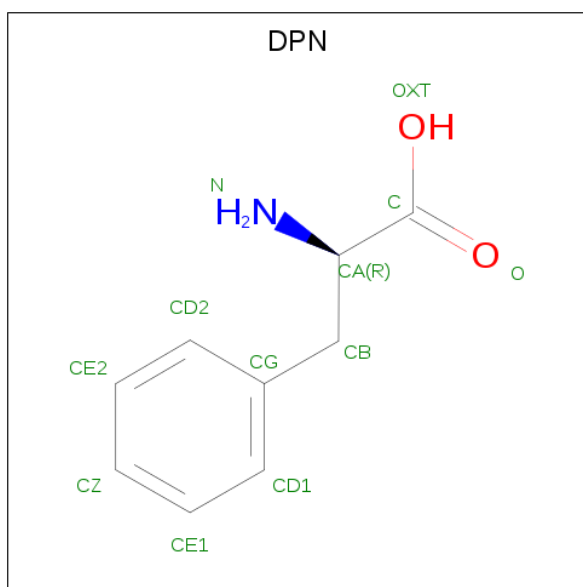
- Molecule 1 is a protein called D-amino acid amidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	362	Total	C	N	O	S	0	0	0
			2811	1775	486	534	16			
1	B	362	Total	C	N	O	S	0	3	0
			2841	1791	496	538	16			
1	C	360	Total	C	N	O	S	0	0	0
			2799	1769	484	530	16			
1	D	355	Total	C	N	O	S	0	2	0
			2772	1756	479	519	18			
1	E	349	Total	C	N	O	S	0	0	0
			2709	1715	467	511	16			
1	F	300	Total	C	N	O	S	0	0	0
			2342	1483	405	439	15			

- Molecule 2 is BARIUM ION (three-letter code: BA) (formula: Ba).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	4	Total	Ba	0	0
			4	4		
2	E	2	Total	Ba	0	0
			2	2		
2	B	2	Total	Ba	0	0
			2	2		
2	C	4	Total	Ba	0	0
			4	4		
2	A	5	Total	Ba	0	0
			5	5		
2	F	3	Total	Ba	0	0
			3	3		

- Molecule 3 is D-PHENYLALANINE (three-letter code: DPN) (formula: C₉H₁₁NO₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			11	9	1	1		
3	B	1	Total	C	N	O	0	0
			11	9	1	1		
3	C	1	Total	C	N	O	0	0
			11	9	1	1		
3	D	1	Total	C	N	O	0	0
			11	9	1	1		
3	E	1	Total	C	N	O	0	0
			11	9	1	1		

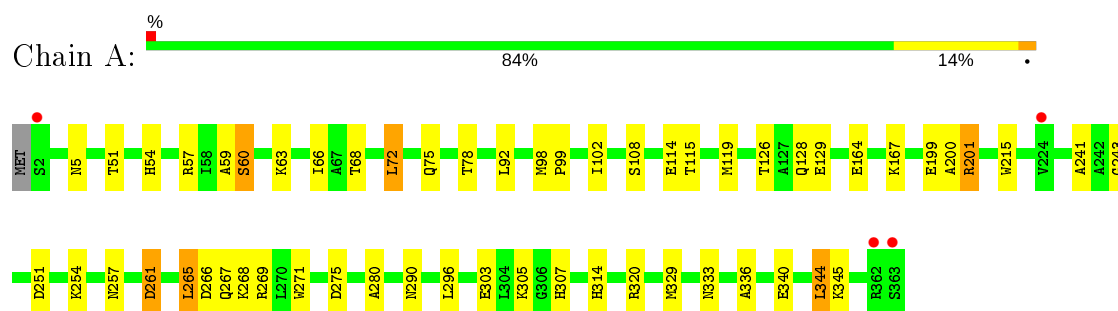
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	125	Total	O	0	0
			125	125		
4	B	164	Total	O	0	0
			164	164		
4	C	158	Total	O	0	0
			158	158		
4	D	138	Total	O	0	0
			138	138		
4	E	70	Total	O	0	0
			70	70		
4	F	90	Total	O	0	0
			90	90		

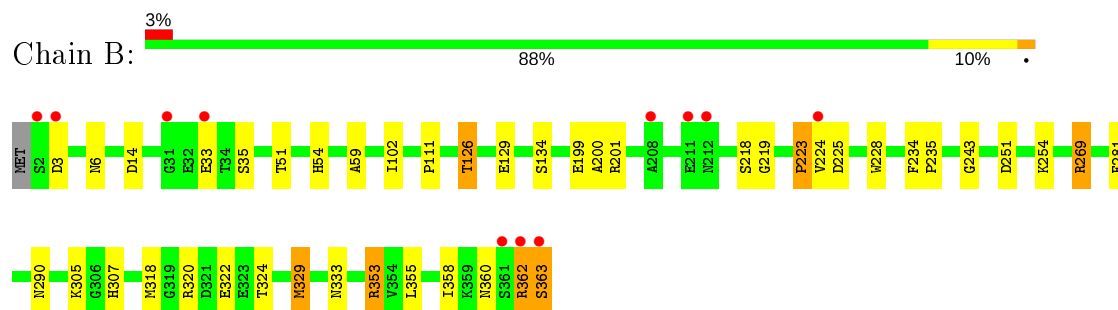
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

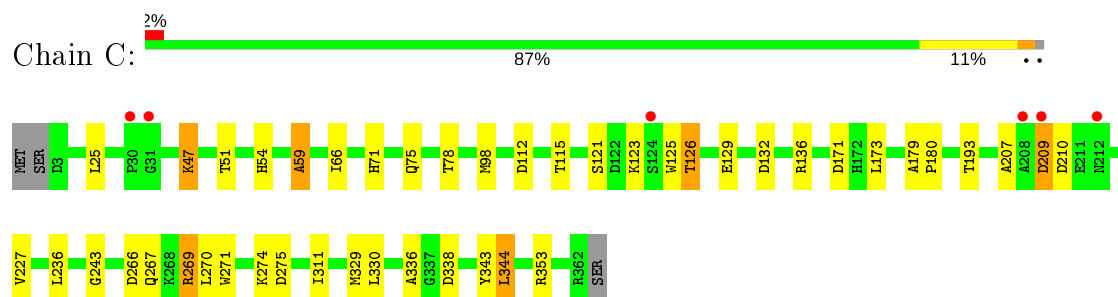
- Molecule 1: D-amino acid amidase



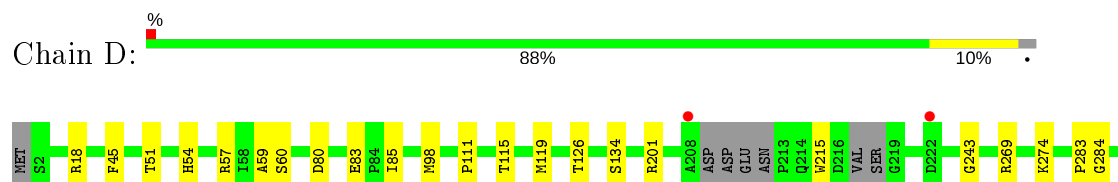
- Molecule 1: D-amino acid amidase



- Molecule 1: D-amino acid amidase

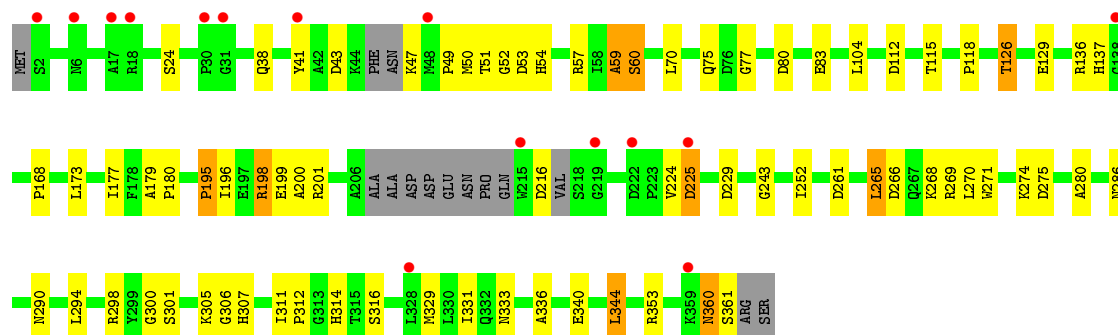
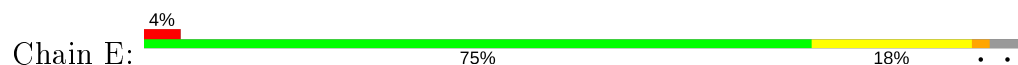


- Molecule 1: D-amino acid amidase

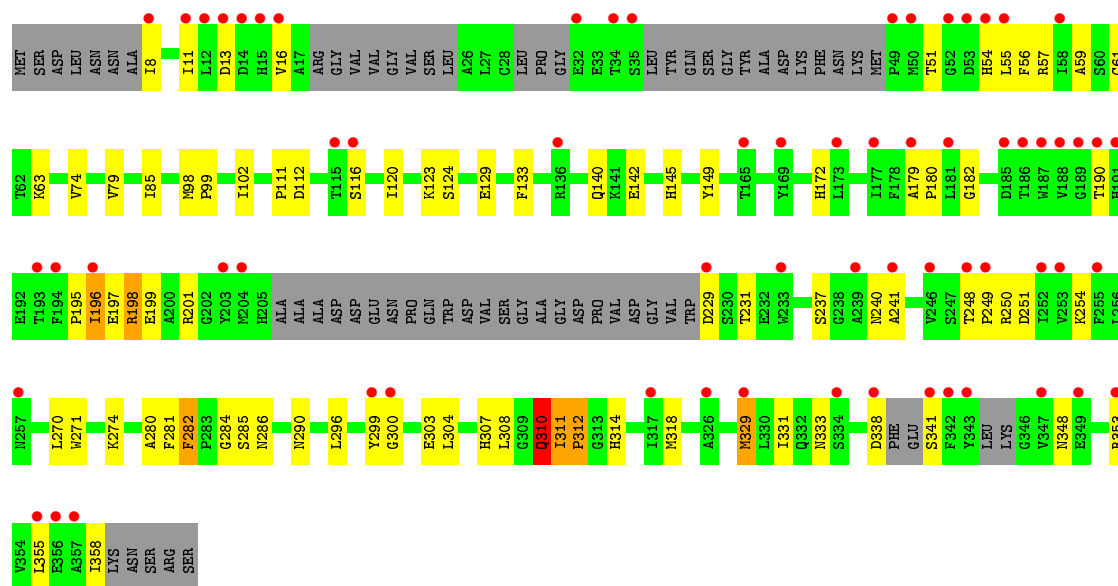




- Molecule 1: D-amino acid amidase



- Molecule 1: D-amino acid amidase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	77.07Å 123.70Å 116.05Å 90.00° 104.44° 90.00°	Depositor
Resolution (Å)	19.87 – 2.40 19.87 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.6 (19.87-2.40) 99.6 (19.87-2.40)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.24 (at 2.41Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.195 , 0.269 0.195 , 0.267	Depositor DCC
R_{free} test set	4106 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	28.6	Xtriage
Anisotropy	0.070	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 42.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	17094	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.98% 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

5.1 Standard geometry

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

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	0.47	0/2883	0.67	5/3910 (0.1%)
1	B	0.49	0/2913	0.68	3/3949 (0.1%)
1	C	0.48	0/2871	0.62	1/3894 (0.0%)
1	D	0.48	0/2845	0.67	5/3853 (0.1%)
1	E	0.44	0/2776	0.61	2/3759 (0.1%)
1	F	0.47	0/2397	0.59	0/3239
All	All	0.47	0/16685	0.64	16/22604 (0.1%)

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	B	0	1
1	E	0	1
All	All	0	2

There are no bond length outliers.

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	59	ALA	C-N-CA	9.31	144.99	121.70
1	A	59	ALA	O-C-N	-9.24	107.92	122.70
1	D	59	ALA	O-C-N	-8.92	108.43	122.70
1	A	60	SER	O-C-N	-8.33	109.38	122.70
1	B	59	ALA	O-C-N	-8.28	109.45	122.70
1	B	59	ALA	C-N-CA	7.73	141.02	121.70
1	C	59	ALA	O-C-N	-7.10	111.35	122.70
1	A	59	ALA	CA-C-N	6.77	132.10	117.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	60	SER	CA-C-N	6.57	131.66	117.20
1	D	59	ALA	CA-C-N	6.49	131.47	117.20
1	E	60	SER	O-C-N	-6.27	112.67	122.70
1	A	59	ALA	C-N-CA	5.96	136.60	121.70
1	B	59	ALA	CA-C-N	5.95	130.30	117.20
1	E	59	ALA	O-C-N	-5.75	113.50	122.70
1	D	60	SER	O-C-N	-5.22	114.35	122.70
1	D	60	SER	CA-C-N	5.09	128.41	117.20

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	223	PRO	Peptide
1	E	60	SER	Mainchain

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2811	0	2709	38	0
1	B	2841	0	2739	26	0
1	C	2799	0	2700	32	0
1	D	2772	0	2687	20	0
1	E	2709	0	2620	40	0
1	F	2342	0	2266	58	0
2	A	5	0	0	0	0
2	B	2	0	0	0	0
2	C	4	0	0	0	0
2	D	4	0	0	0	0
2	E	2	0	0	0	0
2	F	3	0	0	0	0
3	A	11	0	10	1	0
3	B	11	0	10	0	0
3	C	11	0	10	1	0
3	D	11	0	10	1	0
3	E	11	0	10	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	125	0	0	4	0
4	B	164	0	0	3	0
4	C	158	0	0	9	0
4	D	138	0	0	2	0
4	E	70	0	0	2	0
4	F	90	0	0	9	0
All	All	17094	0	15771	210	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 7.

All (210) 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:A:102:ILE:HG21	4:A:3140:HOH:O	1.35	1.25
1:F:331:ILE:HG23	4:F:3090:HOH:O	1.52	1.06
1:A:267:GLN:NE2	1:F:284:GLY:H	1.60	0.98
1:A:51:THR:H	1:A:54:HIS:HD2	0.98	0.97
1:E:75:GLN:HE22	1:E:265:LEU:HA	1.32	0.91
1:A:267:GLN:HE22	1:F:284:GLY:H	0.94	0.91
1:A:51:THR:H	1:A:54:HIS:CD2	1.87	0.91
1:A:98:MET:HB3	1:A:102:ILE:HD11	1.52	0.91
1:C:75:GLN:HE22	1:C:266:ASP:H	1.19	0.89
1:C:126:THR:HG22	1:C:129:GLU:H	1.39	0.88
1:C:75:GLN:HG2	1:C:269:ARG:HD3	1.57	0.87
1:A:267:GLN:HE22	1:F:284:GLY:N	1.75	0.84
1:A:72:LEU:HD13	1:A:265:LEU:HD12	1.58	0.84
1:B:269:ARG:HD2	1:B:269:ARG:N	1.97	0.80
1:F:237:SER:HB3	4:F:3042:HOH:O	1.81	0.80
1:E:195:PRO:HB2	1:E:198:ARG:HG3	1.62	0.79
1:B:51:THR:H	1:B:54:HIS:HD2	1.28	0.79
1:C:126:THR:HG21	4:C:3091:HOH:O	1.82	0.78
1:E:51:THR:H	1:E:54:HIS:HD2	1.33	0.76
1:C:51:THR:H	1:C:54:HIS:HD2	1.30	0.75
1:D:57:ARG:H	1:D:314:HIS:HD2	1.32	0.75
1:D:51:THR:H	1:D:54:HIS:HD2	1.34	0.75
1:C:209:ASP:CB	4:C:3141:HOH:O	2.36	0.73
1:B:223:PRO:HD3	1:B:228:TRP:CZ2	2.24	0.72
1:B:51:THR:H	1:B:54:HIS:CD2	2.07	0.71
1:C:75:GLN:HE22	1:C:266:ASP:N	1.88	0.71
1:F:300:GLY:O	4:F:3089:HOH:O	2.08	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:240:ASN:CG	1:F:241:ALA:H	1.93	0.70
1:E:126:THR:HG22	1:E:129:GLU:H	1.56	0.70
1:C:75:GLN:NE2	1:C:266:ASP:H	1.89	0.70
1:A:257:ASN:O	1:A:261:ASP:HB2	1.90	0.70
1:F:57:ARG:H	1:F:314:HIS:HD2	1.40	0.69
1:F:59:ALA:HB2	1:F:311:ILE:HD13	1.74	0.69
1:C:336:ALA:H	1:C:344:LEU:HD13	1.56	0.69
1:E:80:ASP:O	1:E:83:GLU:HG2	1.92	0.68
1:C:209:ASP:HB3	4:C:3141:HOH:O	1.92	0.67
1:F:270:LEU:O	1:F:274:LYS:HG2	1.94	0.67
1:B:14:ASP:HB2	1:B:353[B]:ARG:HH22	1.59	0.66
1:A:75:GLN:NE2	1:A:266:ASP:H	1.93	0.66
1:A:126:THR:HB	1:A:129:GLU:HB2	1.79	0.64
1:E:75:GLN:NE2	1:E:266:ASP:H	1.94	0.64
1:D:119[A]:MET:CE	1:D:215:TRP:HB2	2.28	0.64
1:B:126:THR:HG22	1:B:129:GLU:H	1.62	0.64
1:E:118:PRO:HA	1:E:216:ASP:HB3	1.78	0.63
1:A:72:LEU:HD13	1:A:265:LEU:CD1	2.28	0.63
1:C:171:ASP:HB3	4:C:3160:HOH:O	1.99	0.62
1:F:111:PRO:HG3	1:F:140:GLN:HB2	1.81	0.62
1:F:195:PRO:HB2	1:F:198:ARG:HG3	1.82	0.62
1:F:190:THR:HB	4:F:3087:HOH:O	1.99	0.61
1:F:51:THR:H	1:F:54:HIS:CD2	2.18	0.61
1:E:24:SER:HB2	1:E:50:MET:HE2	1.82	0.61
1:C:209:ASP:HB2	4:C:3141:HOH:O	1.99	0.60
3:A:1060:DPN:C	4:A:3043:HOH:O	2.49	0.60
1:F:172:HIS:HA	4:F:3094:HOH:O	2.01	0.60
1:F:341:SER:N	4:F:3102:HOH:O	2.35	0.60
1:B:223:PRO:HB2	4:B:3121:HOH:O	2.02	0.60
1:F:51:THR:H	1:F:54:HIS:HD2	1.49	0.60
1:F:314:HIS:HB2	4:F:3073:HOH:O	2.03	0.59
1:F:280:ALA:HB2	1:F:290:ASN:OD1	2.03	0.59
1:B:224:VAL:HG23	1:B:225:ASP:HB3	1.84	0.59
1:E:201:ARG:O	1:E:333:ASN:HB2	2.03	0.59
1:F:355:LEU:O	1:F:358:ILE:HG22	2.04	0.58
1:A:99:PRO:O	1:A:102:ILE:HG13	2.04	0.58
1:F:61:CYS:HB3	1:F:318:MET:SD	2.43	0.58
1:B:269:ARG:HD2	1:B:269:ARG:H	1.70	0.56
1:B:126:THR:HG23	4:B:3058:HOH:O	2.04	0.56
1:F:286:ASN:ND2	1:F:299:TYR:CD1	2.74	0.56
1:A:126:THR:HG22	1:A:128:GLN:H	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:71:HIS:O	1:C:75:GLN:HG3	2.07	0.55
1:A:75:GLN:HE22	1:A:266:ASP:H	1.54	0.55
1:B:224:VAL:HG23	1:B:225:ASP:OD1	2.07	0.55
1:C:210:ASP:HA	1:C:338:ASP:HB2	1.89	0.55
1:D:305:LYS:HE3	1:D:322:GLU:OE1	2.06	0.55
1:D:119[A]:MET:HE2	1:D:215:TRP:HB2	1.89	0.54
1:D:45:PHE:HD1	4:D:3114:HOH:O	1.88	0.54
1:D:353:ARG:NH1	1:D:356:GLU:OE1	2.40	0.54
1:E:316:SER:HB3	1:E:331:ILE:HG23	1.89	0.54
1:E:38:GLN:NE2	1:E:52:GLY:HA2	2.22	0.54
1:A:75:GLN:HE22	1:A:265:LEU:HA	1.73	0.54
1:F:282:PHE:O	1:F:285:SER:OG	2.09	0.54
1:F:133:PHE:HD1	4:F:3037:HOH:O	1.91	0.53
1:D:201:ARG:O	1:D:333:ASN:HB2	2.08	0.53
1:C:179:ALA:HB3	1:C:180:PRO:HD3	1.89	0.53
1:B:111:PRO:O	1:B:134:SER:HB3	2.09	0.53
1:C:123:LYS:HD3	1:C:125:TRP:CE2	2.44	0.52
1:E:77:GLY:HA2	4:E:3040:HOH:O	2.09	0.52
1:A:268:LYS:HD3	1:F:281:PHE:CD2	2.44	0.52
1:B:320:ARG:HD3	4:B:3086:HOH:O	2.10	0.52
1:E:75:GLN:NE2	1:E:265:LEU:HA	2.13	0.52
1:E:51:THR:H	1:E:54:HIS:CD2	2.21	0.52
1:A:271:TRP:CD1	1:A:275:ASP:HB2	2.43	0.52
1:F:57:ARG:H	1:F:314:HIS:CD2	2.26	0.52
1:B:305:LYS:HE3	1:B:322:GLU:OE1	2.10	0.52
1:B:201:ARG:O	1:B:333:ASN:HB2	2.09	0.52
1:E:59:ALA:HB2	1:E:311:ILE:HB	1.90	0.52
1:F:59:ALA:CB	1:F:310:GLN:H	2.23	0.52
1:F:59:ALA:HB3	1:F:310:GLN:H	1.75	0.52
1:D:119[B]:MET:HE1	3:D:1060:DPN:HE2	1.92	0.51
1:F:201:ARG:HB3	1:F:229:ASP:OD2	2.11	0.51
1:C:132:ASP:O	1:C:136:ARG:HG3	2.09	0.51
1:A:126:THR:HG22	1:A:128:GLN:N	2.26	0.51
1:E:224:VAL:O	1:E:225:ASP:HB2	2.11	0.51
1:B:33:GLU:HB2	1:C:209:ASP:OD1	2.10	0.51
1:F:54:HIS:O	1:F:248:THR:HG22	2.11	0.51
1:D:119[A]:MET:HG3	1:D:215:TRP:HB3	1.94	0.51
1:A:340:GLU:OE2	4:A:3142:HOH:O	2.19	0.50
1:F:355:LEU:HG	4:F:3026:HOH:O	2.10	0.50
1:F:13:ASP:HA	1:F:16:VAL:HG22	1.93	0.50
1:F:285:SER:HA	1:F:348:ASN:HD21	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:251:ASP:HA	1:F:254:LYS:HD2	1.93	0.50
1:E:271:TRP:CD1	1:E:275:ASP:HB2	2.46	0.50
3:C:1060:DPN:C	4:C:3074:HOH:O	2.59	0.50
1:F:240:ASN:CG	1:F:241:ALA:N	2.64	0.50
1:E:201:ARG:HD3	1:E:229:ASP:OD2	2.12	0.50
1:C:266:ASP:OD1	1:C:269:ARG:HD2	2.12	0.49
1:D:310:GLN:NE2	1:D:344:LEU:HG	2.27	0.49
1:F:63:LYS:HD2	1:F:149:TYR:OH	2.12	0.49
1:E:75:GLN:HE22	1:E:265:LEU:CA	2.15	0.49
1:C:59:ALA:HB2	1:C:311:ILE:HB	1.94	0.49
1:B:324:THR:HG22	1:B:362:ARG:HH12	1.78	0.49
1:B:225:ASP:OD2	1:B:225:ASP:O	2.31	0.48
1:E:280:ALA:HB2	1:E:290:ASN:OD1	2.13	0.48
1:A:57:ARG:H	1:A:314:HIS:HD2	1.60	0.48
1:F:142:GLU:O	1:F:145:HIS:HB3	2.14	0.48
1:A:68:THR:HG23	1:A:265:LEU:HD13	1.96	0.48
1:D:111:PRO:O	1:D:134:SER:HB3	2.13	0.48
1:B:360:ASN:HA	1:B:363:SER:HB2	1.96	0.48
1:D:274:LYS:HD2	1:D:322:GLU:OE2	2.14	0.48
1:F:85:ILE:HG12	1:F:98:MET:HB2	1.95	0.48
1:A:78:THR:OG1	1:A:164:GLU:OE1	2.32	0.47
1:C:98:MET:HE2	4:C:3012:HOH:O	2.14	0.47
1:A:280:ALA:HB2	1:A:290:ASN:OD1	2.15	0.47
1:E:270:LEU:O	1:E:274:LYS:HG2	2.13	0.47
1:A:201:ARG:O	1:A:333:ASN:HB2	2.14	0.47
1:A:257:ASN:HA	1:A:320:ARG:HH21	1.79	0.47
1:C:66:ILE:HD13	1:C:173:LEU:HD11	1.97	0.46
1:F:299:TYR:HE2	1:F:304:LEU:HD12	1.81	0.46
1:D:80:ASP:O	1:D:83:GLU:HG2	2.14	0.46
1:E:173:LEU:O	1:E:177:ILE:HB	2.16	0.46
1:F:56:PHE:HE1	1:F:333:ASN:OD1	1.99	0.46
4:C:3144:HOH:O	1:E:300:GLY:HA2	2.16	0.46
1:E:126:THR:HG21	4:E:3074:HOH:O	2.15	0.46
1:B:199:GLU:HG2	1:B:200:ALA:O	2.16	0.46
1:A:251:ASP:O	1:A:254:LYS:HB2	2.15	0.45
1:F:249:PRO:HB3	1:F:329:MET:O	2.15	0.45
1:E:252:ILE:HG21	1:E:329:MET:HE2	1.99	0.45
1:F:311:ILE:HB	1:F:312:PRO:HD2	1.98	0.45
1:E:360:ASN:O	1:E:361:SER:HB2	2.17	0.45
1:F:123:LYS:HZ1	1:F:129:GLU:CD	2.20	0.45
1:F:251:ASP:O	1:F:254:LYS:HB2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:98:MET:CE	4:C:3012:HOH:O	2.65	0.44
1:F:98:MET:HB3	1:F:102:ILE:HG21	1.98	0.44
1:A:66:ILE:HG13	1:A:241:ALA:HB1	1.99	0.44
1:F:179:ALA:N	1:F:180:PRO:HD2	2.32	0.44
1:E:199:GLU:HG2	1:E:200:ALA:O	2.17	0.44
1:A:336:ALA:H	1:A:344:LEU:HD13	1.82	0.44
1:E:57:ARG:H	1:E:314:HIS:HD2	1.66	0.44
1:E:43:ASP:O	1:E:47:LYS:HA	2.17	0.43
1:F:55:LEU:H	1:F:199:GLU:HA	1.82	0.43
1:F:8:ILE:HA	1:F:11:ILE:HD12	2.00	0.43
1:B:355:LEU:HA	1:B:358:ILE:HD12	1.99	0.43
1:A:102:ILE:O	1:A:108:SER:HB3	2.18	0.43
1:E:57:ARG:H	1:E:314:HIS:CD2	2.36	0.43
1:E:41:TYR:HA	1:E:49:PRO:HA	2.00	0.43
1:E:179:ALA:HB3	1:E:180:PRO:HD3	2.00	0.43
1:F:296:LEU:HD11	1:F:303:GLU:HB2	2.01	0.43
1:D:283:PRO:HA	1:D:284:GLY:HA2	1.84	0.43
1:F:286:ASN:ND2	1:F:299:TYR:CE1	2.86	0.43
1:F:57:ARG:N	1:F:314:HIS:HD2	2.10	0.43
1:F:250:ARG:HG2	1:F:254:LYS:HE3	2.00	0.43
1:C:123:LYS:HD3	1:C:125:TRP:CZ2	2.54	0.42
1:D:274:LYS:O	1:D:305:LYS:NZ	2.52	0.42
1:D:85:ILE:HD11	1:D:98:MET:HE2	2.01	0.42
1:D:57:ARG:N	1:D:314:HIS:HD2	2.09	0.42
1:C:207:ALA:O	1:C:343:TYR:CE2	2.72	0.42
1:A:119:MET:HG3	1:A:215:TRP:HB3	2.02	0.42
1:E:286:ASN:HB3	1:E:298:ARG:O	2.19	0.42
1:F:338:ASP:O	1:F:341:SER:HB3	2.19	0.42
1:A:296:LEU:HD13	1:A:305:LYS:HG2	2.01	0.42
1:F:56:PHE:CG	1:F:331:ILE:HG21	2.54	0.42
1:F:56:PHE:CE1	1:F:333:ASN:OD1	2.73	0.42
1:B:234:PHE:HA	1:B:235:PRO:HD3	1.93	0.41
1:B:251:ASP:O	1:B:254:LYS:HB3	2.20	0.41
1:A:75:GLN:HE21	1:A:269:ARG:HB2	1.84	0.41
1:A:199:GLU:HG2	1:A:200:ALA:O	2.19	0.41
1:E:136:ARG:HG2	1:E:137:HIS:CE1	2.55	0.41
1:C:25:LEU:HD13	1:C:330:LEU:HD12	2.02	0.41
1:C:271:TRP:CD1	1:C:275:ASP:HB2	2.55	0.41
1:E:118:PRO:HA	1:E:216:ASP:CB	2.46	0.41
1:A:60:SER:O	1:A:63:LYS:HB2	2.20	0.41
1:E:265:LEU:HG	1:E:269:ARG:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:70:LEU:HD23	1:E:104:LEU:HD11	2.03	0.41
1:A:114:GLU:HG2	4:A:3051:HOH:O	2.20	0.41
1:A:296:LEU:HD11	1:A:303:GLU:OE2	2.21	0.41
1:E:38:GLN:HE21	1:E:52:GLY:HA2	1.84	0.41
1:D:335:GLY:HA3	4:D:3081:HOH:O	2.20	0.41
1:E:336:ALA:H	1:E:344:LEU:HD13	1.86	0.41
1:B:318:MET:HB3	1:B:329:MET:SD	2.61	0.41
1:C:47:LYS:HD3	1:C:47:LYS:HA	1.91	0.41
1:F:74:VAL:HA	1:F:79:VAL:O	2.21	0.41
1:C:75:GLN:HE21	1:C:269:ARG:HB2	1.86	0.40
1:C:51:THR:H	1:C:54:HIS:CD2	2.22	0.40
1:E:294:LEU:HD22	1:E:306:GLY:HA2	2.02	0.40
1:F:99:PRO:O	1:F:102:ILE:HG22	2.21	0.40
1:A:265:LEU:HG	1:A:269:ARG:HB3	2.02	0.40
1:B:218:SER:HA	1:B:219:GLY:HA2	1.89	0.40
1:C:353:ARG:HD3	1:C:353:ARG:HA	1.97	0.40
1:D:18:ARG:NH1	1:D:349:GLU:OE1	2.55	0.40
1:B:281:PHE:HB2	1:F:271:TRP:CE2	2.56	0.40
1:C:270:LEU:HG	1:C:274:LYS:HE3	2.04	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	360/363 (99%)	349 (97%)	10 (3%)	1 (0%)	41 55
1	B	363/363 (100%)	346 (95%)	16 (4%)	1 (0%)	41 55
1	C	358/363 (99%)	341 (95%)	15 (4%)	2 (1%)	25 36
1	D	351/363 (97%)	338 (96%)	12 (3%)	1 (0%)	41 55
1	E	341/363 (94%)	322 (94%)	14 (4%)	5 (2%)	10 14

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	286/363 (79%)	264 (92%)	17 (6%)	5 (2%)	9	11
All	All	2059/2178 (94%)	1960 (95%)	84 (4%)	15 (1%)	22	32

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	310	GLN
1	E	360	ASN
1	F	182	GLY
1	A	243	GLY
1	E	243	GLY
1	F	312	PRO
1	B	243	GLY
1	C	47	LYS
1	C	243	GLY
1	F	197	GLU
1	F	196	ILE
1	D	243	GLY
1	E	168	PRO
1	E	195	PRO
1	E	312	PRO

5.3.2 Protein sidechains ⓘ

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	300/301 (100%)	288 (96%)	12 (4%)	31	49
1	B	303/301 (101%)	290 (96%)	13 (4%)	29	46
1	C	298/301 (99%)	285 (96%)	13 (4%)	28	45
1	D	295/301 (98%)	287 (97%)	8 (3%)	44	65
1	E	289/301 (96%)	273 (94%)	16 (6%)	21	35
1	F	251/301 (83%)	237 (94%)	14 (6%)	21	34
All	All	1736/1806 (96%)	1660 (96%)	76 (4%)	29	45

All (76) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	ASN
1	A	72	LEU
1	A	92	LEU
1	A	115	THR
1	A	167	LYS
1	A	201	ARG
1	A	261	ASP
1	A	265	LEU
1	A	307	HIS
1	A	329	MET
1	A	344	LEU
1	A	345	LYS
1	B	3	ASP
1	B	6	ASN
1	B	35	SER
1	B	102	ILE
1	B	126	THR
1	B	269	ARG
1	B	290	ASN
1	B	307	HIS
1	B	329	MET
1	B	353[A]	ARG
1	B	353[B]	ARG
1	B	362	ARG
1	B	363	SER
1	C	78	THR
1	C	112	ASP
1	C	115	THR
1	C	121	SER
1	C	126	THR
1	C	193	THR
1	C	209	ASP
1	C	227	VAL
1	C	236	LEU
1	C	267	GLN
1	C	269	ARG
1	C	329	MET
1	C	344	LEU
1	D	115	THR
1	D	126	THR
1	D	269	ARG
1	D	290	ASN

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Mol	Chain	Res	Type
1	D	307	HIS
1	D	320	ARG
1	D	329	MET
1	D	344	LEU
1	E	53	ASP
1	E	112	ASP
1	E	115	THR
1	E	126	THR
1	E	196	ILE
1	E	198	ARG
1	E	225	ASP
1	E	261	ASP
1	E	265	LEU
1	E	268	LYS
1	E	301	SER
1	E	305	LYS
1	E	307	HIS
1	E	340	GLU
1	E	344	LEU
1	E	353	ARG
1	F	112	ASP
1	F	116	SER
1	F	120	ILE
1	F	124	SER
1	F	196	ILE
1	F	198	ARG
1	F	231	THR
1	F	282	PHE
1	F	307	HIS
1	F	308	LEU
1	F	310	GLN
1	F	311	ILE
1	F	329	MET
1	F	353	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (34) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	5	ASN
1	A	54	HIS
1	A	75	GLN
1	A	163	HIS

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Mol	Chain	Res	Type
1	A	205	HIS
1	A	212	ASN
1	A	267	GLN
1	A	360	ASN
1	B	46	ASN
1	B	54	HIS
1	B	267	GLN
1	B	348	ASN
1	B	360	ASN
1	C	5	ASN
1	C	54	HIS
1	C	75	GLN
1	C	163	HIS
1	C	267	GLN
1	D	6	ASN
1	D	54	HIS
1	D	314	HIS
1	D	360	ASN
1	E	5	ASN
1	E	54	HIS
1	E	75	GLN
1	E	205	HIS
1	E	314	HIS
1	F	9	GLN
1	F	54	HIS
1	F	75	GLN
1	F	163	HIS
1	F	191	HIS
1	F	205	HIS
1	F	314	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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](#)

Of 25 ligands modelled in this entry, 20 are monoatomic - leaving 5 for Mogul analysis.

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.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	362/363 (99%)	-0.26	4 (1%) 80 79	14, 29, 40, 55	0
1	B	362/363 (99%)	-0.26	11 (3%) 50 49	14, 23, 41, 56	0
1	C	360/363 (99%)	-0.35	6 (1%) 70 68	13, 24, 42, 49	0
1	D	355/363 (97%)	-0.34	3 (0%) 86 84	12, 23, 40, 61	0
1	E	349/363 (96%)	0.17	15 (4%) 35 33	18, 37, 58, 74	0
1	F	300/363 (82%)	1.08	65 (21%) 0 0	22, 53, 70, 72	0
All	All	2088/2178 (95%)	-0.02	104 (4%) 28 27	12, 28, 59, 74	0

All (104) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	363	SER	6.8
1	E	31	GLY	6.1
1	D	208	ALA	5.7
1	F	193	THR	5.3
1	F	204	MET	4.8
1	F	248	THR	4.5
1	F	233	TRP	4.4
1	F	189	GLY	4.4
1	C	208	ALA	4.3
1	F	239	ALA	4.1
1	F	50	MET	4.0
1	B	2	SER	3.9
1	F	12	LEU	3.9
1	A	363	SER	3.8
1	F	196	ILE	3.8
1	F	326	ALA	3.8
1	F	342	PHE	3.8
1	F	115	THR	3.7
1	F	15	HIS	3.7

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Mol	Chain	Res	Type	RSRZ
1	B	362	ARG	3.7
1	F	334	SER	3.7
1	B	224	VAL	3.6
1	F	253	VAL	3.6
1	F	55	LEU	3.5
1	F	187	TRP	3.5
1	F	54	HIS	3.4
1	B	31	GLY	3.3
1	F	203	TYR	3.3
1	F	11	ILE	3.2
1	F	249	PRO	3.2
1	F	246	VAL	3.2
1	E	48	MET	3.2
1	F	186	THR	3.1
1	B	361	SER	3.1
1	F	34	THR	3.0
1	F	300	GLY	3.0
1	E	2	SER	2.9
1	F	188	VAL	2.8
1	F	136	ARG	2.8
1	F	35	SER	2.8
1	F	32	GLU	2.8
1	C	124	SER	2.7
1	F	343	TYR	2.7
1	F	14	ASP	2.7
1	E	222	ASP	2.7
1	F	190	THR	2.7
1	F	16	VAL	2.6
1	F	116	SER	2.6
1	F	58	ILE	2.6
1	F	341	SER	2.6
1	E	359	LYS	2.6
1	C	209	ASP	2.6
1	F	165	THR	2.6
1	A	362	ARG	2.5
1	F	173	LEU	2.5
1	E	219	GLY	2.5
1	E	225	ASP	2.5
1	F	49	PRO	2.5
1	F	8	ILE	2.5
1	F	329	MET	2.5
1	E	6	ASN	2.5

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Mol	Chain	Res	Type	RSRZ
1	F	181	LEU	2.4
1	F	347	VAL	2.4
1	F	13	ASP	2.4
1	F	357	ALA	2.4
1	F	229	ASP	2.4
1	F	338	ASP	2.4
1	B	208	ALA	2.4
1	F	179	ALA	2.4
1	F	299	TYR	2.3
1	B	33	GLU	2.3
1	F	241	ALA	2.3
1	F	355	LEU	2.3
1	F	53	ASP	2.3
1	E	18	ARG	2.3
1	F	185	ASP	2.3
1	E	328	LEU	2.3
1	F	317	ILE	2.3
1	E	30	PRO	2.2
1	F	252	ILE	2.2
1	F	191	HIS	2.2
1	E	138	GLY	2.2
1	B	212	ASN	2.2
1	F	194	PHE	2.2
1	D	222	ASP	2.1
1	D	362	ARG	2.1
1	F	353	ARG	2.1
1	B	211	GLU	2.1
1	C	31	GLY	2.1
1	E	215	TRP	2.1
1	F	356	GLU	2.1
1	F	169	TYR	2.1
1	C	30	PRO	2.1
1	E	41	TYR	2.1
1	F	257	ASN	2.1
1	C	212	ASN	2.0
1	F	52	GLY	2.0
1	B	3	ASP	2.0
1	A	224	VAL	2.0
1	A	2	SER	2.0
1	F	177	ILE	2.0
1	E	17	ALA	2.0
1	F	255	PHE	2.0

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Mol	Chain	Res	Type	RSRZ
1	F	349	GLU	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 carbohydrates 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(Å ²)	Q<0.9
2	BA	D	3012	1/1	0.74	0.19	61,61,61,61	1
2	BA	F	3008	1/1	0.78	0.12	49,49,49,49	1
2	BA	A	3018	1/1	0.79	0.08	57,57,57,57	1
2	BA	D	3017	1/1	0.80	0.06	58,58,58,58	1
2	BA	A	3020	1/1	0.85	0.09	66,66,66,66	1
2	BA	B	3019	1/1	0.88	0.11	59,59,59,59	1
2	BA	E	3010	1/1	0.89	0.06	73,73,73,73	1
3	DPN	D	1060	11/12	0.90	0.17	29,31,33,34	0
3	DPN	E	1060	11/12	0.92	0.13	28,31,32,32	0
2	BA	C	3009	1/1	0.93	0.13	71,71,71,71	1
3	DPN	A	1060	11/12	0.93	0.15	22,23,24,26	0
2	BA	F	3006	1/1	0.94	0.06	51,51,51,51	1
2	BA	F	3014	1/1	0.94	0.07	44,44,44,44	1
3	DPN	B	1060	11/12	0.95	0.13	23,26,27,27	0
2	BA	C	3011	1/1	0.96	0.06	53,53,53,53	1
2	BA	A	3004	1/1	0.96	0.04	41,41,41,41	1
3	DPN	C	1060	11/12	0.97	0.11	13,16,19,19	0
2	BA	A	3007	1/1	0.97	0.10	59,59,59,59	1
2	BA	D	3013	1/1	0.98	0.05	59,59,59,59	1
2	BA	E	3016	1/1	0.98	0.11	36,36,36,36	1
2	BA	C	3001	1/1	0.99	0.04	29,29,29,29	0
2	BA	D	3015	1/1	0.99	0.07	29,29,29,29	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	BA	A	3003	1/1	1.00	0.05	28,28,28,28	1
2	BA	C	3005	1/1	1.00	0.01	37,37,37,37	1
2	BA	B	3002	1/1	1.00	0.04	28,28,28,28	1

6.5 Other polymers [i](#)

There are no such residues in this entry.