Full wwPDB X-ray Structure Validation Report ⓘ

Nov 13, 2023 – 01:56 PM JST

PDB ID	:	5XEP
Title	:	Crystal structure of BRP39, a chitinase-like protein, at 2.6 Angstorm resolution
Authors	:	Mohanty, A.K.; Fisher, A.J.; Choudhary, S.; Kaushik, J.K.
Deposited on	:	2017-04-05
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:

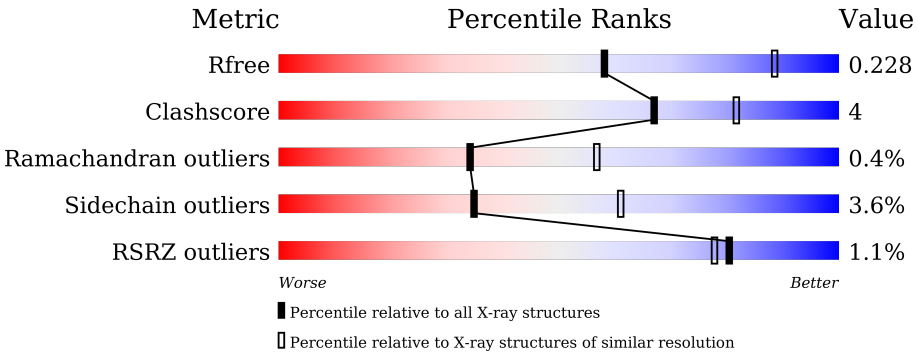
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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}	130704	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (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 <=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	381	85% 9% • 5%
1	B	381	83% 10% • 6%
1	C	381	81% 11% • 6%
1	D	381	86% 8% • 5%
1	E	381	85% 8% • 6%
1	F	381	83% 9% • 6%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 17726 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.

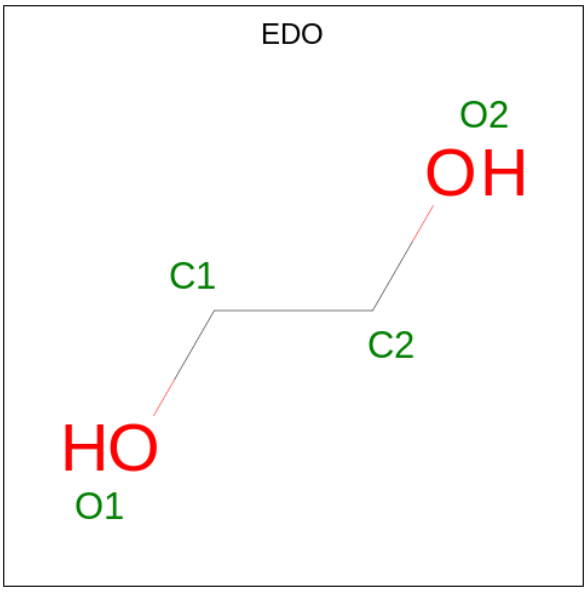
- Molecule 1 is a protein called Chitinase-3-like protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	362	Total	C	N	O	S	0	1	0
			2906	1870	493	534	9			
1	B	360	Total	C	N	O	S	0	0	0
			2890	1860	490	531	9			
1	C	360	Total	C	N	O	S	0	0	0
			2875	1852	484	530	9			
1	D	361	Total	C	N	O	S	0	0	0
			2883	1856	488	530	9			
1	E	358	Total	C	N	O	S	0	0	0
			2866	1844	485	528	9			
1	F	357	Total	C	N	O	S	0	1	0
			2860	1841	484	526	9			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	104	GLY	GLU	engineered mutation	UNP Q61362
A	340	ARG	GLY	engineered mutation	UNP Q61362
B	104	GLY	GLU	engineered mutation	UNP Q61362
B	340	ARG	GLY	engineered mutation	UNP Q61362
C	104	GLY	GLU	engineered mutation	UNP Q61362
C	340	ARG	GLY	engineered mutation	UNP Q61362
D	104	GLY	GLU	engineered mutation	UNP Q61362
D	340	ARG	GLY	engineered mutation	UNP Q61362
E	104	GLY	GLU	engineered mutation	UNP Q61362
E	340	ARG	GLY	engineered mutation	UNP Q61362
F	104	GLY	GLU	engineered mutation	UNP Q61362
F	340	ARG	GLY	engineered mutation	UNP Q61362

- Molecule 2 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



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

- Molecule 3 is water.

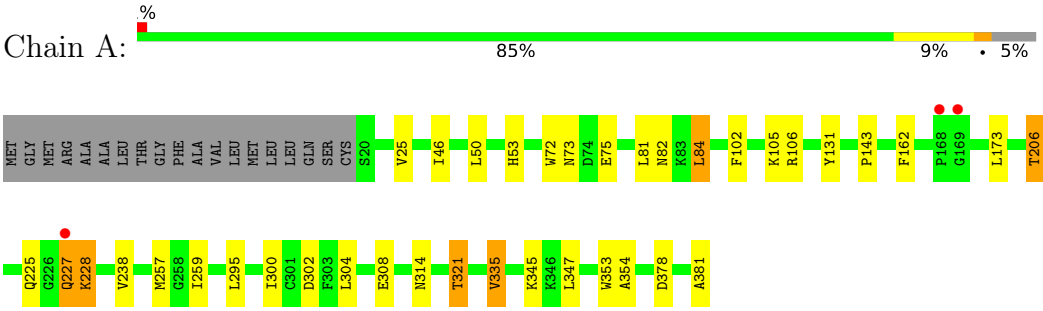
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	107	Total O 107 107	0	0
3	B	110	Total O 110 110	0	0
3	C	50	Total O 50 50	0	0
3	D	56	Total O 56 56	0	0
3	E	60	Total O 60 60	0	0
3	F	55	Total O 55 55	0	0

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.

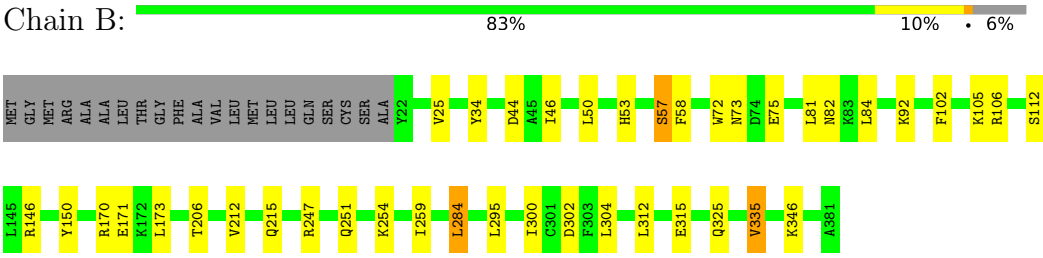
• Molecule 1: Chitinase-3-like protein 1

Chain A:



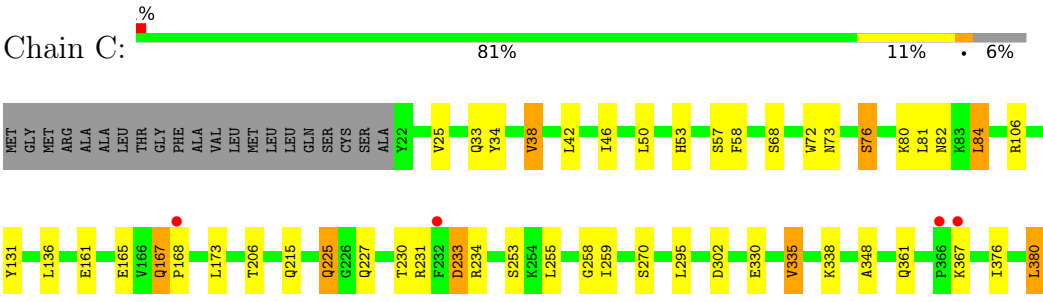
• Molecule 1: Chitinase-3-like protein 1

Chain B:



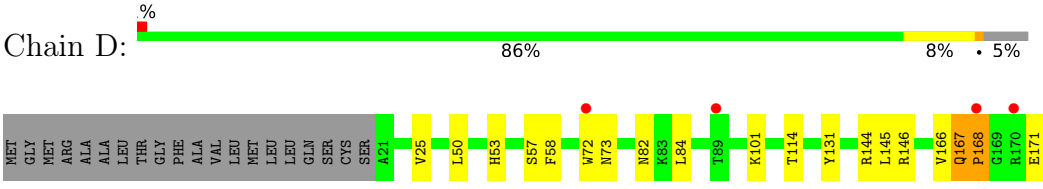
• Molecule 1: Chitinase-3-like protein 1

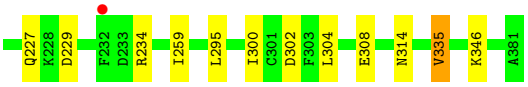
Chain C:



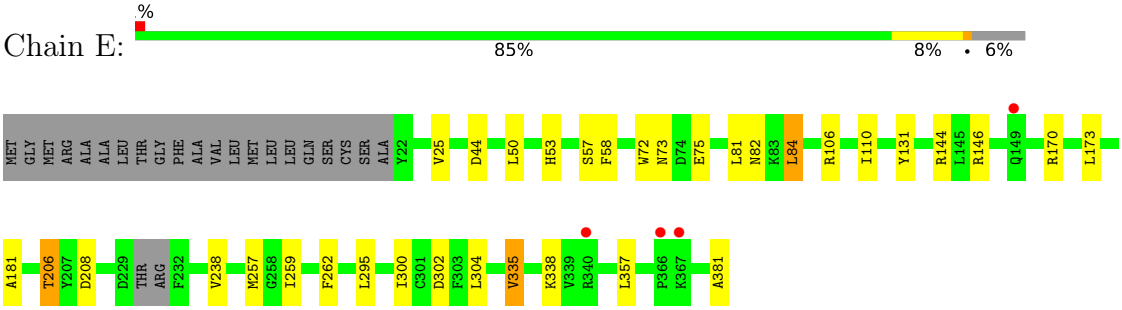
• Molecule 1: Chitinase-3-like protein 1

Chain D:

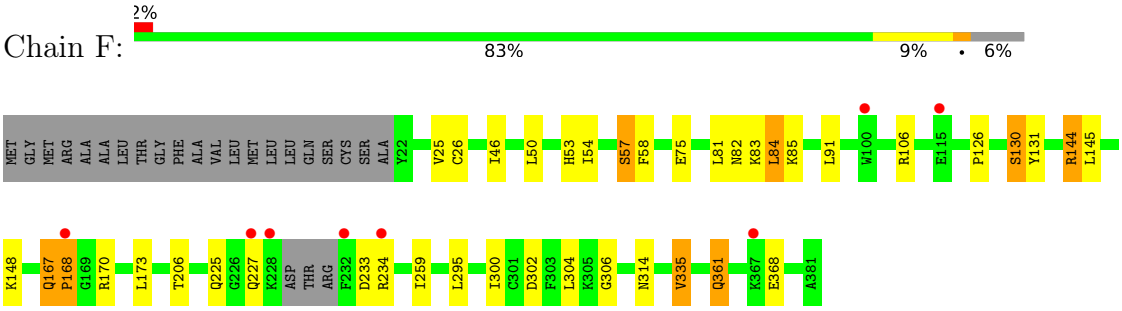




• Molecule 1: Chitinase-3-like protein 1



• Molecule 1: Chitinase-3-like protein 1



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	130.61Å 81.32Å 229.33Å 90.00° 105.86° 90.00°	Depositor
Resolution (Å)	38.27 – 2.60 38.27 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.7 (38.27-2.60) 99.7 (38.27-2.60)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.99 (at 2.61Å)	Xtriage
Refinement program	PHENIX 1.11.1_2575	Depositor
R, R_{free}	0.190 , 0.231 0.191 , 0.228	Depositor DCC
R_{free} test set	3610 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å^2)	37.3	Xtriage
Anisotropy	0.530	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 47.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.45$, $< L^2 > = 0.27$	Xtriage
Estimated twinning fraction	0.023 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	17726	wwPDB-VP
Average B, all atoms (Å^2)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 31.29 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.1336e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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: EDO

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	0.28	0/2982	0.50	0/4029
1	B	0.28	0/2963	0.50	0/4003
1	C	0.29	0/2947	0.52	0/3984
1	D	0.28	0/2956	0.50	0/3995
1	E	0.28	0/2937	0.53	1/3967 (0.0%)
1	F	0.30	0/2934	0.51	0/3964
All	All	0.28	0/17719	0.51	1/23942 (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	C	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	E	146	ARG	NE-CZ-NH2	-6.09	117.25	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	225	GLN	Sidechain

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	2906	0	2856	24	0
1	B	2890	0	2841	32	0
1	C	2875	0	2813	28	0
1	D	2883	0	2824	16	0
1	E	2866	0	2813	18	0
1	F	2860	0	2806	23	0
2	A	8	0	12	0	0
3	A	107	0	0	7	1
3	B	110	0	0	9	1
3	C	50	0	0	5	0
3	D	56	0	0	3	0
3	E	60	0	0	6	0
3	F	55	0	0	5	0
All	All	17726	0	16965	135	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 4.

All (135) 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:B:144:ARG:HH21	1:B:146:ARG:HE	1.07	0.97
1:F:167:GLN:HB3	1:F:168:PRO:HD3	1.56	0.87
1:E:381:ALA:O	3:E:401:HOH:O	1.94	0.86
1:B:112:SER:O	1:D:167:GLN:NE2	2.09	0.85
1:C:82:ASN:ND2	1:C:131:TYR:O	2.14	0.81
1:C:258:GLY:O	3:C:401:HOH:O	1.99	0.79
1:A:82:ASN:ND2	1:A:131:TYR:O	2.19	0.76
1:B:44:ASP:O	3:B:401:HOH:O	2.03	0.76
1:A:214:ARG:NH1	3:A:1107:HOH:O	2.20	0.74
1:A:227:GLN:OE1	3:A:1101:HOH:O	2.05	0.74
1:A:162:PHE:O	3:A:1102:HOH:O	2.05	0.73
1:E:82:ASN:ND2	1:E:131:TYR:O	2.20	0.73
1:C:225:GLN:CD	1:C:234:ARG:HA	2.08	0.73
1:F:82:ASN:ND2	1:F:131:TYR:O	2.22	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:82:ASN:ND2	1:D:131:TYR:O	2.22	0.73
1:A:143:PRO:O	3:A:1103:HOH:O	2.05	0.73
1:E:181:ALA:O	3:E:402:HOH:O	2.07	0.73
1:B:144:ARG:NH1	3:B:403:HOH:O	2.22	0.72
1:F:361:GLN:OE1	3:F:401:HOH:O	2.07	0.72
1:F:126:PRO:O	1:F:130:SER:OG	2.08	0.71
1:A:378:ASP:OD1	3:A:1104:HOH:O	2.08	0.71
1:B:82:ASN:ND2	1:B:131:TYR:O	2.23	0.71
1:B:215:GLN:NE2	3:B:404:HOH:O	2.23	0.68
1:B:150:TYR:OH	1:D:167:GLN:OE1	2.09	0.68
1:F:233:ASP:OD2	3:F:402:HOH:O	2.11	0.67
1:D:308:GLU:OE2	3:D:402:HOH:O	2.13	0.66
1:F:368:GLU:OE1	3:F:404:HOH:O	2.14	0.65
1:C:215:GLN:OE1	3:C:402:HOH:O	2.14	0.65
1:C:270:SER:O	3:C:403:HOH:O	2.14	0.65
1:B:144:ARG:NH2	1:B:146:ARG:HE	1.89	0.65
1:E:208:ASP:OD1	3:E:404:HOH:O	2.15	0.64
1:E:44:ASP:O	3:E:403:HOH:O	2.15	0.63
1:A:345:LYS:HB3	1:A:347:LEU:HD13	1.82	0.61
1:C:76:SER:O	1:C:80:LYS:HG3	2.00	0.61
1:F:227:GLN:OE1	1:F:314:ASN:ND2	2.30	0.60
1:B:146:ARG:NH2	1:C:33:GLN:OE1	2.25	0.60
1:A:227:GLN:NE2	1:A:314:ASN:OD1	2.35	0.59
1:D:72:TRP:CE2	1:D:73:ASN:HB3	2.37	0.58
1:D:101:LYS:NZ	3:D:401:HOH:O	2.08	0.57
1:C:230:THR:H	1:C:233:ASP:HB2	1.69	0.57
1:B:144:ARG:HH21	1:B:146:ARG:NE	1.90	0.57
1:F:25:VAL:HG22	1:F:53:HIS:HB2	1.88	0.56
1:F:225:GLN:OE1	1:F:234:ARG:HG2	2.06	0.56
1:B:25:VAL:HG22	1:B:53:HIS:HB2	1.88	0.55
1:F:83:LYS:NZ	3:F:413:HOH:O	2.39	0.54
1:A:72:TRP:CE2	1:A:73:ASN:HB3	2.43	0.53
1:A:225:GLN:HE21	1:A:228:LYS:HB2	1.73	0.53
1:B:144:ARG:NH1	3:B:409:HOH:O	2.41	0.53
1:A:25:VAL:HG22	1:A:53:HIS:HB2	1.89	0.53
1:B:284:LEU:HD22	1:B:325:GLN:NE2	2.24	0.53
1:B:92:LYS:NZ	1:B:171:GLU:OE2	2.41	0.53
1:C:376:ILE:O	1:C:380:LEU:HD22	2.08	0.53
1:E:144:ARG:NH1	3:E:410:HOH:O	2.41	0.53
1:D:144:ARG:HH12	1:D:146:ARG:CZ	2.22	0.52
1:C:46:ILE:O	3:C:404:HOH:O	2.18	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:144:ARG:HB2	1:F:144:ARG:NH1	2.25	0.52
1:C:25:VAL:HG22	1:C:53:HIS:HB2	1.92	0.52
1:B:105:LYS:HE2	1:C:34:TYR:CE2	2.45	0.51
1:B:72:TRP:CE2	1:B:73:ASN:HB3	2.46	0.51
1:F:144:ARG:HB2	1:F:144:ARG:HH11	1.74	0.51
1:C:121:VAL:HG12	1:C:161:GLU:HG3	1.90	0.51
1:F:26:CYS:HB2	1:F:54:ILE:HD13	1.92	0.51
1:E:72:TRP:CE2	1:E:73:ASN:HB3	2.46	0.50
1:F:85:LYS:HG2	1:F:91:LEU:HB3	1.93	0.50
1:A:102:PHE:CZ	1:A:106:ARG:HG2	2.47	0.50
1:D:167:GLN:HB2	1:D:168:PRO:HD3	1.94	0.49
1:A:210:HIS:O	3:A:1105:HOH:O	2.20	0.49
1:D:229:ASP:OD1	1:D:234:ARG:NE	2.38	0.49
1:E:25:VAL:HG22	1:E:53:HIS:HB2	1.94	0.49
1:D:172:LYS:O	3:D:403:HOH:O	2.20	0.48
1:B:75:GLU:HG2	1:B:131:TYR:CE1	2.49	0.48
1:B:57:SER:HA	1:B:58:PHE:HA	1.64	0.47
1:A:381:ALA:O	3:A:1106:HOH:O	2.20	0.47
1:F:167:GLN:CB	1:F:168:PRO:HD3	2.38	0.47
1:A:75:GLU:HG2	1:A:131:TYR:CE1	2.50	0.47
1:C:128:LEU:HD11	1:C:136:LEU:HB2	1.96	0.47
1:D:25:VAL:HG22	1:D:53:HIS:HB2	1.96	0.47
1:D:57:SER:HA	1:D:58:PHE:HA	1.68	0.46
1:E:106:ARG:HH21	1:E:110:ILE:HD11	1.80	0.46
1:D:259:ILE:HG21	1:D:335:VAL:HG22	1.97	0.46
1:A:259:ILE:HG21	1:A:335:VAL:HG22	1.98	0.45
1:E:170:ARG:NH2	3:E:418:HOH:O	2.50	0.45
1:A:46:ILE:HB	1:A:84:LEU:HD21	1.99	0.45
1:B:170:ARG:O	3:B:402:HOH:O	2.21	0.45
1:F:167:GLN:HB3	1:F:168:PRO:CD	2.36	0.45
1:C:81:LEU:O	1:C:84:LEU:HB2	2.17	0.44
1:E:259:ILE:HG21	1:E:335:VAL:HG22	1.98	0.44
1:A:308:GLU:HB2	1:A:321:THR:HG22	1.99	0.44
1:B:102:PHE:CZ	1:B:106:ARG:HG2	2.53	0.44
1:B:251:GLN:HB2	1:B:254:LYS:HG2	2.00	0.44
1:F:46:ILE:HB	1:F:84:LEU:HD21	1.99	0.44
1:F:300:ILE:O	1:F:304:LEU:HG	2.17	0.44
1:C:57:SER:HA	1:C:58:PHE:HA	1.66	0.44
1:E:57:SER:HA	1:E:58:PHE:HA	1.66	0.44
1:C:38:VAL:HG12	1:C:361:GLN:OE1	2.18	0.43
1:E:75:GLU:HG2	1:E:131:TYR:CE1	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:231:ARG:O	1:C:234:ARG:HG2	2.18	0.43
1:A:81:LEU:O	1:A:84:LEU:HB2	2.18	0.43
1:B:81:LEU:O	1:B:84:LEU:HB2	2.19	0.43
1:E:81:LEU:O	1:E:84:LEU:HB2	2.18	0.43
1:B:46:ILE:HB	1:B:84:LEU:HD21	2.01	0.43
1:B:300:ILE:O	1:B:304:LEU:HG	2.18	0.43
1:B:251:GLN:NE2	3:B:420:HOH:O	2.51	0.43
1:F:57:SER:HA	1:F:58:PHE:HA	1.65	0.43
1:F:259:ILE:HG21	1:F:335:VAL:HG22	2.00	0.43
1:B:75:GLU:HG3	3:B:417:HOH:O	2.18	0.42
1:B:312:LEU:HB3	1:B:315:GLU:OE1	2.20	0.42
1:B:82:ASN:ND2	3:B:410:HOH:O	2.41	0.42
1:C:225:GLN:OE1	1:C:234:ARG:HA	2.19	0.42
1:A:353:TRP:HA	1:A:354:ALA:HA	1.86	0.42
1:A:206:THR:HB	1:A:238:VAL:HG22	2.02	0.42
1:A:300:ILE:O	1:A:304:LEU:HG	2.19	0.42
1:C:72:TRP:CE2	1:C:73:ASN:HB3	2.55	0.42
1:C:259:ILE:HG21	1:C:335:VAL:HG22	2.02	0.42
1:B:259:ILE:HG21	1:B:335:VAL:HG22	2.02	0.42
1:E:262:PHE:HB3	1:E:357:LEU:HD13	2.00	0.42
1:B:112:SER:HB2	1:D:167:GLN:NE2	2.35	0.41
1:C:253:SER:O	1:C:348:ALA:HB2	2.20	0.41
1:C:42:LEU:HD13	1:C:80:LYS:NZ	2.35	0.41
1:A:105:LYS:HG2	1:B:34:TYR:CE1	2.55	0.41
1:F:306:GLY:O	3:F:406:HOH:O	2.22	0.41
1:D:300:ILE:O	1:D:304:LEU:HG	2.21	0.41
1:E:300:ILE:O	1:E:304:LEU:HG	2.21	0.41
1:A:257:MET:HB2	1:A:347:LEU:HD23	2.02	0.41
1:C:46:ILE:HB	1:C:84:LEU:HD21	2.02	0.41
1:C:106:ARG:HA	1:C:106:ARG:HD2	1.86	0.41
1:C:330:GLU:OE2	1:C:338:LYS:NZ	2.47	0.41
1:E:257:MET:HE3	1:E:338:LYS:HB3	2.03	0.41
1:C:255:LEU:HD23	1:C:255:LEU:HA	1.94	0.41
1:E:206:THR:HB	1:E:238:VAL:HG22	2.03	0.41
1:C:68:SER:HB2	3:C:429:HOH:O	2.20	0.40
1:F:75:GLU:HG2	1:F:131:TYR:CE1	2.56	0.40
1:B:212:VAL:HB	3:B:437:HOH:O	2.20	0.40
1:D:227:GLN:HG2	1:D:314:ASN:ND2	2.36	0.40
1:F:54:ILE:HG21	1:F:81:LEU:HD11	2.04	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)
3:A:1165:HOH:O	3:B:465:HOH:O[4_545]	2.05	0.15

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	361/381 (95%)	357 (99%)	4 (1%)	0	100	100
1	B	358/381 (94%)	356 (99%)	2 (1%)	0	100	100
1	C	358/381 (94%)	351 (98%)	4 (1%)	3 (1%)	19	39
1	D	359/381 (94%)	348 (97%)	7 (2%)	4 (1%)	14	30
1	E	354/381 (93%)	351 (99%)	3 (1%)	0	100	100
1	F	354/381 (93%)	349 (99%)	3 (1%)	2 (1%)	25	47
All	All	2144/2286 (94%)	2112 (98%)	23 (1%)	9 (0%)	34	57

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	167	GLN
1	D	168	PRO
1	F	167	GLN
1	D	166	VAL
1	D	171	GLU
1	C	367	LYS
1	F	168	PRO
1	C	168	PRO
1	C	167	GLN

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	306/320 (96%)	296 (97%)	10 (3%)	38	64
1	B	305/320 (95%)	295 (97%)	10 (3%)	38	64
1	C	302/320 (94%)	288 (95%)	14 (5%)	27	51
1	D	302/320 (94%)	292 (97%)	10 (3%)	38	64
1	E	302/320 (94%)	295 (98%)	7 (2%)	50	75
1	F	301/320 (94%)	286 (95%)	15 (5%)	24	47
All	All	1818/1920 (95%)	1752 (96%)	66 (4%)	35	61

All (66) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	50	LEU
1	A	84	LEU
1	A	173	LEU
1	A	206	THR
1	A	227	GLN
1	A	228	LYS
1	A	295	LEU
1	A	302	ASP
1	A	321	THR
1	A	335	VAL
1	B	50	LEU
1	B	57	SER
1	B	173	LEU
1	B	206	THR
1	B	247	ARG
1	B	284	LEU
1	B	295	LEU
1	B	302	ASP
1	B	335	VAL
1	B	346	LYS
1	C	38	VAL
1	C	50	LEU
1	C	76	SER
1	C	84	LEU
1	C	165	GLU
1	C	167	GLN
1	C	173	LEU

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Mol	Chain	Res	Type
1	C	206	THR
1	C	227	GLN
1	C	233	ASP
1	C	295	LEU
1	C	302	ASP
1	C	335	VAL
1	C	380	LEU
1	D	50	LEU
1	D	84	LEU
1	D	114	THR
1	D	145	LEU
1	D	173	LEU
1	D	206	THR
1	D	295	LEU
1	D	302	ASP
1	D	335	VAL
1	D	346	LYS
1	E	50	LEU
1	E	84	LEU
1	E	173	LEU
1	E	206	THR
1	E	295	LEU
1	E	302	ASP
1	E	335	VAL
1	F	50	LEU
1	F	57	SER
1	F	84	LEU
1	F	106	ARG
1	F	130	SER
1	F	144	ARG
1	F	145	LEU
1	F	148	LYS
1	F	170	ARG
1	F	173	LEU
1	F	206	THR
1	F	295	LEU
1	F	302	ASP
1	F	335	VAL
1	F	361	GLN

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

Mol	Chain	Res	Type
1	A	225	GLN
1	D	243	GLN
1	F	361	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)

2 ligands are 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	$\#\|Z\| > 2$
2	EDO	A	1002	-	3,3,3	0.45	0	2,2,2	0.35	0
2	EDO	A	1001	-	3,3,3	0.44	0	2,2,2	0.41	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	EDO	A	1002	-	-	1/1/1/1	-
2	EDO	A	1001	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1002	EDO	O1-C1-C2-O2

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, 95^{th} 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	362/381 (95%)	-0.21	3 (0%) 86 84	11, 32, 63, 100	0
1	B	360/381 (94%)	-0.37	0 100 100	11, 32, 57, 71	0
1	C	360/381 (94%)	-0.11	4 (1%) 80 78	20, 50, 80, 111	0
1	D	361/381 (94%)	-0.27	5 (1%) 75 71	20, 47, 76, 102	0
1	E	358/381 (93%)	-0.16	4 (1%) 80 78	21, 45, 71, 108	0
1	F	357/381 (93%)	-0.08	8 (2%) 62 56	24, 50, 79, 95	0
All	All	2158/2286 (94%)	-0.20	24 (1%) 80 78	11, 43, 73, 111	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	168	PRO	5.7
1	E	367	LYS	4.6
1	C	366	PRO	4.5
1	C	232	PHE	3.7
1	F	232	PHE	3.4
1	A	168	PRO	3.3
1	A	169	GLY	3.2
1	E	366	PRO	3.0
1	C	367	LYS	2.8
1	F	100	TRP	2.8
1	D	170	ARG	2.8
1	D	89	THR	2.7
1	E	149	GLN	2.7
1	C	168	PRO	2.6
1	D	72	TRP	2.5
1	F	115	GLU	2.5
1	A	227	GLN	2.4
1	F	228	LYS	2.4
1	D	168	PRO	2.3

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Mol	Chain	Res	Type	RSRZ
1	F	234	ARG	2.2
1	F	227	GLN	2.1
1	F	367	LYS	2.0
1	D	232	PHE	2.0
1	E	340	ARG	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 monosaccharides 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, 95^{th} 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	EDO	A	1002	4/4	0.89	0.10	43,46,52,56	0
2	EDO	A	1001	4/4	0.95	0.17	13,16,24,27	0

6.5 Other polymers (i)

There are no such residues in this entry.