Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 02:59 PM GMT

PDB ID	:	4B3L
Title	:	Family 1 6-phospho-beta-D glycosidase from Streptococcus pyogenes
Authors	:	Stepper, J.; Dabin, J.; Ekloef, J.M.; Thongpoo, P.; Kongsaeree, P.T.; Taylor, E.J.; Turkenburg, J.P.; Brumer, H.; Davies, G.J.
Deposited on	:	2012-07-24
Resolution	:	2.51 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

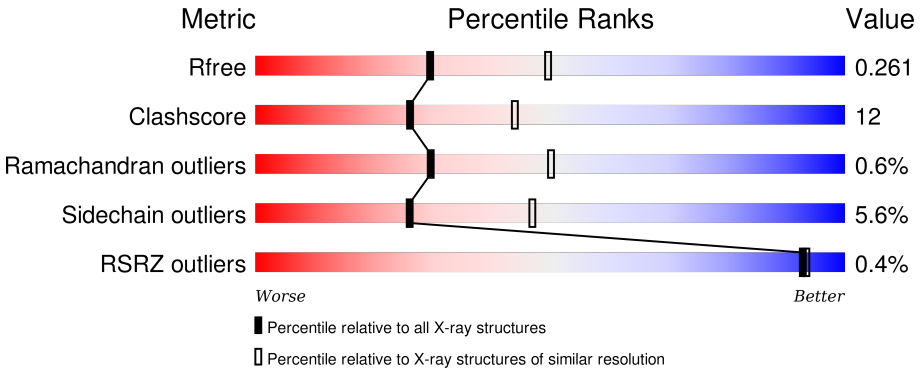
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

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 2.51 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}	91344	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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. 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	479	74% 21%
1	B	479	77% 17%
1	C	479	71% 23%
1	D	479	77% 17%
1	E	479	% 70% 22%

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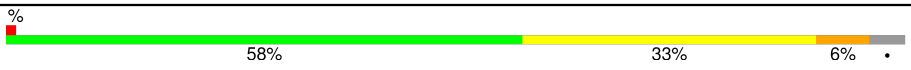
Mol	Chain	Length	Quality of chain
1	F	479	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 22619 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 BETA-GLUCOSIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	461	Total	C	N	O	S	0	0	0
			3767	2435	636	686	10			
1	B	461	Total	C	N	O	S	0	0	0
			3767	2435	636	686	10			
1	C	461	Total	C	N	O	S	0	0	0
			3767	2435	636	686	10			
1	D	461	Total	C	N	O	S	0	0	0
			3767	2435	636	686	10			
1	E	461	Total	C	N	O	S	0	0	0
			3767	2435	636	686	10			
1	F	461	Total	C	N	O	S	0	0	0
			3767	2435	636	686	10			

- Molecule 2 is water.

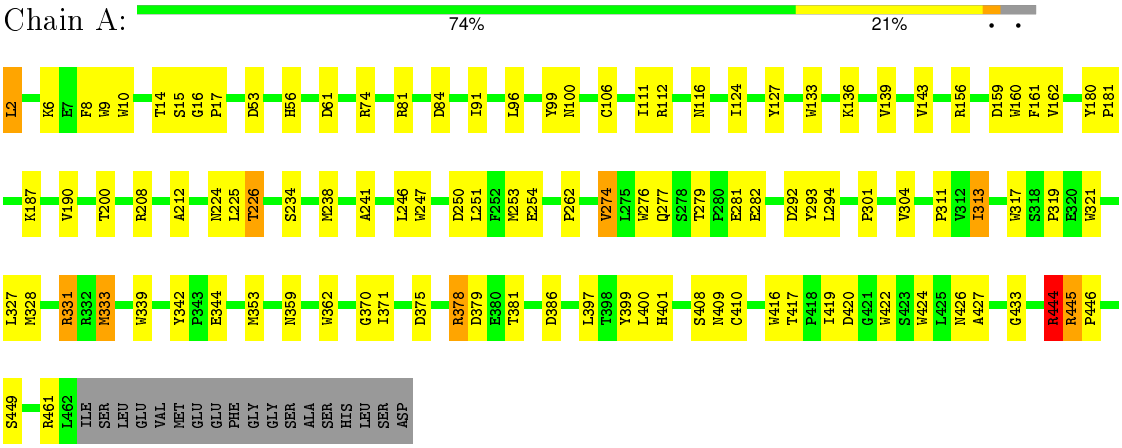
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	O	0	0
			1	1		
2	B	4	Total	O	0	0
			4	4		
2	C	3	Total	O	0	0
			3	3		
2	D	5	Total	O	0	0
			5	5		
2	E	1	Total	O	0	0
			1	1		
2	F	3	Total	O	0	0
			3	3		

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 errors 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.

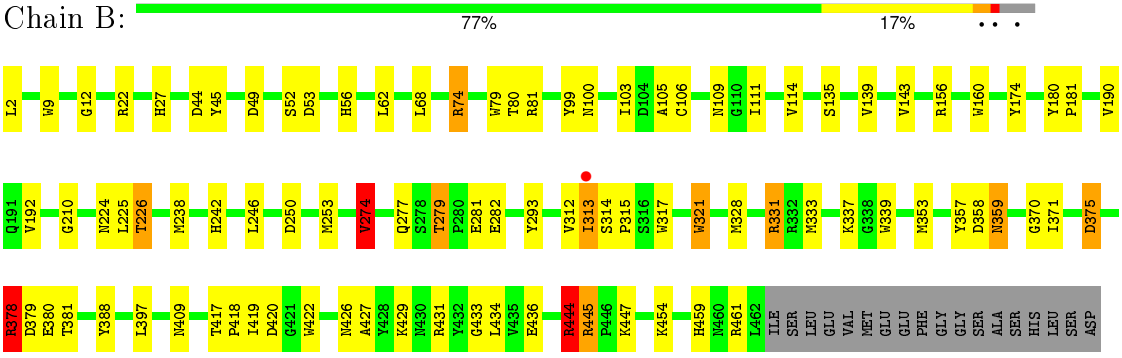
- Molecule 1: BETA-GLUCOSIDASE

Chain A:



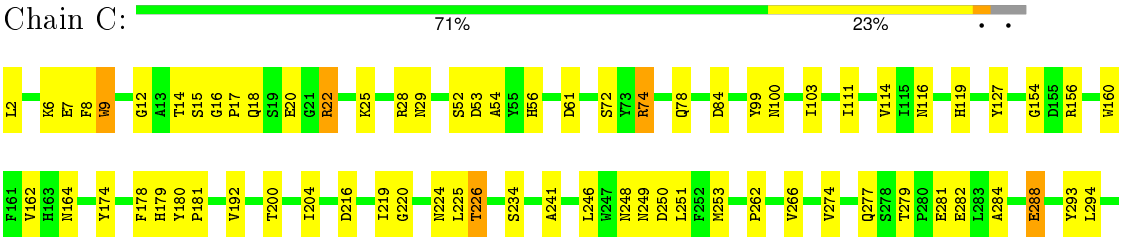
- Molecule 1: BETA-GLUCOSIDASE

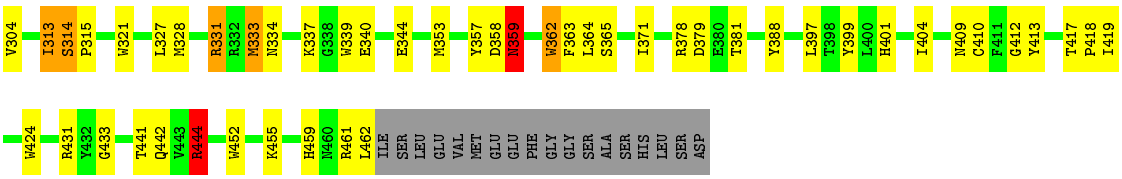
Chain B:



- Molecule 1: BETA-GLUCOSIDASE

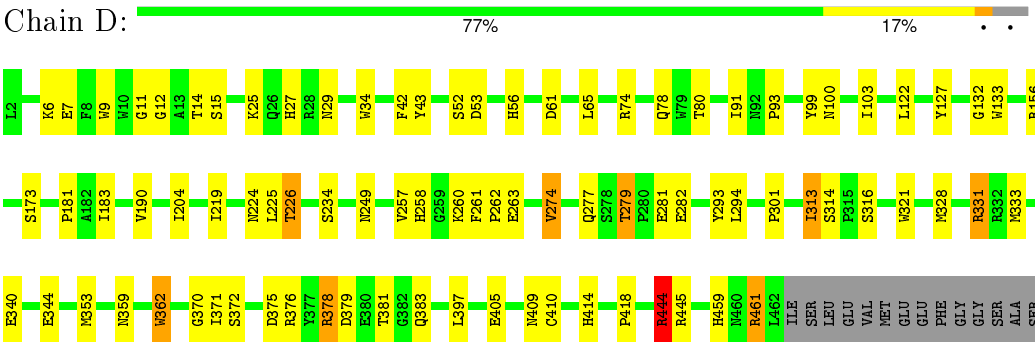
Chain C:





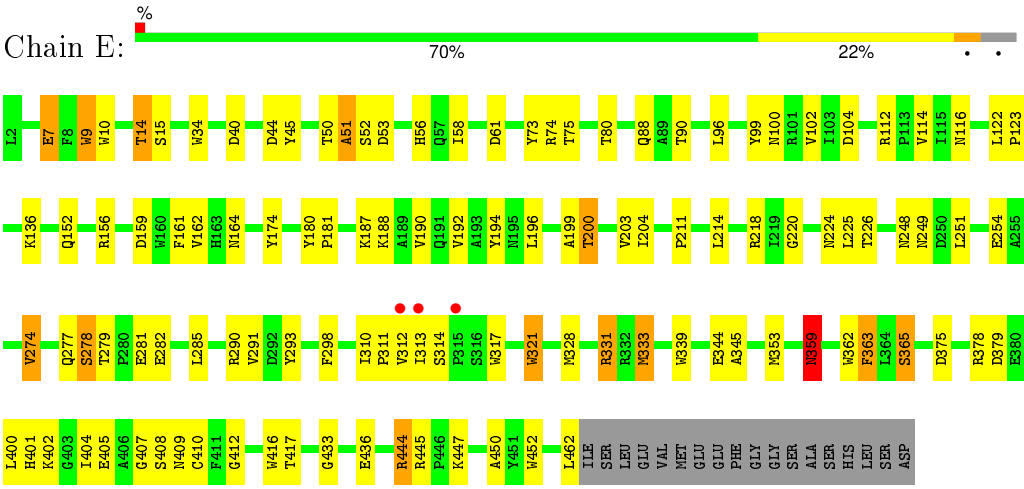
• Molecule 1: BETA-GLUCOSIDASE

Chain D:



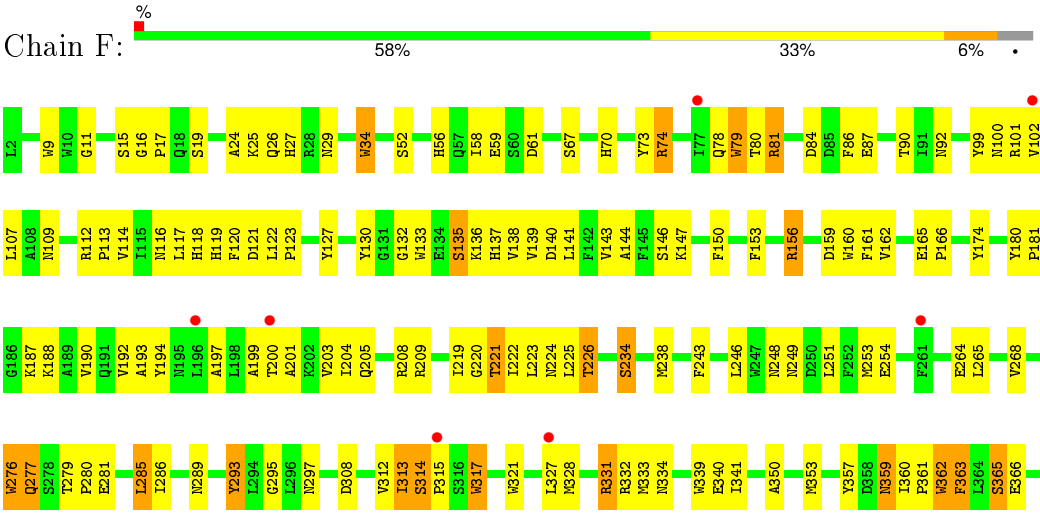
• Molecule 1: BETA-GLUCOSIDASE

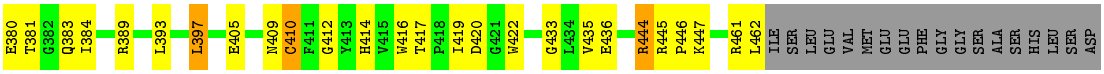
Chain E:



• Molecule 1: BETA-GLUCOSIDASE

Chain F:




E380
T381
S382
Q383
I384
R389
L393
L397
E405
N409
C410
F411
G412
Y413
H414
V415
W416
T417
P418
I419
D420
G421
W422
G433
L434
V435
E436
R444
R445
P446
K447
R461
L462
ILE
SER
LEU
GLU
VAL
MET
GLU
GLU
PHE
GLY
GLY
SER
ALA
SER
HIS
LEU
SER
ASP

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	107.83Å 198.04Å 107.88Å 90.00° 118.51° 90.00°	Depositor
Resolution (Å)	94.75 – 2.51 99.02 – 2.51	Depositor EDS
% Data completeness (in resolution range)	99.5 (94.75-2.51) 99.3 (99.02-2.51)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.32 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.7.0025	Depositor
R, R_{free}	0.205 , 0.261 0.205 , 0.261	Depositor DCC
R_{free} test set	6762 reflections (5.29%)	DCC
Wilson B-factor (Å^2)	47.9	Xtriage
Anisotropy	0.055	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	(Not available) , (Not available)	EDS
Estimated twinning fraction	0.023 for -h-l,k,h 0.023 for l,k,-h-l 0.032 for h,-k,-h-l 0.034 for -h-l,-k,l 0.087 for l,-k,h	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.28$	Xtriage
Outliers	0 of 134562 reflections	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	22619	wwPDB-VP
Average B, all atoms (Å^2)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.11% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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	0.87	8/3891 (0.2%)	0.88	7/5304 (0.1%)
1	B	0.89	7/3891 (0.2%)	0.88	6/5304 (0.1%)
1	C	0.86	7/3891 (0.2%)	0.89	8/5304 (0.2%)
1	D	0.86	6/3891 (0.2%)	0.85	1/5304 (0.0%)
1	E	0.82	6/3891 (0.2%)	0.84	0/5304
1	F	0.91	8/3891 (0.2%)	0.91	2/5304 (0.0%)
All	All	0.87	42/23346 (0.2%)	0.87	24/31824 (0.1%)

All (42) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	339	TRP	CD2-CE2	6.69	1.49	1.41
1	D	339	TRP	CD2-CE2	6.69	1.49	1.41
1	E	339	TRP	CD2-CE2	6.51	1.49	1.41
1	F	34	TRP	CD2-CE2	6.50	1.49	1.41
1	B	339	TRP	CD2-CE2	6.48	1.49	1.41
1	D	9	TRP	CD2-CE2	6.42	1.49	1.41
1	D	160	TRP	CD2-CE2	6.40	1.49	1.41
1	A	160	TRP	CD2-CE2	6.33	1.49	1.41
1	F	9	TRP	CD2-CE2	6.30	1.49	1.41
1	A	317	TRP	CD2-CE2	6.29	1.48	1.41
1	F	79	TRP	CD2-CE2	6.06	1.48	1.41
1	F	339	TRP	CD2-CE2	6.02	1.48	1.41
1	C	424	TRP	CD2-CE2	5.94	1.48	1.41
1	A	424	TRP	CD2-CE2	5.87	1.48	1.41
1	D	362	TRP	CD2-CE2	5.87	1.48	1.41
1	A	133	TRP	CD2-CE2	5.85	1.48	1.41
1	F	276	TRP	CD2-CE2	5.74	1.48	1.41
1	C	339	TRP	CD2-CE2	5.71	1.48	1.41
1	E	321	TRP	CD2-CE2	5.70	1.48	1.41
1	E	452	TRP	CD2-CE2	5.68	1.48	1.41
1	A	276	TRP	CD2-CE2	5.62	1.48	1.41
1	B	79	TRP	CD2-CE2	5.61	1.48	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	362	TRP	CD2-CE2	5.58	1.48	1.41
1	E	10	TRP	CD2-CE2	5.58	1.48	1.41
1	B	9	TRP	CD2-CE2	5.56	1.48	1.41
1	D	34	TRP	CD2-CE2	5.54	1.48	1.41
1	F	422	TRP	CD2-CE2	5.54	1.48	1.41
1	B	317	TRP	CD2-CE2	5.53	1.48	1.41
1	B	422	TRP	CD2-CE2	5.50	1.48	1.41
1	B	160	TRP	CD2-CE2	5.38	1.47	1.41
1	D	321	TRP	CD2-CE2	5.36	1.47	1.41
1	F	317	TRP	CD2-CE2	5.33	1.47	1.41
1	C	321	TRP	CD2-CE2	5.32	1.47	1.41
1	C	452	TRP	CD2-CE2	5.25	1.47	1.41
1	C	9	TRP	CD2-CE2	5.23	1.47	1.41
1	E	9	TRP	CD2-CE2	5.22	1.47	1.41
1	E	34	TRP	CD2-CE2	5.21	1.47	1.41
1	C	160	TRP	CD2-CE2	5.15	1.47	1.41
1	A	422	TRP	CD2-CE2	5.12	1.47	1.41
1	B	321	TRP	CD2-CE2	5.08	1.47	1.41
1	A	321	TRP	CD2-CE2	5.06	1.47	1.41
1	C	362	TRP	CD2-CE2	5.00	1.47	1.41

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	444	ARG	NE-CZ-NH2	-9.72	115.44	120.30
1	C	444	ARG	NE-CZ-NH1	8.95	124.77	120.30
1	C	444	ARG	NE-CZ-NH2	-7.59	116.51	120.30
1	C	431	ARG	NE-CZ-NH1	7.30	123.95	120.30
1	B	429	LYS	CD-CE-NZ	-6.62	96.47	111.70
1	B	444	ARG	NE-CZ-NH1	6.47	123.54	120.30
1	B	444	ARG	NE-CZ-NH2	-6.44	117.08	120.30
1	C	74	ARG	NE-CZ-NH2	-6.43	117.08	120.30
1	A	84	ASP	CB-CG-OD2	-6.19	112.73	118.30
1	C	84	ASP	CB-CG-OD1	5.83	123.55	118.30
1	A	444	ARG	NE-CZ-NH1	5.74	123.17	120.30
1	A	74	ARG	NE-CZ-NH1	5.74	123.17	120.30
1	C	22	ARG	NE-CZ-NH1	5.69	123.15	120.30
1	B	74	ARG	NE-CZ-NH2	-5.65	117.47	120.30
1	A	84	ASP	CB-CG-OD1	5.61	123.35	118.30
1	D	444	ARG	NE-CZ-NH2	-5.61	117.50	120.30
1	C	358	ASP	CB-CG-OD1	5.55	123.30	118.30
1	C	84	ASP	CB-CG-OD2	-5.48	113.37	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	F	107	LEU	CA-CB-CG	-5.40	102.89	115.30
1	A	378	ARG	NE-CZ-NH2	-5.21	117.69	120.30
1	A	327	LEU	CA-CB-CG	5.13	127.11	115.30
1	B	238	MET	CG-SD-CE	-5.12	92.01	100.20
1	F	156	ARG	NE-CZ-NH1	5.09	122.84	120.30
1	B	378	ARG	NE-CZ-NH1	5.06	122.83	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3767	0	3574	78	0
1	B	3767	0	3574	74	0
1	C	3767	0	3574	79	0
1	D	3767	0	3574	64	0
1	E	3767	0	3574	93	0
1	F	3767	0	3574	155	0
2	A	1	0	0	0	0
2	B	4	0	0	2	0
2	C	3	0	0	0	0
2	D	5	0	0	0	0
2	E	1	0	0	0	0
2	F	3	0	0	0	0
All	All	22619	0	21444	540	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 12.

All (540) 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:224:ASN:OD1	1:B:226:THR:HG23	1.35	1.23
1:F:331:ARG:CG	1:F:331:ARG:HH11	1.47	1.22

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:331:ARG:CG	1:B:331:ARG:HH11	1.54	1.16
1:A:224:ASN:OD1	1:A:226:THR:HG23	1.46	1.16
1:F:331:ARG:HG2	1:F:331:ARG:HH11	1.10	1.15
1:C:224:ASN:OD1	1:C:226:THR:HG23	1.48	1.13
1:E:331:ARG:HG2	1:E:331:ARG:HH11	1.09	1.13
1:A:331:ARG:HH11	1:A:331:ARG:CG	1.63	1.11
1:E:112:ARG:HD3	1:E:159:ASP:OD2	1.54	1.07
1:E:224:ASN:OD1	1:E:226:THR:HG23	1.56	1.05
1:E:331:ARG:CG	1:E:331:ARG:HH11	1.69	1.04
1:A:331:ARG:HH11	1:A:331:ARG:HG2	0.91	1.04
1:B:331:ARG:HG3	1:B:331:ARG:HH11	1.23	1.03
1:F:81:ARG:HH11	1:F:81:ARG:HG3	1.21	1.01
1:F:359:ASN:HD21	1:F:409:ASN:H	1.06	0.98
1:C:379:ASP:OD1	1:C:381:THR:HG22	1.64	0.96
1:A:331:ARG:NH1	1:A:331:ARG:HG2	1.72	0.96
1:B:224:ASN:OD1	1:B:226:THR:CG2	2.13	0.95
1:F:199:ALA:O	1:F:203:VAL:HG23	1.67	0.94
1:F:331:ARG:CG	1:F:331:ARG:NH1	2.21	0.92
1:F:224:ASN:OD1	1:F:226:THR:HG23	1.68	0.92
1:D:331:ARG:HG2	1:D:331:ARG:HH11	1.35	0.91
1:A:379:ASP:OD1	1:A:381:THR:HG22	1.70	0.91
1:E:282:GLU:HA	1:E:285:LEU:HD12	1.52	0.91
1:F:331:ARG:HG2	1:F:331:ARG:NH1	1.79	0.90
1:B:331:ARG:HG2	1:B:331:ARG:HH11	1.34	0.90
1:F:331:ARG:HH11	1:F:331:ARG:HG3	1.35	0.89
1:B:331:ARG:NH1	1:B:331:ARG:CG	2.26	0.89
1:E:136:LYS:HZ3	1:E:194:TYR:HE2	1.13	0.89
1:C:328:MET:O	1:C:331:ARG:HD3	1.75	0.87
1:E:188:LYS:O	1:E:192:VAL:HG23	1.74	0.86
1:C:174:TYR:CE2	1:C:192:VAL:HG21	2.11	0.85
1:B:100:ASN:ND2	1:B:156:ARG:HH22	1.75	0.85
1:B:279:THR:HG22	1:B:282:GLU:H	1.44	0.82
1:C:225:LEU:HD22	1:C:353:MET:HE3	1.62	0.82
1:E:52:SER:O	1:E:444:ARG:NH2	2.13	0.81
1:F:297:ASN:ND2	1:F:366:GLU:HB2	1.95	0.81
1:F:160:TRP:HB2	1:F:219:ILE:CG2	2.11	0.81
1:B:100:ASN:HD21	1:B:156:ARG:HH22	1.23	0.81
1:F:122:LEU:HD12	1:F:123:PRO:HD2	1.63	0.80
1:D:279:THR:HG22	1:D:282:GLU:H	1.47	0.80
1:D:353:MET:HA	1:D:353:MET:HE2	1.62	0.80
1:B:445:ARG:HH11	1:B:445:ARG:CG	1.94	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:224:ASN:OD1	1:A:226:THR:CG2	2.28	0.79
1:D:53:ASP:OD1	1:D:56:HIS:HD2	1.66	0.79
1:F:112:ARG:HD3	1:F:159:ASP:OD2	1.82	0.79
1:F:81:ARG:NH1	1:F:81:ARG:HG3	1.96	0.78
1:B:445:ARG:HH11	1:B:445:ARG:HG3	1.49	0.77
1:E:254:GLU:HG3	1:E:262:PRO:HG3	1.65	0.77
1:B:359:ASN:HD21	1:B:409:ASN:H	1.32	0.76
1:C:100:ASN:HD22	1:C:156:ARG:HH12	1.32	0.76
1:D:224:ASN:OD1	1:D:226:THR:CG2	2.34	0.75
1:C:224:ASN:OD1	1:C:226:THR:CG2	2.33	0.75
1:B:242:HIS:ND1	2:B:2003:HOH:O	1.83	0.75
1:A:190:VAL:HG21	1:A:274:VAL:CG1	2.16	0.75
1:D:359:ASN:HD21	1:D:409:ASN:H	1.30	0.75
1:F:160:TRP:HB2	1:F:219:ILE:HG22	1.70	0.74
1:C:100:ASN:ND2	1:C:156:ARG:HH12	1.86	0.74
1:F:61:ASP:OD1	1:F:444:ARG:NH1	2.21	0.74
1:D:331:ARG:NH1	1:D:333:MET:HB2	2.02	0.74
1:F:162:VAL:HG21	1:F:200:THR:HG23	1.70	0.72
1:C:53:ASP:OD1	1:C:56:HIS:HD2	1.73	0.72
1:D:331:ARG:HH12	1:D:333:MET:HB2	1.53	0.71
1:D:331:ARG:NH1	1:D:331:ARG:HG2	2.03	0.71
1:F:26:GLN:OE1	1:F:92:ASN:ND2	2.23	0.71
1:B:331:ARG:NH1	1:B:331:ARG:HG3	1.99	0.71
1:B:44:ASP:O	1:B:45:TYR:HB2	1.88	0.71
1:A:331:ARG:CG	1:A:331:ARG:NH1	2.35	0.71
1:F:74:ARG:HA	1:F:114:VAL:O	1.90	0.71
1:E:331:ARG:CG	1:E:331:ARG:NH1	2.37	0.71
1:D:224:ASN:OD1	1:D:226:THR:HG22	1.91	0.70
1:B:434:LEU:O	1:B:447:LYS:HG3	1.91	0.70
1:F:277:GLN:NE2	1:F:277:GLN:HA	2.06	0.70
1:F:15:SER:O	1:F:19:SER:OG	2.08	0.70
1:A:253:MET:CE	1:A:353:MET:HE1	2.22	0.70
1:F:275:LEU:HD12	1:F:276:TRP:H	1.56	0.69
1:F:225:LEU:HD13	1:F:253:MET:HG3	1.74	0.69
1:F:52:SER:O	1:F:444:ARG:NH2	2.25	0.69
1:B:331:ARG:NH1	1:B:331:ARG:HG2	1.97	0.69
1:B:279:THR:CG2	1:B:281:GLU:HB2	2.22	0.69
1:E:100:ASN:HD21	1:E:156:ARG:HH22	1.39	0.69
1:B:53:ASP:OD1	1:B:56:HIS:HD2	1.76	0.69
1:E:381:THR:HG23	1:E:445:ARG:NH2	2.08	0.68
1:D:379:ASP:OD1	1:D:381:THR:CG2	2.41	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:459:HIS:O	1:C:461:ARG:HG3	1.93	0.68
1:F:359:ASN:HD21	1:F:409:ASN:N	1.86	0.68
1:F:188:LYS:O	1:F:192:VAL:HG23	1.93	0.68
1:D:160:TRP:HB2	1:D:219:ILE:HG13	1.76	0.68
1:F:190:VAL:O	1:F:193:ALA:HB3	1.94	0.68
1:A:127:TYR:CZ	1:A:181:PRO:HG3	2.28	0.68
1:A:61:ASP:OD1	1:A:444:ARG:HD2	1.94	0.67
1:C:417:THR:O	1:C:433:GLY:HA2	1.94	0.67
1:A:359:ASN:HD21	1:A:408:SER:HA	1.59	0.67
1:E:328:MET:O	1:E:331:ARG:HD2	1.94	0.66
1:E:14:THR:OG1	1:E:15:SER:N	2.28	0.66
1:B:328:MET:O	1:B:331:ARG:HD2	1.96	0.66
1:E:194:TYR:CZ	1:E:278:SER:HB2	2.31	0.66
1:F:234:SER:O	1:F:238:MET:HB2	1.94	0.66
1:E:225:LEU:HD22	1:E:353:MET:CE	2.25	0.66
1:A:328:MET:O	1:A:331:ARG:HD2	1.96	0.66
1:C:225:LEU:CD2	1:C:353:MET:CE	2.73	0.66
1:A:139:VAL:O	1:A:143:VAL:HG23	1.96	0.66
1:E:359:ASN:HD21	1:E:409:ASN:H	1.44	0.65
1:C:25:LYS:NZ	1:C:78:GLN:HE22	1.94	0.65
1:B:105:ALA:O	1:B:109:ASN:ND2	2.24	0.65
1:E:104:ASP:OD1	1:E:156:ARG:NH1	2.29	0.65
1:F:80:THR:HG23	1:F:123:PRO:HG3	1.79	0.65
1:E:225:LEU:HD22	1:E:353:MET:HE2	1.78	0.65
1:F:87:GLU:OE2	1:F:130:TYR:OH	2.15	0.64
1:E:331:ARG:NH1	1:E:331:ARG:HG2	1.92	0.64
1:F:160:TRP:HB2	1:F:219:ILE:HG23	1.79	0.64
1:D:100:ASN:ND2	1:D:156:ARG:HH12	1.95	0.64
1:C:359:ASN:HD21	1:C:409:ASN:H	1.44	0.64
1:F:105:ALA:O	1:F:109:ASN:HB2	1.98	0.64
1:F:58:ILE:HG12	1:F:102:VAL:HG22	1.79	0.64
1:E:56:HIS:CD2	1:F:56:HIS:CD2	2.86	0.64
1:C:2:LEU:HG	1:C:401:HIS:CE1	2.33	0.63
1:B:331:ARG:H	1:B:331:ARG:HD3	1.62	0.63
1:F:204:ILE:HG23	1:F:219:ILE:CD1	2.28	0.63
1:A:253:MET:CE	1:A:353:MET:CE	2.77	0.63
1:D:379:ASP:OD1	1:D:381:THR:HG23	1.98	0.63
1:E:379:ASP:OD1	1:E:381:THR:HG22	1.99	0.63
1:F:275:LEU:HD12	1:F:276:TRP:N	2.14	0.63
1:A:53:ASP:OD1	1:A:56:HIS:HD2	1.83	0.62
1:D:99:TYR:O	1:D:103:ILE:HG12	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:103:ILE:N	1:F:103:ILE:HD13	2.15	0.62
1:E:174:TYR:CE2	1:E:192:VAL:HG21	2.34	0.62
1:E:100:ASN:ND2	1:E:156:ARG:HH22	1.98	0.62
1:F:84:ASP:HB3	1:F:90:THR:OG1	1.99	0.61
1:C:2:LEU:HG	1:C:401:HIS:ND1	2.15	0.61
1:D:375:ASP:OD1	1:D:378:ARG:HD2	2.00	0.61
1:C:225:LEU:HD22	1:C:353:MET:CE	2.30	0.61
1:E:258:HIS:HA	1:E:290:ARG:NH1	2.16	0.61
1:C:6:LYS:O	1:C:7:GLU:HB2	2.01	0.61
1:F:277:GLN:HE21	1:F:277:GLN:HA	1.62	0.61
1:B:174:TYR:CE2	1:B:192:VAL:HG21	2.35	0.61
1:F:11:GLY:HA2	1:F:70:HIS:ND1	2.14	0.61
1:D:169:VAL:O	1:D:173:SER:HB2	2.00	0.61
1:B:225:LEU:HD13	1:B:253:MET:HG3	1.83	0.61
1:F:208:ARG:NH2	1:F:219:ILE:HD11	2.15	0.61
1:F:205:GLN:HB2	1:F:289:ASN:ND2	2.16	0.61
1:D:353:MET:HA	1:D:353:MET:CE	2.28	0.60
1:B:445:ARG:HG3	1:B:445:ARG:NH1	2.16	0.60
1:F:58:ILE:O	1:F:61:ASP:HB2	2.00	0.60
1:D:53:ASP:OD1	1:D:56:HIS:CD2	2.53	0.60
1:D:362:TRP:O	1:D:410:CYS:HA	2.00	0.60
1:A:253:MET:HE1	1:A:353:MET:CE	2.32	0.60
1:A:279:THR:HG22	1:A:282:GLU:H	1.67	0.60
1:C:331:ARG:HG3	1:C:340:GLU:HG3	1.82	0.60
1:A:112:ARG:HD3	1:A:159:ASP:OD2	2.00	0.60
1:A:253:MET:HE1	1:A:353:MET:HE1	1.83	0.60
1:F:219:ILE:HD12	1:F:219:ILE:O	2.02	0.59
1:F:81:ARG:CG	1:F:81:ARG:HH11	2.07	0.59
1:F:143:VAL:O	1:F:146:SER:OG	2.16	0.59
1:F:359:ASN:ND2	1:F:409:ASN:H	1.88	0.59
1:B:328:MET:O	1:B:331:ARG:CD	2.50	0.59
1:E:220:GLY:HA2	1:E:291:VAL:HG12	1.84	0.59
1:A:375:ASP:O	1:A:378:ARG:HG3	2.01	0.59
1:F:59:GLU:OE2	1:F:101:ARG:HB3	2.02	0.59
1:B:378:ARG:HH22	1:B:436:GLU:CD	2.06	0.58
1:C:251:LEU:HD23	1:C:251:LEU:C	2.24	0.58
1:C:246:LEU:HA	1:C:250:ASP:HB2	1.85	0.58
1:E:225:LEU:CD2	1:E:353:MET:HE2	2.34	0.58
1:A:136:LYS:NZ	1:A:282:GLU:OE1	2.34	0.58
1:B:100:ASN:HD22	1:B:156:ARG:HH12	1.51	0.58
1:D:224:ASN:OD1	1:D:226:THR:HG23	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:99:TYR:O	1:C:103:ILE:HG12	2.04	0.58
1:E:133:TRP:HB2	1:E:192:VAL:HG13	1.86	0.58
1:F:378:ARG:HH22	1:F:436:GLU:CD	2.06	0.58
1:E:279:THR:HG22	1:E:281:GLU:H	1.69	0.58
1:D:379:ASP:OD1	1:D:381:THR:HG22	2.04	0.58
1:B:314:SER:HB2	1:B:321:TRP:CZ2	2.39	0.58
1:D:331:ARG:CG	1:D:331:ARG:NH1	2.67	0.57
1:D:225:LEU:HD22	1:D:353:MET:HE3	1.86	0.57
1:F:353:MET:HE2	1:F:353:MET:HA	1.86	0.57
1:F:264:GLU:O	1:F:268:VAL:HG23	2.04	0.57
1:C:419:ILE:HD13	1:C:444:ARG:HD3	1.86	0.57
1:C:251:LEU:HD23	1:C:251:LEU:O	2.04	0.57
1:E:74:ARG:HA	1:E:114:VAL:O	2.05	0.57
1:D:100:ASN:HD22	1:D:156:ARG:HH12	1.52	0.57
1:C:225:LEU:CD2	1:C:353:MET:HE2	2.34	0.57
1:F:162:VAL:HG23	1:F:221:THR:HG22	1.87	0.57
1:C:74:ARG:HB2	1:C:114:VAL:HB	1.86	0.57
1:A:251:LEU:HD23	1:A:251:LEU:O	2.05	0.56
1:E:194:TYR:OH	1:E:278:SER:HB2	2.06	0.56
1:E:251:LEU:C	1:E:251:LEU:HD23	2.24	0.56
1:A:379:ASP:CG	1:A:381:THR:HG22	2.26	0.56
1:A:331:ARG:HH12	1:A:333:MET:HB3	1.70	0.56
1:A:190:VAL:HG21	1:A:274:VAL:HG13	1.87	0.56
1:E:417:THR:O	1:E:433:GLY:HA2	2.06	0.56
1:F:365:SER:O	1:F:414:HIS:HB2	2.06	0.56
1:F:204:ILE:HG23	1:F:219:ILE:HD13	1.87	0.56
1:F:363:PHE:HB2	1:F:412:GLY:O	2.06	0.56
1:B:379:ASP:OD1	1:B:381:THR:HG22	2.06	0.56
1:F:435:VAL:HG22	1:F:446:PRO:HA	1.87	0.56
1:F:103:ILE:O	1:F:106:CYS:HB2	2.06	0.55
1:F:331:ARG:HG3	1:F:331:ARG:NH1	2.04	0.55
1:B:44:ASP:O	1:B:45:TYR:CB	2.51	0.55
1:F:116:ASN:ND2	1:F:118:HIS:O	2.31	0.55
1:B:314:SER:HB2	1:B:321:TRP:HZ2	1.72	0.55
1:D:190:VAL:HG21	1:D:274:VAL:HG13	1.88	0.55
1:A:2:LEU:HG	1:A:401:HIS:ND1	2.21	0.55
1:F:246:LEU:HD13	1:F:265:LEU:HB2	1.88	0.55
1:F:360:ILE:HD12	1:F:361:PRO:O	2.07	0.55
1:E:122:LEU:HD21	1:E:132:GLY:HA2	1.88	0.55
1:C:225:LEU:HD13	1:C:253:MET:HG3	1.88	0.55
1:C:362:TRP:O	1:C:410:CYS:HA	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:328:MET:O	1:A:331:ARG:CD	2.55	0.55
1:C:294:LEU:O	1:C:362:TRP:HA	2.07	0.55
1:F:357:TYR:O	1:F:360:ILE:HG23	2.06	0.54
1:A:253:MET:HE2	1:A:353:MET:CE	2.37	0.54
1:A:208:ARG:HH21	1:A:292:ASP:CG	2.10	0.54
1:D:370:GLY:O	1:D:371:ILE:HD13	2.07	0.54
1:E:362:TRP:O	1:E:410:CYS:HA	2.08	0.54
1:C:61:ASP:OD1	1:C:444:ARG:HD2	2.06	0.54
1:A:344:GLU:HG3	1:A:399:TYR:CZ	2.42	0.54
1:B:81:ARG:HD2	1:B:99:TYR:CE2	2.43	0.54
1:E:61:ASP:OD1	1:E:444:ARG:HD2	2.07	0.54
1:F:146:SER:HB2	1:F:150:PHE:CE2	2.43	0.54
1:D:328:MET:O	1:D:331:ARG:HD2	2.08	0.54
1:F:378:ARG:NH2	1:F:436:GLU:OE1	2.41	0.54
1:F:435:VAL:HG13	1:F:445:ARG:C	2.28	0.54
1:A:331:ARG:H	1:A:331:ARG:HD3	1.74	0.53
1:F:160:TRP:CB	1:F:219:ILE:HG22	2.36	0.53
1:F:222:ILE:HA	1:F:295:GLY:O	2.08	0.53
1:F:317:TRP:HD1	1:F:321:TRP:CZ3	2.26	0.53
1:D:279:THR:HG23	1:D:281:GLU:OE1	2.09	0.53
1:F:104:ASP:OD1	1:F:156:ARG:NH1	2.31	0.53
1:C:379:ASP:CG	1:C:381:THR:HG22	2.29	0.53
1:A:253:MET:HE2	1:A:353:MET:HE1	1.90	0.53
1:F:27:HIS:HB2	1:F:80:THR:HB	1.89	0.53
1:C:22:ARG:NH2	1:C:28:ARG:HG2	2.24	0.53
1:F:99:TYR:HB2	1:F:153:PHE:CZ	2.43	0.53
1:F:251:LEU:HD23	1:F:251:LEU:C	2.29	0.53
1:F:116:ASN:HA	1:F:161:PHE:O	2.09	0.53
1:C:284:ALA:O	1:C:288:GLU:HB2	2.08	0.53
1:C:12:GLY:HA3	1:C:418:PRO:HG3	1.91	0.53
1:D:378:ARG:HA	1:D:383:GLN:O	2.09	0.52
1:F:225:LEU:HD12	1:F:249:ASN:HB3	1.91	0.52
1:F:417:THR:O	1:F:433:GLY:HA2	2.10	0.52
1:F:139:VAL:HG13	1:F:199:ALA:HB2	1.92	0.52
1:E:56:HIS:CD2	1:F:56:HIS:NE2	2.77	0.52
1:E:256:ALA:O	1:E:291:VAL:HG22	2.09	0.52
1:B:370:GLY:HA2	1:B:431:ARG:O	2.09	0.52
1:C:333:MET:HG3	1:C:334:ASN:N	2.25	0.52
1:F:25:LYS:NZ	1:F:78:GLN:HE22	2.07	0.52
1:A:106:CYS:HB3	1:A:111:ILE:O	2.10	0.51
1:F:362:TRP:O	1:F:410:CYS:HA	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:384:ILE:HB	1:F:447:LYS:HG2	1.93	0.51
1:E:196:LEU:O	1:E:200:THR:OG1	2.28	0.51
1:F:204:ILE:HD12	1:F:219:ILE:HB	1.91	0.51
1:E:381:THR:HG23	1:E:445:ARG:HH22	1.75	0.51
1:D:459:HIS:O	1:D:461:ARG:HG2	2.11	0.51
1:D:353:MET:HE2	1:D:353:MET:CA	2.39	0.51
1:D:91:ILE:O	1:D:93:PRO:HD3	2.10	0.51
1:F:100:ASN:ND2	1:F:156:ARG:HH22	2.08	0.51
1:F:29:ASN:HD22	1:F:78:GLN:NE2	2.08	0.51
1:A:208:ARG:NH2	1:A:292:ASP:OD1	2.43	0.51
1:E:397:LEU:O	1:E:400:LEU:HB3	2.11	0.51
1:F:15:SER:HB3	1:F:119:HIS:CD2	2.47	0.50
1:F:174:TYR:CE2	1:F:192:VAL:HG21	2.47	0.50
1:E:53:ASP:OD1	1:E:56:HIS:HD2	1.92	0.50
1:D:6:LYS:O	1:D:7:GLU:HB2	2.10	0.50
1:A:294:LEU:O	1:A:362:TRP:HA	2.11	0.50
1:A:53:ASP:OD1	1:A:56:HIS:CD2	2.65	0.50
1:F:378:ARG:HA	1:F:383:GLN:O	2.11	0.50
1:A:331:ARG:HH12	1:A:333:MET:CB	2.24	0.50
1:B:379:ASP:OD1	1:B:381:THR:CG2	2.60	0.50
1:A:370:GLY:O	1:A:371:ILE:HD13	2.12	0.50
1:F:16:GLY:N	1:F:17:PRO:CD	2.75	0.50
1:E:331:ARG:NH1	1:E:333:MET:HB2	2.27	0.50
1:F:251:LEU:HD12	1:F:265:LEU:HD21	1.91	0.50
1:C:248:ASN:C	1:C:249:ASN:HD22	2.15	0.50
1:A:379:ASP:OD1	1:A:381:THR:CG2	2.51	0.50
1:F:161:PHE:HD2	1:F:221:THR:N	2.10	0.50
1:F:248:ASN:C	1:F:249:ASN:HD22	2.15	0.50
1:B:426:ASN:O	1:B:427:ALA:C	2.49	0.50
1:C:251:LEU:CD2	1:C:251:LEU:C	2.80	0.49
1:F:297:ASN:HD22	1:F:366:GLU:H	1.59	0.49
1:E:74:ARG:NH2	1:E:164:ASN:OD1	2.44	0.49
1:E:180:TYR:CG	1:E:181:PRO:HA	2.48	0.49
1:A:331:ARG:NH1	1:A:333:MET:HB3	2.26	0.49
1:A:386:ASP:OD2	1:A:449:SER:HB3	2.12	0.49
1:D:6:LYS:O	1:D:7:GLU:CB	2.61	0.49
1:F:297:ASN:HD22	1:F:366:GLU:N	2.11	0.49
1:E:200:THR:O	1:E:204:ILE:HG12	2.13	0.49
1:A:127:TYR:CE1	1:A:181:PRO:HG3	2.47	0.49
1:F:137:HIS:CD2	1:F:141:LEU:HD11	2.48	0.49
1:E:80:THR:HG22	1:E:123:PRO:HB3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:190:VAL:HG21	1:E:274:VAL:HG22	1.94	0.48
1:A:251:LEU:HD23	1:A:251:LEU:C	2.33	0.48
1:A:241:ALA:HA	1:A:304:VAL:HG21	1.96	0.48
1:F:268:VAL:O	1:F:272:ASP:OD1	2.31	0.48
1:E:344:GLU:HG3	1:E:399:TYR:CZ	2.48	0.48
1:E:96:LEU:HD11	1:E:152:GLN:HE21	1.78	0.48
1:C:127:TYR:CZ	1:C:181:PRO:HG3	2.48	0.48
1:F:366:GLU:HG2	1:F:416:TRP:HE3	1.77	0.48
1:A:417:THR:O	1:A:433:GLY:HA2	2.13	0.48
1:F:130:TYR:CE2	1:F:137:HIS:HD2	2.30	0.48
1:D:100:ASN:HD21	1:D:156:ARG:HH22	1.60	0.48
1:F:201:ALA:HB2	1:F:286:ILE:HA	1.95	0.48
1:B:100:ASN:ND2	1:B:156:ARG:NH2	2.54	0.48
1:B:99:TYR:O	1:B:103:ILE:HG12	2.14	0.48
1:A:8:PHE:HD2	1:A:10:TRP:CE2	2.31	0.48
1:C:25:LYS:HZ2	1:C:78:GLN:HE22	1.59	0.48
1:C:25:LYS:HZ2	1:C:78:GLN:NE2	2.12	0.48
1:E:187:LYS:HA	1:E:274:VAL:HG23	1.95	0.48
1:D:257:VAL:HG12	1:D:258:HIS:CD2	2.49	0.48
1:B:225:LEU:HD22	1:B:353:MET:CE	2.44	0.48
1:F:317:TRP:HA	1:F:321:TRP:CZ2	2.49	0.48
1:E:375:ASP:OD1	1:E:378:ARG:NH1	2.46	0.48
1:F:383:GLN:HG2	1:F:384:ILE:N	2.29	0.48
1:B:246:LEU:HA	1:B:250:ASP:HB2	1.96	0.48
1:F:397:LEU:HB3	1:F:462:LEU:HD11	1.96	0.48
1:A:100:ASN:ND2	1:A:156:ARG:HH22	2.12	0.48
1:F:133:TRP:O	1:F:192:VAL:HG22	2.14	0.48
1:E:56:HIS:NE2	1:F:56:HIS:CD2	2.82	0.48
1:C:6:LYS:O	1:C:7:GLU:CB	2.62	0.47
1:F:29:ASN:HD22	1:F:78:GLN:HE21	1.61	0.47
1:B:52:SER:O	1:B:444:ARG:NH2	2.40	0.47
1:F:205:GLN:OE1	1:F:285:LEU:CD2	2.61	0.47
1:E:9:TRP:HB2	1:E:412:GLY:HA3	1.96	0.47
1:C:344:GLU:HG3	1:C:399:TYR:CZ	2.49	0.47
1:C:371:ILE:HG13	1:C:388:TYR:CE1	2.48	0.47
1:D:11:GLY:O	1:D:414:HIS:HA	2.15	0.47
1:A:91:ILE:HG21	1:A:96:LEU:HD22	1.96	0.47
1:D:42:PHE:O	1:D:43:TYR:C	2.52	0.47
1:C:25:LYS:HZ3	1:C:78:GLN:HE22	1.62	0.47
1:C:362:TRP:CZ2	1:C:410:CYS:HB2	2.49	0.47
1:D:14:THR:OG1	1:D:15:SER:N	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:279:THR:HG22	1:C:282:GLU:H	1.78	0.47
1:C:20:GLU:HA	1:C:54:ALA:HB3	1.95	0.47
1:E:331:ARG:HG3	1:E:331:ARG:NH1	2.24	0.47
1:F:122:LEU:HD12	1:F:123:PRO:CD	2.38	0.47
1:D:127:TYR:HA	1:D:132:GLY:N	2.29	0.47
1:F:136:LYS:O	1:F:139:VAL:HB	2.14	0.47
1:C:401:HIS:O	1:C:404:ILE:N	2.47	0.47
1:B:378:ARG:NH2	1:B:436:GLU:OE1	2.47	0.47
1:F:201:ALA:CB	1:F:286:ILE:HA	2.45	0.47
1:E:133:TRP:CB	1:E:192:VAL:HG13	2.45	0.47
1:E:416:TRP:CD1	1:E:417:THR:HB	2.50	0.47
1:C:162:VAL:HG11	1:C:200:THR:HA	1.97	0.47
1:A:444:ARG:HG2	1:A:444:ARG:H	1.54	0.47
1:E:50:THR:O	1:E:51:ALA:C	2.53	0.46
1:A:162:VAL:HG11	1:A:200:THR:HA	1.95	0.46
1:F:314:SER:HA	1:F:315:PRO:HD2	1.65	0.46
1:D:25:LYS:NZ	1:D:78:GLN:HE22	2.12	0.46
1:B:313:ILE:HD12	1:B:314:SER:H	1.80	0.46
1:E:127:TYR:HA	1:E:132:GLY:N	2.31	0.46
1:C:279:THR:HG23	1:C:281:GLU:OE1	2.16	0.46
1:F:81:ARG:O	1:F:81:ARG:HG2	2.16	0.46
1:F:362:TRP:CE2	1:F:410:CYS:HB2	2.51	0.46
1:D:127:TYR:CZ	1:D:181:PRO:HG3	2.50	0.46
1:C:241:ALA:HA	1:C:304:VAL:HG21	1.97	0.46
1:E:211:PRO:HG2	1:E:214:LEU:HD12	1.98	0.46
1:D:29:ASN:HD22	1:D:78:GLN:NE2	2.14	0.46
1:A:419:ILE:O	1:A:420:ASP:C	2.53	0.46
1:C:200:THR:O	1:C:204:ILE:HG13	2.15	0.46
1:B:279:THR:HG22	1:B:282:GLU:N	2.21	0.46
1:C:225:LEU:HD21	1:C:353:MET:HE2	1.98	0.46
1:F:208:ARG:HH21	1:F:219:ILE:HD11	1.80	0.46
1:F:243:PHE:O	1:F:246:LEU:HB2	2.15	0.46
1:F:127:TYR:HA	1:F:132:GLY:N	2.31	0.46
1:E:88:GLN:HB2	1:E:90:THR:HG23	1.97	0.46
1:B:459:HIS:O	1:B:461:ARG:HG3	2.16	0.46
1:E:199:ALA:O	1:E:203:VAL:HG23	2.15	0.45
1:E:248:ASN:C	1:E:249:ASN:HD22	2.20	0.45
1:E:7:GLU:OE1	1:E:7:GLU:HA	2.16	0.45
1:A:100:ASN:ND2	1:A:156:ARG:HH12	2.15	0.45
1:C:180:TYR:CG	1:C:181:PRO:HA	2.51	0.45
1:C:174:TYR:CD2	1:C:192:VAL:HG21	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:61:ASP:OD2	1:E:444:ARG:NH1	2.50	0.45
1:B:357:TYR:O	1:B:359:ASN:N	2.49	0.45
1:B:313:ILE:HD13	1:B:313:ILE:HA	1.73	0.45
1:E:298:PHE:CZ	1:E:345:ALA:HB3	2.51	0.45
1:D:344:GLU:H	1:D:344:GLU:CD	2.19	0.45
1:C:14:THR:OG1	1:C:15:SER:N	2.49	0.45
1:A:416:TRP:CD1	1:A:417:THR:HB	2.52	0.45
1:A:254:GLU:HG3	1:A:262:PRO:HG3	1.99	0.45
1:F:389:ARG:O	1:F:393:LEU:HG	2.17	0.45
1:A:251:LEU:C	1:A:251:LEU:CD2	2.85	0.45
1:E:254:GLU:HB2	1:E:262:PRO:HD3	1.97	0.45
1:C:359:ASN:ND2	1:C:409:ASN:H	2.13	0.45
1:E:317:TRP:HA	1:E:321:TRP:CZ2	2.51	0.45
1:A:9:TRP:CD1	1:A:9:TRP:N	2.84	0.45
1:B:357:TYR:C	1:B:359:ASN:H	2.20	0.45
1:D:331:ARG:NH2	1:D:333:MET:SD	2.90	0.45
1:F:80:THR:CG2	1:F:123:PRO:HG3	2.46	0.45
1:F:140:ASP:O	1:F:143:VAL:HB	2.17	0.45
1:C:16:GLY:N	1:C:17:PRO:CD	2.80	0.45
1:E:122:LEU:HD13	1:E:133:TRP:CE2	2.51	0.45
1:F:317:TRP:CD1	1:F:321:TRP:CZ3	3.04	0.45
1:A:100:ASN:HD21	1:A:156:ARG:HH22	1.64	0.45
1:A:16:GLY:N	1:A:17:PRO:CD	2.80	0.45
1:B:353:MET:HE1	1:B:357:TYR:CD2	2.53	0.44
1:F:277:GLN:NE2	1:F:277:GLN:CA	2.77	0.44
1:A:359:ASN:HD21	1:A:409:ASN:H	1.65	0.44
1:A:100:ASN:HD22	1:A:156:ARG:HH12	1.65	0.44
1:C:353:MET:HE1	1:C:357:TYR:CD2	2.51	0.44
1:F:159:ASP:HA	1:F:293:TYR:OH	2.17	0.44
1:C:25:LYS:NZ	1:C:78:GLN:NE2	2.64	0.44
1:B:381:THR:O	1:B:381:THR:OG1	2.35	0.44
1:F:144:ALA:O	1:F:147:LYS:HB2	2.18	0.44
1:B:139:VAL:O	1:B:143:VAL:HG23	2.18	0.44
1:B:371:ILE:HG13	1:B:388:TYR:CE1	2.52	0.44
1:F:313:ILE:HA	1:F:313:ILE:HD13	1.58	0.44
1:E:404:ILE:O	1:E:407:GLY:N	2.44	0.44
1:C:178:PHE:O	1:C:179:HIS:HD2	2.00	0.44
1:E:99:TYR:O	1:E:102:VAL:HB	2.17	0.44
1:A:279:THR:HG23	1:A:281:GLU:OE1	2.18	0.44
1:C:52:SER:O	1:C:444:ARG:NH2	2.42	0.44
1:A:14:THR:OG1	1:A:15:SER:N	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:445:ARG:HH11	1:D:445:ARG:HG3	1.81	0.44
1:D:249:ASN:N	1:D:249:ASN:HD22	2.14	0.44
1:A:445:ARG:HA	1:A:446:PRO:HD3	1.67	0.44
1:F:334:ASN:HB2	1:F:341:ILE:HD11	1.98	0.44
1:A:253:MET:CE	1:A:353:MET:HE3	2.48	0.43
1:D:122:LEU:HD21	1:D:132:GLY:CA	2.48	0.43
1:F:160:TRP:CB	1:F:219:ILE:CG2	2.91	0.43
1:D:225:LEU:CD2	1:D:353:MET:HE3	2.46	0.43
1:B:225:LEU:HD22	1:B:353:MET:HE3	2.00	0.43
1:B:312:VAL:HG23	1:B:313:ILE:N	2.33	0.43
1:B:314:SER:HA	1:B:315:PRO:HD2	1.91	0.43
1:D:61:ASP:O	1:D:65:LEU:HG	2.18	0.43
1:B:419:ILE:O	1:B:420:ASP:C	2.55	0.43
1:C:8:PHE:CE1	1:C:412:GLY:N	2.86	0.43
1:E:74:ARG:HB2	1:E:114:VAL:HB	1.99	0.43
1:F:194:TYR:O	1:F:197:ALA:HB3	2.19	0.43
1:D:12:GLY:HA3	1:D:418:PRO:HG3	1.99	0.43
1:C:313:ILE:HD13	1:C:313:ILE:HA	1.67	0.43
1:F:419:ILE:O	1:F:420:ASP:C	2.57	0.43
1:F:190:VAL:HG21	1:F:274:VAL:HG13	2.00	0.43
1:A:180:TYR:CG	1:A:181:PRO:HA	2.53	0.43
1:B:375:ASP:O	1:B:378:ARG:HG2	2.19	0.43
1:C:216:ASP:OD1	1:C:216:ASP:N	2.52	0.43
1:E:44:ASP:O	1:E:45:TYR:HB2	2.18	0.43
1:A:313:ILE:HD12	1:A:313:ILE:HA	1.84	0.43
1:F:297:ASN:HD22	1:F:366:GLU:HB2	1.78	0.43
1:E:344:GLU:HG3	1:E:399:TYR:CE1	2.54	0.43
1:E:312:VAL:HG23	1:E:313:ILE:N	2.33	0.43
1:C:9:TRP:CD1	1:C:9:TRP:N	2.85	0.43
1:F:328:MET:O	1:F:331:ARG:HD3	2.19	0.43
1:F:122:LEU:HD21	1:F:132:GLY:HA3	2.00	0.43
1:B:445:ARG:HH11	1:B:445:ARG:HG2	1.81	0.43
1:E:58:ILE:HG12	1:E:102:VAL:HG22	2.00	0.43
1:F:135:SER:OG	1:F:138:VAL:HG23	2.18	0.43
1:E:162:VAL:HG11	1:E:200:THR:HA	2.00	0.42
1:C:15:SER:OG	1:C:18:GLN:NE2	2.43	0.42
1:D:122:LEU:HD13	1:D:133:TRP:CE2	2.54	0.42
1:B:74:ARG:HB2	1:B:114:VAL:HB	2.01	0.42
1:E:7:GLU:OE1	1:E:7:GLU:CA	2.68	0.42
1:C:262:PRO:O	1:C:266:VAL:HG23	2.19	0.42
1:D:301:PRO:HD2	1:D:340:GLU:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:313:ILE:HD13	1:D:313:ILE:HA	1.66	0.42
1:B:242:HIS:CE1	2:B:2003:HOH:O	2.53	0.42
1:C:53:ASP:OD1	1:C:56:HIS:CD2	2.63	0.42
1:F:222:ILE:HG23	1:F:365:SER:OG	2.18	0.42
1:E:127:TYR:HA	1:E:132:GLY:H	1.84	0.42
1:A:246:LEU:HA	1:A:250:ASP:HB2	2.00	0.42
1:F:204:ILE:HD12	1:F:219:ILE:HD13	2.00	0.42
1:E:61:ASP:CG	1:E:444:ARG:HH11	2.23	0.42
1:B:379:ASP:CG	1:B:381:THR:HG22	2.40	0.42
1:D:371:ILE:HG22	1:D:372:SER:N	2.34	0.42
1:F:78:GLN:O	1:F:79:TRP:C	2.56	0.42
1:B:12:GLY:HA3	1:B:418:PRO:HG3	2.02	0.42
1:C:441:THR:O	1:C:442:GLN:HB2	2.20	0.42
1:E:122:LEU:HD21	1:E:132:GLY:CA	2.49	0.42
1:F:86:PHE:O	1:F:141:LEU:HD22	2.19	0.42
1:F:161:PHE:HA	1:F:220:GLY:O	2.20	0.42
1:E:116:ASN:ND2	1:E:164:ASN:HB2	2.35	0.42
1:F:243:PHE:O	1:F:246:LEU:N	2.53	0.42
1:B:27:HIS:HB2	1:B:80:THR:HB	2.02	0.42
1:B:68:LEU:O	1:B:454:LYS:HB2	2.18	0.42
1:F:223:LEU:HB3	1:F:224:ASN:H	1.70	0.42
1:A:301:PRO:HG3	1:A:342:TYR:HB3	2.01	0.42
1:B:190:VAL:HG21	1:B:274:VAL:HG13	2.02	0.42
1:E:363:PHE:CZ	1:E:365:SER:HB3	2.54	0.42
1:C:314:SER:HA	1:C:315:PRO:HD2	1.74	0.41
1:B:279:THR:HG21	1:B:281:GLU:HB2	2.01	0.41
1:D:6:LYS:C	1:D:7:GLU:HG2	2.40	0.41
1:B:461:ARG:HB2	1:B:461:ARG:HE	1.57	0.41
1:A:397:LEU:HD12	1:A:397:LEU:HA	1.92	0.41
1:B:417:THR:O	1:B:433:GLY:HA2	2.19	0.41
1:F:328:MET:O	1:F:331:ARG:CD	2.68	0.41
1:B:314:SER:O	1:B:315:PRO:C	2.57	0.41
1:F:332:ARG:O	1:F:340:GLU:HA	2.20	0.41
1:E:447:LYS:O	1:E:450:ALA:HB3	2.21	0.41
1:D:52:SER:O	1:D:444:ARG:NH2	2.48	0.41
1:D:294:LEU:O	1:D:362:TRP:HA	2.20	0.41
1:B:180:TYR:CG	1:B:181:PRO:HA	2.56	0.41
1:D:376:ARG:HB2	1:D:376:ARG:HE	1.51	0.41
1:F:117:LEU:HB2	1:F:162:VAL:O	2.21	0.41
1:E:313:ILE:HD13	1:E:313:ILE:HA	1.90	0.41
1:F:180:TYR:CG	1:F:181:PRO:HA	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:74:ARG:HB2	1:F:114:VAL:HB	2.02	0.41
1:C:116:ASN:ND2	1:C:164:ASN:HB2	2.34	0.41
1:A:81:ARG:HD2	1:A:99:TYR:CE2	2.55	0.41
1:C:219:ILE:HG12	1:C:220:GLY:N	2.36	0.41
1:E:73:TYR:CE1	1:E:75:THR:HB	2.56	0.41
1:E:401:HIS:O	1:E:402:LYS:C	2.57	0.41
1:B:106:CYS:HB3	1:B:111:ILE:O	2.21	0.41
1:F:350:ALA:O	1:F:353:MET:HB2	2.20	0.41
1:A:400:LEU:HD11	1:A:410:CYS:SG	2.61	0.41
1:D:261:PHE:HA	1:D:262:PRO:HD3	1.95	0.41
1:A:247:TRP:NE1	1:A:319:PRO:HG3	2.36	0.41
1:C:225:LEU:HD21	1:C:353:MET:CE	2.49	0.41
1:A:225:LEU:HD13	1:A:253:MET:HG3	2.03	0.41
1:A:225:LEU:HD22	1:A:353:MET:HE3	2.02	0.41
1:D:122:LEU:HD21	1:D:132:GLY:HA2	2.01	0.41
1:D:27:HIS:HB2	1:D:80:THR:HB	2.02	0.41
1:B:22:ARG:HD3	1:B:49:ASP:OD1	2.21	0.41
1:E:161:PHE:HA	1:E:220:GLY:O	2.21	0.41
1:C:72:SER:HA	1:C:111:ILE:HG23	2.03	0.41
1:F:297:ASN:ND2	1:F:366:GLU:CB	2.77	0.40
1:B:357:TYR:C	1:B:359:ASN:N	2.74	0.40
1:C:29:ASN:HD22	1:C:78:GLN:NE2	2.18	0.40
1:E:362:TRP:CZ2	1:E:410:CYS:HB2	2.56	0.40
1:F:397:LEU:HD13	1:F:397:LEU:HA	1.98	0.40
1:F:366:GLU:HG2	1:F:416:TRP:CE3	2.57	0.40
1:B:62:LEU:HD23	1:B:62:LEU:HA	1.98	0.40
1:A:426:ASN:O	1:A:427:ALA:C	2.60	0.40
1:F:199:ALA:O	1:F:203:VAL:CG2	2.54	0.40
1:F:200:THR:O	1:F:204:ILE:HG12	2.22	0.40
1:F:185:ASP:OD2	1:F:188:LYS:HG3	2.21	0.40
1:D:204:ILE:HG12	1:D:219:ILE:HD13	2.02	0.40
1:F:78:GLN:HG3	1:F:121:ASP:OD2	2.21	0.40
1:F:353:MET:CE	1:F:353:MET:HA	2.49	0.40
1:E:180:TYR:CD1	1:E:181:PRO:HA	2.56	0.40
1:C:15:SER:HB3	1:C:119:HIS:CD2	2.57	0.40
1:F:279:THR:HA	1:F:280:PRO:HD3	1.86	0.40
1:E:310:ILE:HA	1:E:311:PRO:HD3	1.87	0.40
1:C:364:LEU:HD23	1:C:413:TYR:CD1	2.56	0.40
1:F:165:GLU:HA	1:F:166:PRO:HD2	1.92	0.40
1:C:331:ARG:NH1	1:C:333:MET:HB2	2.36	0.40
1:E:436:GLU:O	1:E:444:ARG:HA	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:297:ASN:ND2	1:F:366:GLU:N	2.69	0.40
1:F:435:VAL:HG13	1:F:446:PRO:N	2.37	0.40
1:E:397:LEU:HB3	1:E:462:LEU:HD11	2.02	0.40
1:A:116:ASN:HA	1:A:161:PHE:O	2.21	0.40
1:A:124:ILE:HG13	1:A:124:ILE:O	2.22	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	459/479 (96%)	438 (95%)	20 (4%)	1 (0%)	52	75
1	B	459/479 (96%)	429 (94%)	26 (6%)	4 (1%)	21	37
1	C	459/479 (96%)	425 (93%)	32 (7%)	2 (0%)	39	61
1	D	459/479 (96%)	424 (92%)	34 (7%)	1 (0%)	52	75
1	E	459/479 (96%)	425 (93%)	30 (6%)	4 (1%)	21	37
1	F	459/479 (96%)	409 (89%)	46 (10%)	4 (1%)	21	37
All	All	2754/2874 (96%)	2550 (93%)	188 (7%)	16 (1%)	30	50

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	359	ASN
1	B	375	ASP
1	D	336	ASP
1	E	274	VAL
1	E	359	ASN
1	F	24	ALA
1	B	274	VAL

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Mol	Chain	Res	Type
1	E	51	ALA
1	F	375	ASP
1	B	358	ASP
1	F	73	TYR
1	A	212	ALA
1	E	262	PRO
1	C	154	GLY
1	B	210	GLY
1	F	113	PRO

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	389/404 (96%)	373 (96%)	16 (4%)	37	63
1	B	389/404 (96%)	372 (96%)	17 (4%)	35	60
1	C	389/404 (96%)	369 (95%)	20 (5%)	29	52
1	D	389/404 (96%)	369 (95%)	20 (5%)	29	52
1	E	389/404 (96%)	370 (95%)	19 (5%)	31	55
1	F	389/404 (96%)	351 (90%)	38 (10%)	10	19
All	All	2334/2424 (96%)	2204 (94%)	130 (6%)	26	47

All (130) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	LEU
1	A	6	LYS
1	A	187	LYS
1	A	226	THR
1	A	234	SER
1	A	238	MET
1	A	274	VAL
1	A	277	GLN
1	A	293	TYR

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Mol	Chain	Res	Type
1	A	311	PRO
1	A	313	ILE
1	A	331	ARG
1	A	333	MET
1	A	444	ARG
1	A	445	ARG
1	A	461	ARG
1	B	2	LEU
1	B	135	SER
1	B	226	THR
1	B	274	VAL
1	B	277	GLN
1	B	279	THR
1	B	293	TYR
1	B	313	ILE
1	B	331	ARG
1	B	333	MET
1	B	337	LYS
1	B	359	ASN
1	B	378	ARG
1	B	380	GLU
1	B	397	LEU
1	B	444	ARG
1	B	445	ARG
1	C	226	THR
1	C	234	SER
1	C	274	VAL
1	C	277	GLN
1	C	288	GLU
1	C	293	TYR
1	C	313	ILE
1	C	314	SER
1	C	327	LEU
1	C	331	ARG
1	C	333	MET
1	C	337	LYS
1	C	359	ASN
1	C	363	PHE
1	C	365	SER
1	C	378	ARG
1	C	397	LEU
1	C	444	ARG

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Mol	Chain	Res	Type
1	C	455	LYS
1	C	462	LEU
1	D	74	ARG
1	D	183	ILE
1	D	226	THR
1	D	234	SER
1	D	260	LYS
1	D	263	GLU
1	D	274	VAL
1	D	277	GLN
1	D	279	THR
1	D	293	TYR
1	D	313	ILE
1	D	314	SER
1	D	316	SER
1	D	331	ARG
1	D	337	LYS
1	D	378	ARG
1	D	397	LEU
1	D	405	GLU
1	D	444	ARG
1	D	461	ARG
1	E	7	GLU
1	E	14	THR
1	E	40	ASP
1	E	200	THR
1	E	218	ARG
1	E	277	GLN
1	E	278	SER
1	E	293	TYR
1	E	314	SER
1	E	331	ARG
1	E	333	MET
1	E	359	ASN
1	E	363	PHE
1	E	365	SER
1	E	381	THR
1	E	397	LEU
1	E	405	GLU
1	E	408	SER
1	E	444	ARG
1	F	34	TRP

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Mol	Chain	Res	Type
1	F	67	SER
1	F	74	ARG
1	F	81	ARG
1	F	120	PHE
1	F	135	SER
1	F	183	ILE
1	F	184	VAL
1	F	185	ASP
1	F	187	LYS
1	F	209	ARG
1	F	221	THR
1	F	226	THR
1	F	234	SER
1	F	254	GLU
1	F	274	VAL
1	F	277	GLN
1	F	281	GLU
1	F	285	LEU
1	F	293	TYR
1	F	308	ASP
1	F	312	VAL
1	F	313	ILE
1	F	314	SER
1	F	327	LEU
1	F	331	ARG
1	F	333	MET
1	F	359	ASN
1	F	363	PHE
1	F	365	SER
1	F	375	ASP
1	F	380	GLU
1	F	381	THR
1	F	397	LEU
1	F	405	GLU
1	F	410	CYS
1	F	444	ARG
1	F	461	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (70) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	56	HIS

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Mol	Chain	Res	Type
1	A	57	GLN
1	A	78	GLN
1	A	100	ASN
1	A	152	GLN
1	A	249	ASN
1	A	289	ASN
1	A	297	ASN
1	A	359	ASN
1	A	367	ASN
1	A	383	GLN
1	A	430	ASN
1	B	56	HIS
1	B	100	ASN
1	B	152	GLN
1	B	249	ASN
1	B	297	ASN
1	B	359	ASN
1	B	383	GLN
1	B	459	HIS
1	C	18	GLN
1	C	56	HIS
1	C	78	GLN
1	C	100	ASN
1	C	119	HIS
1	C	152	GLN
1	C	179	HIS
1	C	205	GLN
1	C	248	ASN
1	C	249	ASN
1	C	289	ASN
1	C	297	ASN
1	C	359	ASN
1	C	367	ASN
1	C	383	GLN
1	D	56	HIS
1	D	78	GLN
1	D	100	ASN
1	D	152	GLN
1	D	179	HIS
1	D	249	ASN
1	D	258	HIS
1	D	289	ASN

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Mol	Chain	Res	Type
1	D	297	ASN
1	D	359	ASN
1	D	383	GLN
1	D	459	HIS
1	E	56	HIS
1	E	100	ASN
1	E	152	GLN
1	E	249	ASN
1	E	289	ASN
1	E	297	ASN
1	E	359	ASN
1	E	367	ASN
1	E	385	GLN
1	E	426	ASN
1	F	56	HIS
1	F	78	GLN
1	F	100	ASN
1	F	119	HIS
1	F	137	HIS
1	F	152	GLN
1	F	164	ASN
1	F	249	ASN
1	F	277	GLN
1	F	289	ASN
1	F	297	ASN
1	F	359	ASN
1	F	367	ASN

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

There are no carbohydrates in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

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, 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	461/479 (96%)	-0.24	0 100 100	24, 40, 63, 93	1 (0%)
1	B	461/479 (96%)	-0.29	1 (0%) 95 96	25, 41, 63, 84	1 (0%)
1	C	461/479 (96%)	-0.24	0 100 100	26, 44, 67, 91	1 (0%)
1	D	461/479 (96%)	-0.27	0 100 100	25, 42, 64, 82	1 (0%)
1	E	461/479 (96%)	-0.15	3 (0%) 89 90	28, 48, 70, 103	2 (0%)
1	F	461/479 (96%)	0.11	7 (1%) 76 79	27, 53, 75, 97	2 (0%)
All	All	2766/2874 (96%)	-0.18	11 (0%) 93 93	24, 45, 69, 103	8 (0%)

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	315	PRO	4.3
1	F	200	THR	3.2
1	B	313	ILE	2.8
1	E	312	VAL	2.7
1	F	77	ILE	2.5
1	F	315	PRO	2.3
1	F	196	LEU	2.3
1	F	327	LEU	2.2
1	F	102	VAL	2.1
1	E	313	ILE	2.0
1	F	261	PHE	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.