



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 12:38 PM UTC

PDB ID : 1C9T / pdb_00001c9t
Title : COMPLEX OF BDELLASTASIN WITH BOVINE TRYPSIN
Authors : Rester, U.; Bode, W.; Moser, M.; Parry, M.A.; Huber, R.; Auerswald, E.
Deposited on : 1999-08-03
Resolution : 3.30 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

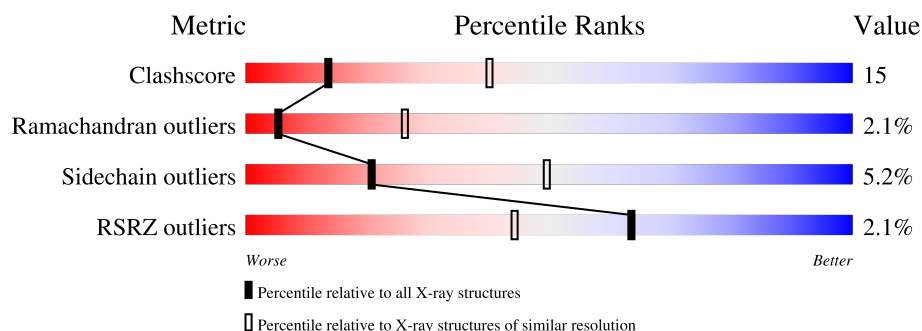
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 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))
Clashscore	190562	1209 (3.32-3.28)
Ramachandran outliers	187476	1188 (3.32-3.28)
Sidechain outliers	187428	1187 (3.32-3.28)
RSRZ outliers	180081	1169 (3.32-3.28)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	223	73% 26% .
1	B	223	62% 36% .
1	C	223	70% 28% .
1	D	223	67% 30% .
1	E	223	66% 33% .
1	F	223	66% 31% ..

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Mol	Chain	Length	Quality of chain
2	G	59	63%27%10%
2	H	59	54%31%5%10%
2	I	59	69%17%•10%
2	J	59	56%24%10%10%
2	K	59	63%24%•10%
2	L	59	59%27%•10%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 12224 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 TRYPSIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	223	Total	C	N	O	S	175	0	0
			1629	1012	279	324	14			
1	B	223	Total	C	N	O	S	175	0	0
			1629	1012	279	324	14			
1	C	223	Total	C	N	O	S	175	0	0
			1629	1012	279	324	14			
1	D	223	Total	C	N	O	S	175	0	0
			1629	1012	279	324	14			
1	E	223	Total	C	N	O	S	175	0	0
			1629	1012	279	324	14			
1	F	223	Total	C	N	O	S	175	0	0
			1629	1012	279	324	14			

- Molecule 2 is a protein called BDELLASTASIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	G	53	Total	C	N	O	S	39	0	0
			384	229	65	79	11			
2	H	53	Total	C	N	O	S	120	0	0
			384	229	65	79	11			
2	I	53	Total	C	N	O	S	126	0	0
			384	229	65	79	11			
2	J	53	Total	C	N	O	S	35	0	0
			384	229	65	79	11			
2	K	53	Total	C	N	O	S	67	0	0
			384	229	65	79	11			
2	L	53	Total	C	N	O	S	54	0	0
			384	229	65	79	11			

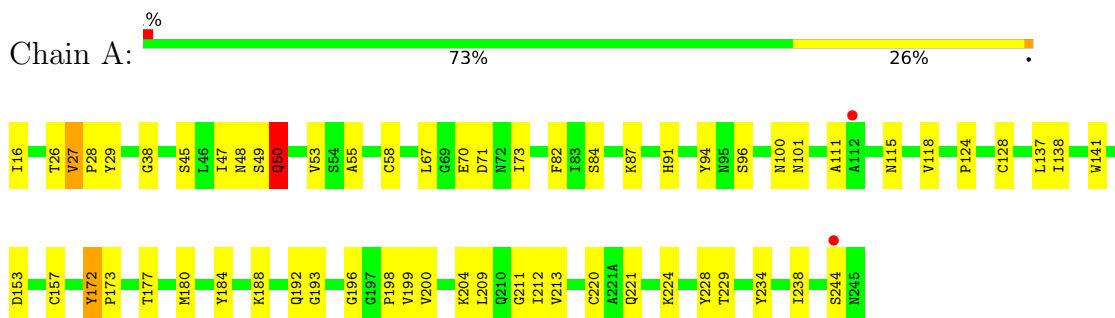
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	25	Total 25	O 25	0	0
3	B	25	Total 25	O 25	0	0
3	C	25	Total 25	O 25	0	0
3	D	24	Total 24	O 24	0	0
3	E	25	Total 25	O 25	0	0
3	F	21	Total 21	O 21	0	0
3	J	1	Total 1	O 1	0	0

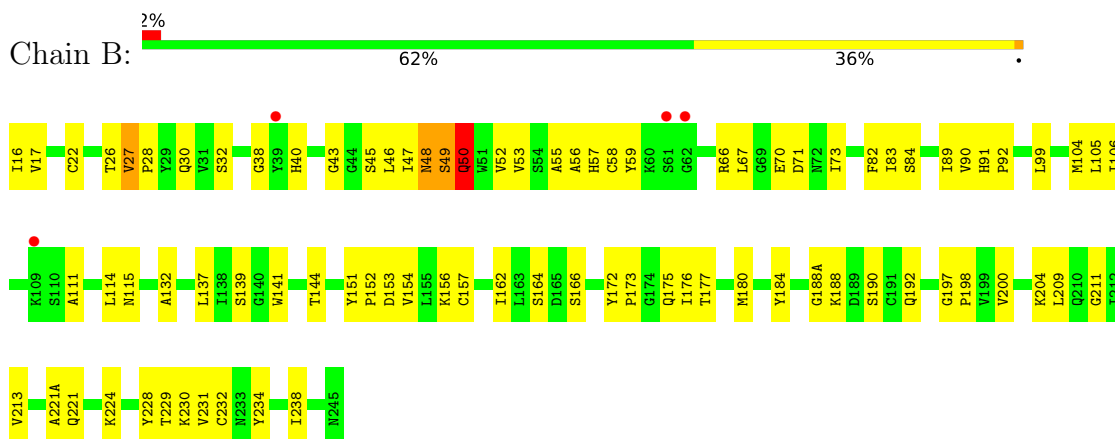
3 Residue-property plots

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: TRYPSIN



• Molecule 1: TRYPSIN

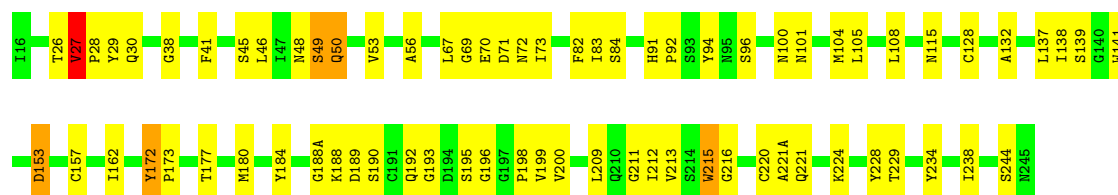


• Molecule 1: TRYPSIN



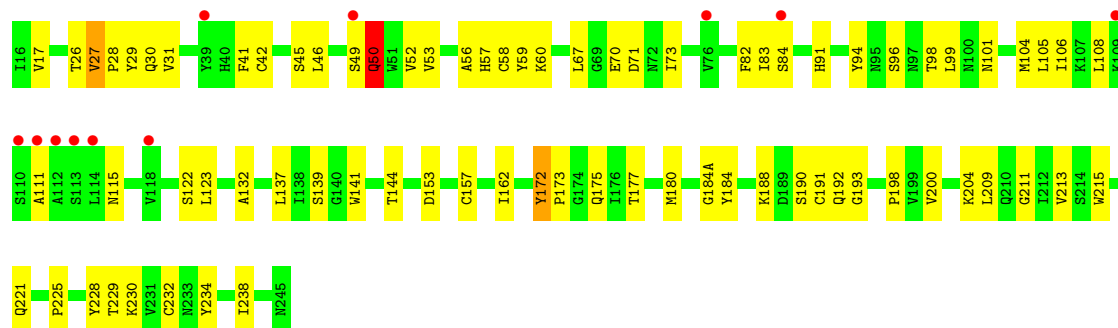
• Molecule 1: TRYPSIN

Chain D:  67% 30% .



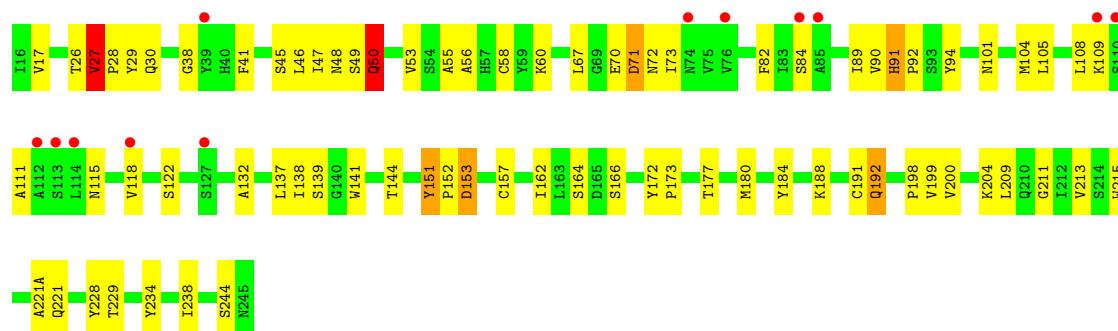
• Molecule 1: TRYPSIN

Chain E:  5% 66% 33% .



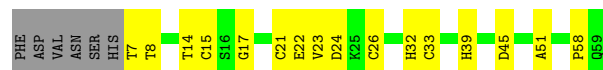
• Molecule 1: TRYPSIN

Chain F:  5% 66% 31% ..



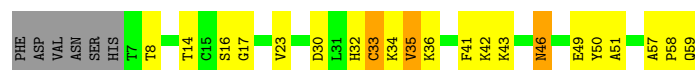
• Molecule 2: BDELLASTASIN

Chain G:  63% 27% 10%

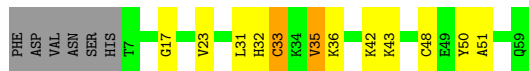


• Molecule 2: BDELLASTASIN

Chain H:  54% 31% 5% 10%



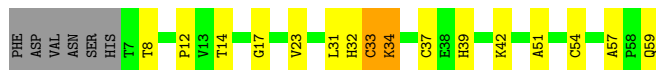
• Molecule 2: BDELLASTASIN

Chain I:  69% 17% 10%

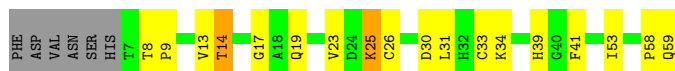
• Molecule 2: BDELLASTASIN

Chain J:  56% 24% 10% 10%

• Molecule 2: BDELLASTASIN

Chain K:  63% 24% 10%

• Molecule 2: BDELLASTASIN

Chain L:  59% 27% 10%

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	95.22Å 108.78Å 95.71Å 90.00° 93.70° 90.00°	Depositor
Resolution (Å)	8.00 – 3.30 8.00 – 3.31	Depositor EDS
% Data completeness (in resolution range)	(Not available) (8.00-3.30) 79.3 (8.00-3.31)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.09 (at 3.32Å)	Xtriage
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.208 , 0.287 0.232 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	40.7	Xtriage
Anisotropy	0.330	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 107.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.349 for l,-k,h	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	12224	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.67% 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

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	0.65	0/1660	1.01	10/2250 (0.4%)
1	B	0.64	0/1660	1.04	12/2250 (0.5%)
1	C	0.63	0/1660	1.01	11/2250 (0.5%)
1	D	0.64	0/1660	1.03	9/2250 (0.4%)
1	E	0.62	0/1660	1.01	10/2250 (0.4%)
1	F	0.62	0/1660	1.03	12/2250 (0.5%)
2	G	0.63	0/390	1.14	1/524 (0.2%)
2	H	0.59	0/390	1.08	3/524 (0.6%)
2	I	0.59	0/390	1.05	1/524 (0.2%)
2	J	0.67	0/390	1.11	2/524 (0.4%)
2	K	0.67	0/390	1.06	2/524 (0.4%)
2	L	0.71	0/390	1.12	2/524 (0.4%)
All	All	0.64	0/12300	1.04	75/16644 (0.5%)

There are no bond length outliers.

All (75) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	27	VAL	CA-C-N	8.98	129.16	119.28
1	F	27	VAL	C-N-CA	8.98	129.16	119.28
1	D	27	VAL	CA-C-N	8.25	128.35	119.28
1	D	27	VAL	C-N-CA	8.25	128.35	119.28
1	C	27	VAL	CA-C-N	7.96	127.63	119.19
1	C	27	VAL	C-N-CA	7.96	127.63	119.19
2	J	33	CYS	N-CA-C	-7.69	100.17	110.55
1	A	38	GLY	N-CA-C	-7.56	104.42	114.25
2	G	33	CYS	N-CA-C	-7.47	100.47	110.55
1	A	71	ASP	N-CA-C	-7.45	100.25	111.34
1	D	38	GLY	N-CA-C	-7.29	104.77	114.25
1	D	71	ASP	N-CA-C	-7.24	100.56	111.34
1	A	91	HIS	CA-C-N	7.18	128.82	119.84
1	A	91	HIS	C-N-CA	7.18	128.82	119.84
1	D	91	HIS	CA-C-N	7.18	128.81	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	91	HIS	C-N-CA	7.18	128.81	119.84
1	F	71	ASP	N-CA-C	-6.95	100.98	111.34
2	L	33	CYS	N-CA-C	-6.94	101.58	110.53
1	E	27	VAL	CA-C-N	6.94	126.91	119.28
1	E	27	VAL	C-N-CA	6.94	126.91	119.28
1	B	71	ASP	N-CA-C	-6.86	101.12	111.34
1	A	27	VAL	CA-C-N	6.86	126.46	119.19
1	A	27	VAL	C-N-CA	6.86	126.46	119.19
1	E	71	ASP	N-CA-C	-6.78	101.25	111.34
1	C	71	ASP	N-CA-C	-6.69	101.38	111.34
1	B	43	GLY	N-CA-C	-6.66	104.80	112.79
1	B	89	ILE	N-CA-C	6.63	117.29	107.15
1	F	50	GLN	N-CA-C	6.43	121.29	113.38
2	L	34	LYS	N-CA-C	6.34	120.23	111.55
1	F	91	HIS	CA-C-N	6.27	127.68	119.84
1	F	91	HIS	C-N-CA	6.27	127.68	119.84
1	E	91	HIS	CA-C-N	6.20	127.58	119.84
1	E	91	HIS	C-N-CA	6.20	127.58	119.84
1	B	91	HIS	CA-C-N	6.16	127.54	119.84
1	B	91	HIS	C-N-CA	6.16	127.54	119.84
2	K	33	CYS	N-CA-C	-6.04	102.40	110.55
1	D	172	TYR	CA-C-N	6.02	127.37	119.84
1	D	172	TYR	C-N-CA	6.02	127.37	119.84
1	D	215	TRP	N-CA-C	6.01	116.21	108.34
2	K	34	LYS	N-CA-C	5.85	120.21	112.25
1	A	172	TYR	CA-C-N	5.85	127.15	119.84
1	A	172	TYR	C-N-CA	5.85	127.15	119.84
2	H	33	CYS	N-CA-C	-5.78	102.75	110.55
1	C	91	HIS	CA-C-N	5.74	127.02	119.84
1	C	91	HIS	C-N-CA	5.74	127.02	119.84
1	F	38	GLY	N-CA-C	-5.72	106.61	114.67
1	B	38	GLY	N-CA-C	-5.68	106.87	114.25
1	C	125	THR	N-CA-C	-5.67	107.00	114.04
1	C	197	GLY	CA-C-N	5.67	126.15	120.14
1	C	197	GLY	C-N-CA	5.67	126.15	120.14
1	B	99	LEU	N-CA-C	-5.55	105.81	112.58
1	E	172	TYR	CA-C-N	5.52	126.74	119.84
1	E	172	TYR	C-N-CA	5.52	126.74	119.84
1	A	50	GLN	N-CA-C	5.46	120.10	113.38
2	J	34	LYS	N-CA-C	5.43	118.99	111.55
1	E	50	GLN	N-CA-C	5.42	120.05	113.38
1	B	27	VAL	CA-C-N	5.39	125.21	119.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	27	VAL	C-N-CA	5.39	125.21	119.28
2	H	30	ASP	N-CA-C	-5.36	106.74	113.28
1	E	123	LEU	N-CA-C	-5.32	102.47	110.24
1	C	151	TYR	CA-C-N	5.29	125.19	119.85
1	C	151	TYR	C-N-CA	5.29	125.19	119.85
2	I	33	CYS	N-CA-C	-5.29	103.41	110.55
2	H	35	VAL	CB-CA-C	-5.28	102.64	111.29
1	A	193	GLY	N-CA-C	-5.24	107.77	114.85
1	F	89	ILE	N-CA-C	5.21	115.86	107.73
1	F	172	TYR	CA-C-N	5.20	126.34	119.84
1	F	172	TYR	C-N-CA	5.20	126.34	119.84
1	B	197	GLY	CA-C-N	5.18	125.64	120.14
1	B	197	GLY	C-N-CA	5.18	125.64	120.14
1	B	50	GLN	N-CA-C	5.12	119.80	113.50
1	E	193	GLY	N-CA-C	-5.11	107.49	114.64
1	F	151	TYR	CA-C-N	5.08	124.98	119.85
1	F	151	TYR	C-N-CA	5.08	124.98	119.85
1	C	89	ILE	N-CA-C	5.08	115.65	107.73

There are no chirality outliers.

There are no planarity outliers.

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	1629	0	1588	36	0
1	B	1629	0	1588	47	0
1	C	1629	0	1588	40	0
1	D	1629	0	1588	42	0
1	E	1629	0	1588	47	0
1	F	1629	0	1588	44	0
2	G	384	0	347	5	0
2	H	384	0	347	15	0
2	I	384	0	347	10	0
2	J	384	0	347	15	0
2	K	384	0	347	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	L	384	0	347	8	0
3	A	25	0	0	4	0
3	B	25	0	0	1	0
3	C	25	0	0	5	0
3	D	24	0	0	3	0
3	E	25	0	0	3	0
3	F	21	0	0	3	0
3	J	1	0	0	1	0
All	All	12224	0	11610	300	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 15.

All (300) 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)
2:L:9:PRO:HA	2:L:14:THR:HG22	1.58	0.85
1:E:45:SER:OG	1:E:198:PRO:HB3	1.81	0.80
1:E:215:TRP:CE3	2:K:31:LEU:HD11	2.15	0.80
1:D:215:TRP:CE3	2:J:31:LEU:HD21	2.17	0.79
2:H:35:VAL:HG12	2:H:36:LYS:H	1.49	0.77
1:F:45:SER:OG	1:F:198:PRO:HB3	1.86	0.74
2:L:19:GLN:OE1	2:L:26:CYS:HB3	1.90	0.72
1:E:215:TRP:CZ3	2:K:31:LEU:HD11	2.26	0.70
2:J:42:LYS:HG2	2:J:50:TYR:CD1	2.26	0.70
1:C:45:SER:OG	1:C:198:PRO:HB3	1.94	0.67
1:B:234:TYR:O	1:B:238:ILE:HG13	1.93	0.67
2:G:32:HIS:HD2	2:G:51:ALA:O	1.79	0.66
1:E:56:ALA:HA	1:E:104:MET:HB2	1.80	0.64
1:E:137:LEU:HD11	1:E:157:CYS:HB3	1.80	0.63
1:F:56:ALA:HA	1:F:104:MET:HB2	1.80	0.62
2:H:43:LYS:HG2	2:H:49:GLU:HG2	1.80	0.62
1:D:26:THR:C	1:D:28:PRO:HD3	2.25	0.62
1:C:234:TYR:O	1:C:238:ILE:HG13	2.01	0.61
1:B:230:LYS:HG2	1:B:232:CYS:SG	2.41	0.61
1:B:45:SER:OG	1:B:198:PRO:HB3	2.00	0.60
2:H:35:VAL:HG12	2:H:36:LYS:N	2.16	0.60
2:H:43:LYS:CG	2:H:49:GLU:HG2	2.32	0.60
2:J:42:LYS:HG2	2:J:50:TYR:HD1	1.65	0.60
1:C:30:GLN:NE2	1:C:139:SER:OG	2.34	0.59
1:F:26:THR:C	1:F:28:PRO:HD3	2.28	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:137:LEU:HD11	1:F:157:CYS:HB3	1.86	0.58
1:B:137:LEU:HD11	1:B:157:CYS:HB3	1.83	0.58
2:I:32:HIS:CD2	2:I:51:ALA:HA	2.39	0.58
1:B:56:ALA:HA	1:B:104:MET:HB2	1.86	0.57
1:F:132:ALA:HA	1:F:162:ILE:HG22	1.85	0.57
2:L:25:LYS:NZ	2:L:25:LYS:HB3	2.20	0.57
1:F:213:VAL:HA	1:F:228:TYR:CD1	2.40	0.57
1:A:101:ASN:HA	1:A:234:TYR:OH	2.05	0.57
1:E:101:ASN:HA	1:E:234:TYR:OH	2.03	0.57
2:I:33:CYS:SG	2:I:35:VAL:HG23	2.45	0.57
1:F:53:VAL:HG11	1:F:209:LEU:HD21	1.85	0.56
1:D:56:ALA:HA	1:D:104:MET:HB2	1.86	0.56
1:D:234:TYR:O	1:D:238:ILE:HG13	2.05	0.56
1:B:190:SER:OG	2:H:34:LYS:HE3	2.05	0.56
1:A:234:TYR:O	1:A:238:ILE:HG13	2.06	0.56
1:D:45:SER:OG	1:D:198:PRO:HB3	2.06	0.56
2:H:46:ASN:OD1	2:H:46:ASN:N	2.38	0.56
1:B:53:VAL:HG11	1:B:209:LEU:HD21	1.88	0.55
2:I:42:LYS:HG2	2:I:50:TYR:CD1	2.41	0.55
1:E:53:VAL:HG13	3:E:246:HOH:O	2.06	0.55
1:A:177:THR:OG1	1:A:180:MET:HG3	2.06	0.55
1:C:16:ILE:N	3:C:252:HOH:O	2.39	0.55
1:E:184:TYR:CD1	1:E:188:LYS:HB2	2.42	0.55
1:F:184:TYR:CD1	1:F:188:LYS:HB2	2.43	0.54
2:G:39:HIS:CD2	2:G:58:PRO:HG3	2.42	0.54
1:F:105:LEU:HD11	1:F:238:ILE:HA	1.89	0.54
1:F:215:TRP:CZ3	2:L:31:LEU:HD11	2.42	0.54
1:C:56:ALA:HA	1:C:104:MET:HB2	1.90	0.54
1:E:122:SER:HB2	1:E:204:LYS:HD3	1.90	0.54
1:F:56:ALA:HB1	1:F:90:VAL:HG13	1.89	0.54
1:A:213:VAL:HA	1:A:228:TYR:CD1	2.43	0.54
1:E:184:TYR:HD1	1:E:188:LYS:HB2	1.73	0.54
1:C:53:VAL:HG13	3:C:246:HOH:O	2.07	0.53
2:I:33:CYS:SG	2:I:35:VAL:CG2	2.96	0.53
1:E:46:LEU:HD22	1:E:67:LEU:HD23	1.90	0.53
1:E:177:THR:OG1	1:E:180:MET:HG3	2.07	0.53
2:J:15:CYS:SG	2:J:21:CYS:HB2	2.48	0.53
1:E:191:CYS:CA	2:K:34:LYS:HD3	2.38	0.53
1:B:55:ALA:O	1:B:58:CYS:HB2	2.09	0.53
1:A:138:ILE:HG12	1:A:199:VAL:HG22	1.91	0.53
1:E:67:LEU:N	1:E:67:LEU:HD12	2.24	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:39:HIS:CD2	2:L:58:PRO:HG3	2.44	0.53
1:A:137:LEU:HD11	1:A:157:CYS:HB3	1.89	0.53
1:A:138:ILE:HD13	1:A:228:TYR:OH	2.09	0.52
1:E:190:SER:O	2:K:34:LYS:HE2	2.09	0.52
1:E:70:GLU:HB2	1:E:141:TRP:CH2	2.43	0.52
1:F:221(A):ALA:HA	3:F:254:HOH:O	2.08	0.52
1:A:70:GLU:HB2	1:A:141:TRP:CH2	2.44	0.52
1:F:184:TYR:HD1	1:F:188:LYS:HB2	1.72	0.52
1:F:70:GLU:HB2	1:F:141:TRP:CH2	2.44	0.52
1:B:40:HIS:O	2:H:36:LYS:HE2	2.10	0.52
1:A:184:TYR:CD1	1:A:188:LYS:HB2	2.46	0.51
1:A:200:VAL:HG13	1:A:204:LYS:O	2.10	0.51
1:C:70:GLU:HB2	1:C:141:TRP:CH2	2.45	0.51
1:D:94:TYR:HA	1:D:101:ASN:HB2	1.92	0.51
1:A:26:THR:C	1:A:28:PRO:HD3	2.36	0.51
1:A:220:CYS:HA	3:A:269:HOH:O	2.10	0.51
1:D:70:GLU:HB2	1:D:141:TRP:CH2	2.46	0.51
1:E:211:GLY:HA2	1:E:229:THR:O	2.10	0.51
1:C:137:LEU:HD11	1:C:157:CYS:HB3	1.91	0.51
1:B:30:GLN:NE2	1:B:139:SER:OG	2.43	0.51
2:I:50:TYR:CE2	2:L:58:PRO:HD2	2.46	0.51
1:C:100:ASN:O	1:C:101:ASN:HB2	2.11	0.50
1:D:69:GLY:HA2	3:D:252:HOH:O	2.10	0.50
1:E:230:LYS:HG2	1:E:232:CYS:SG	2.51	0.50
1:A:67:LEU:HD12	1:A:67:LEU:N	2.26	0.50
1:C:25:ASN:ND2	3:C:253:HOH:O	2.44	0.50
2:K:32:HIS:CD2	2:K:51:ALA:O	2.64	0.50
1:B:67:LEU:HD12	1:B:67:LEU:H	1.76	0.50
1:D:27:VAL:N	1:D:28:PRO:HD3	2.26	0.50
1:D:100:ASN:O	1:D:101:ASN:HB2	2.11	0.50
2:J:15:CYS:N	2:J:26:CYS:SG	2.84	0.50
1:E:191:CYS:N	2:K:34:LYS:HD3	2.27	0.50
1:B:211:GLY:HA2	1:B:231:VAL:HG23	1.94	0.50
1:E:213:VAL:HA	1:E:228:TYR:CD1	2.47	0.50
1:E:105:LEU:HD11	1:E:238:ILE:HA	1.93	0.50
1:C:184:TYR:CD1	1:C:188:LYS:HB2	2.47	0.49
1:C:26:THR:C	1:C:28:PRO:HD3	2.37	0.49
1:F:27:VAL:N	1:F:28:PRO:HD3	2.28	0.49
1:F:122:SER:HB2	1:F:204:LYS:HD3	1.93	0.49
2:J:44:ASP:OD2	2:J:48:CYS:N	2.46	0.49
1:B:132:ALA:HA	1:B:162:ILE:HG22	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:30:GLN:NE2	1:F:139:SER:OG	2.45	0.49
1:C:138:ILE:HD13	1:C:228:TYR:OH	2.12	0.48
1:D:213:VAL:HA	1:D:228:TYR:CD1	2.48	0.48
1:B:211:GLY:HA2	1:B:229:THR:O	2.12	0.48
1:D:41:PHE:HA	2:J:36:LYS:HB3	1.95	0.48
1:B:184:TYR:CD1	1:B:188:LYS:HB2	2.48	0.48
1:B:213:VAL:HA	1:B:228:TYR:CD1	2.49	0.48
1:D:101:ASN:HA	1:D:234:TYR:OH	2.13	0.48
1:D:137:LEU:HD11	1:D:157:CYS:HB3	1.96	0.48
1:D:215:TRP:CZ3	2:J:31:LEU:HD21	2.48	0.48
2:J:32:HIS:CD2	2:J:41:PHE:CD1	3.01	0.48
1:A:45:SER:OG	1:A:198:PRO:HB3	2.13	0.48
1:E:53:VAL:HG11	1:E:209:LEU:CD2	2.44	0.48
1:A:184:TYR:HD1	1:A:188:LYS:HB2	1.78	0.48
1:B:17:VAL:HA	1:B:144:THR:O	2.14	0.48
1:B:57:HIS:NE2	2:H:33:CYS:HB2	2.28	0.48
1:B:70:GLU:HB2	1:B:141:TRP:CH2	2.49	0.48
1:C:105:LEU:HD11	1:C:238:ILE:HA	1.96	0.48
1:B:67:LEU:HD12	1:B:67:LEU:N	2.29	0.48
1:A:94:TYR:CZ	1:A:96:SER:HA	2.49	0.47
1:C:29:TYR:CZ	1:C:200:VAL:HG21	2.48	0.47
1:D:193:GLY:HA2	2:J:36:LYS:HB2	1.95	0.47
1:A:196:GLY:HA2	1:A:212:ILE:CG2	2.45	0.47
1:C:211:GLY:HA2	1:C:231:VAL:HG23	1.95	0.47
1:F:67:LEU:HD12	1:F:67:LEU:N	2.29	0.47
1:A:211:GLY:HA2	1:A:229:THR:O	2.14	0.47
2:J:32:HIS:HD2	2:J:51:ALA:O	1.96	0.47
1:F:211:GLY:HA2	1:F:229:THR:O	2.13	0.47
1:E:26:THR:C	1:E:28:PRO:HD3	2.39	0.47
1:E:94:TYR:HA	1:E:101:ASN:HB2	1.96	0.47
1:F:53:VAL:HG11	1:F:209:LEU:CD2	2.45	0.47
2:K:32:HIS:HD2	2:K:51:ALA:O	1.98	0.47
1:D:188(A):GLY:H	1:D:221(A):ALA:HB1	1.80	0.47
1:D:211:GLY:HA2	1:D:229:THR:O	2.14	0.47
2:J:33:CYS:SG	2:J:35:VAL:CG2	3.03	0.47
2:G:15:CYS:SG	2:G:21:CYS:HB2	2.56	0.46
1:A:29:TYR:CZ	1:A:200:VAL:HG21	2.51	0.46
1:B:16:ILE:N	3:B:252:HOH:O	2.49	0.46
1:C:151:TYR:CD1	2:I:36:LYS:HE3	2.51	0.46
1:B:114:LEU:HD12	1:F:244:SER:HA	1.96	0.46
1:C:50:GLN:HG3	1:C:111:ALA:HA	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:29:TYR:CZ	1:D:200:VAL:HG21	2.50	0.46
1:E:59:TYR:HB2	1:E:104:MET:SD	2.56	0.46
1:C:41:PHE:O	1:C:42:CYS:SG	2.74	0.46
1:C:98:THR:O	1:C:99:LEU:HB2	2.16	0.46
1:C:211:GLY:HA2	1:C:229:THR:O	2.15	0.46
1:D:128:CYS:HB3	3:D:267:HOH:O	2.16	0.46
1:A:177:THR:HG23	1:A:180:MET:HE3	1.97	0.46
1:E:30:GLN:NE2	1:E:139:SER:OG	2.49	0.46
1:B:200:VAL:HA	1:B:204:LYS:O	2.16	0.46
1:B:213:VAL:CG1	2:H:34:LYS:HD2	2.46	0.46
2:H:32:HIS:HD2	2:H:41:PHE:CD2	2.34	0.46
2:H:33:CYS:SG	2:H:35:VAL:HG23	2.55	0.46
1:B:32:SER:HB3	1:B:66:ARG:HB2	1.98	0.45
1:F:17:VAL:HA	1:F:144:THR:O	2.15	0.45
1:F:50:GLN:HG3	1:F:111:ALA:HA	1.96	0.45
1:F:101:ASN:HA	1:F:234:TYR:OH	2.17	0.45
1:C:101:ASN:HA	1:C:234:TYR:OH	2.16	0.45
1:B:105:LEU:HD11	1:B:238:ILE:HA	1.98	0.45
1:F:91:HIS:CG	1:F:92:PRO:HD2	2.52	0.45
2:J:15:CYS:HB3	2:J:19:GLN:HB2	1.99	0.45
1:B:46:LEU:HD22	1:B:67:LEU:HD23	1.98	0.45
2:G:15:CYS:N	2:G:26:CYS:SG	2.89	0.45
1:A:124:PRO:HD3	1:A:209:LEU:O	2.17	0.45
1:E:200:VAL:HA	1:E:204:LYS:O	2.17	0.45
1:F:118:VAL:HG13	3:F:264:HOH:O	2.16	0.45
1:B:177:THR:OG1	1:B:180:MET:HG3	2.17	0.45
1:E:190:SER:C	2:K:34:LYS:HE2	2.41	0.45
1:B:48:ASN:O	1:B:49:SER:C	2.61	0.44
1:D:46:LEU:HD22	1:D:67:LEU:HD23	1.98	0.44
1:E:41:PHE:CZ	1:E:60:LYS:HD2	2.52	0.44
1:D:94:TYR:CZ	1:D:96:SER:HA	2.53	0.44
1:D:199:VAL:HG21	1:D:228:TYR:CD1	2.53	0.44
1:E:50:GLN:HG3	1:E:111:ALA:HA	2.00	0.44
1:E:198:PRO:HG2	3:E:266:HOH:O	2.16	0.44
1:F:41:PHE:CZ	1:F:60:LYS:HD2	2.53	0.44
1:C:213:VAL:HA	1:C:228:TYR:CD1	2.53	0.44
1:B:47:ILE:O	1:B:48:ASN:HB3	2.18	0.43
1:C:47:ILE:O	1:C:48:ASN:HB3	2.16	0.43
1:C:94:TYR:HA	1:C:101:ASN:HB2	2.00	0.43
1:C:25:ASN:HA	3:C:255:HOH:O	2.17	0.43
2:H:32:HIS:CD2	2:H:51:ALA:O	2.71	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:57:ALA:HB1	2:H:58:PRO:HD2	2.00	0.43
1:B:83:ILE:HG22	1:B:84:SER:O	2.19	0.43
1:F:67:LEU:HD12	1:F:67:LEU:H	1.82	0.43
1:F:72:ASN:HA	1:F:153:ASP:O	2.18	0.43
1:C:184:TYR:HD1	1:C:188:LYS:HB2	1.83	0.43
1:E:172:TYR:CE1	1:E:225:PRO:HD2	2.53	0.43
1:A:48:ASN:O	1:A:50:GLN:N	2.50	0.43
1:C:32:SER:HB3	1:C:66:ARG:HB2	2.00	0.43
1:C:48:ASN:O	1:C:50:GLN:N	2.52	0.43
1:D:216:GLY:HA3	3:J:79:HOH:O	2.18	0.43
1:E:57:HIS:NE2	2:K:33:CYS:HB2	2.33	0.43
1:C:27:VAL:N	1:C:28:PRO:HD3	2.34	0.43
1:D:72:ASN:HA	1:D:153:ASP:O	2.19	0.43
1:F:55:ALA:O	1:F:58:CYS:HB2	2.18	0.43
2:I:31:LEU:HD23	2:I:31:LEU:C	2.43	0.43
1:D:48:ASN:O	1:D:50:GLN:N	2.52	0.43
1:D:220:CYS:HA	3:D:268:HOH:O	2.18	0.43
1:F:200:VAL:HA	1:F:204:LYS:O	2.19	0.43
1:E:29:TYR:CZ	1:E:200:VAL:HG21	2.54	0.43
1:F:177:THR:OG1	1:F:180:MET:HG3	2.19	0.43
1:C:210:GLN:NE2	3:C:267:HOH:O	2.52	0.42
1:D:184:TYR:CD1	1:D:188:LYS:HB2	2.53	0.42
1:E:67:LEU:HD12	1:E:67:LEU:H	1.83	0.42
1:F:94:TYR:HA	1:F:101:ASN:HB2	2.01	0.42
2:K:37:CYS:HB3	2:K:54:CYS:HB3	1.67	0.42
1:D:53:VAL:HG11	1:D:209:LEU:CD2	2.49	0.42
1:D:172:TYR:HA	1:D:173:PRO:HD2	1.87	0.42
1:E:94:TYR:CZ	1:E:96:SER:HA	2.54	0.42
2:I:32:HIS:CD2	2:I:51:ALA:O	2.73	0.42
1:B:52:VAL:HB	1:B:106:ILE:HB	2.00	0.42
1:F:234:TYR:O	1:F:238:ILE:HG13	2.19	0.42
1:B:164:SER:C	1:B:166:SER:N	2.77	0.42
1:E:41:PHE:HE1	1:E:58:CYS:O	2.02	0.42
1:F:164:SER:C	1:F:166:SER:N	2.77	0.42
2:L:41:PHE:HD2	2:L:53:ILE:O	2.03	0.42
1:B:26:THR:C	1:B:28:PRO:HD3	2.44	0.42
1:D:189:ASP:OD2	1:D:190:SER:N	2.51	0.42
1:F:29:TYR:CZ	1:F:200:VAL:HG21	2.55	0.42
1:F:71:ASP:HA	3:F:255:HOH:O	2.19	0.42
1:A:50:GLN:HG3	1:A:111:ALA:HA	2.02	0.42
2:J:32:HIS:CD2	2:J:51:ALA:O	2.72	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:16:ILE:N	3:A:252:HOH:O	2.52	0.42
1:A:172:TYR:HA	1:A:173:PRO:HD2	1.81	0.42
1:A:213:VAL:HG22	1:A:228:TYR:HE1	1.85	0.42
1:D:195:SER:OG	2:J:34:LYS:C	2.63	0.42
1:E:53:VAL:HG11	1:E:209:LEU:HD21	2.01	0.42
1:A:53:VAL:HG11	1:A:209:LEU:CD2	2.50	0.41
1:B:188(A):GLY:H	1:B:221(A):ALA:HB1	1.85	0.41
1:D:83:ILE:HG21	1:D:108:LEU:HB3	2.02	0.41
1:F:108:LEU:O	1:F:109:LYS:C	2.62	0.41
1:A:94:TYR:HA	1:A:101:ASN:HB2	2.02	0.41
1:A:177:THR:CG2	1:A:180:MET:HE3	2.50	0.41
1:B:48:ASN:O	1:B:50:GLN:N	2.53	0.41
1:C:53:VAL:HG11	1:C:209:LEU:HD21	2.02	0.41
1:D:132:ALA:HA	1:D:162:ILE:HG22	2.01	0.41
1:A:100:ASN:O	1:A:101:ASN:HB2	2.20	0.41
1:D:30:GLN:NE2	1:D:139:SER:OG	2.53	0.41
1:E:98:THR:O	1:E:99:LEU:HB2	2.19	0.41
1:E:132:ALA:HA	1:E:162:ILE:HG22	2.02	0.41
2:H:42:LYS:HG2	2:H:50:TYR:CD1	2.55	0.41
1:B:22:CYS:SG	1:B:156:LYS:C	3.04	0.41
1:B:59:TYR:CD1	1:B:59:TYR:C	2.99	0.41
1:D:53:VAL:HG11	1:D:209:LEU:HD21	2.02	0.41
1:E:41:PHE:O	1:E:42:CYS:SG	2.79	0.41
2:G:22:GLU:O	2:G:24:ASP:N	2.54	0.41
1:A:47:ILE:O	1:A:48:ASN:HB3	2.21	0.41
1:D:48:ASN:O	1:D:49:SER:C	2.63	0.41
1:D:177:THR:OG1	1:D:180:MET:HG3	2.20	0.41
1:E:83:ILE:HG21	1:E:108:LEU:HB3	2.01	0.41
1:E:172:TYR:HE1	1:E:225:PRO:HD2	1.86	0.41
1:B:154:VAL:HG23	1:B:156:LYS:HE2	2.02	0.41
1:D:196:GLY:HA2	1:D:212:ILE:CG2	2.51	0.41
1:B:53:VAL:HG11	1:B:209:LEU:CD2	2.49	0.41
1:B:151:TYR:HA	1:B:152:PRO:HD2	1.89	0.41
1:B:172:TYR:HB2	1:B:176:ILE:HG12	2.02	0.41
1:B:184:TYR:HD1	1:B:188:LYS:HB2	1.84	0.41
1:C:50:GLN:HG3	1:C:111:ALA:CA	2.51	0.41
1:F:46:LEU:HD22	1:F:67:LEU:HD23	2.03	0.41
1:F:47:ILE:CD1	1:F:53:VAL:HB	2.51	0.41
1:F:151:TYR:HA	1:F:152:PRO:HD2	1.88	0.41
2:H:32:HIS:HD2	2:H:41:PHE:CE2	2.39	0.41
2:K:39:HIS:CE1	2:K:57:ALA:HA	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:55:ALA:O	1:A:58:CYS:HB2	2.20	0.41
1:A:118:VAL:HG13	3:A:264:HOH:O	2.20	0.41
1:A:224:LYS:HA	1:A:224:LYS:HD3	1.94	0.41
1:C:188(A):GLY:H	1:C:221(A):ALA:HB1	1.86	0.41
1:D:224:LYS:HA	1:D:224:LYS:HD3	1.86	0.41
1:E:17:VAL:HA	1:E:144:THR:O	2.21	0.41
1:E:184(A):GLY:HA3	3:E:259:HOH:O	2.21	0.41
1:B:56:ALA:HB1	1:B:90:VAL:HG13	2.02	0.40
1:B:173:PRO:C	1:B:175:GLN:H	2.29	0.40
1:C:50:GLN:HG3	1:C:111:ALA:HB2	2.03	0.40
1:C:53:VAL:HG11	1:C:209:LEU:CD2	2.50	0.40
1:C:164:SER:C	1:C:166:SER:N	2.78	0.40
1:C:199:VAL:HG21	1:C:228:TYR:CD1	2.56	0.40
1:E:173:PRO:C	1:E:175:GLN:H	2.28	0.40
1:F:138:ILE:HG12	1:F:199:VAL:HG22	2.03	0.40
2:I:43:LYS:HA	2:I:48:CYS:O	2.20	0.40
1:B:50:GLN:HG3	1:B:111:ALA:HA	2.03	0.40
1:B:224:LYS:HD3	1:B:224:LYS:HA	1.88	0.40
1:A:128:CYS:HB3	3:A:268:HOH:O	2.20	0.40
1:C:173:PRO:C	1:C:175:GLN:H	2.29	0.40
1:E:52:VAL:HB	1:E:106:ILE:HB	2.04	0.40
1:F:191:CYS:O	1:F:192:GLN:C	2.65	0.40
2:I:42:LYS:HG2	2:I:50:TYR:CE1	2.56	0.40
1:A:47:ILE:HD11	1:A:53:VAL:HB	2.04	0.40
1:C:52:VAL:HB	1:C:106:ILE:HB	2.03	0.40
1:D:138:ILE:HG12	1:D:199:VAL:HG22	2.02	0.40
1:F:47:ILE:O	1:F:48:ASN:HB3	2.21	0.40
1:D:105:LEU:HD11	1:D:238:ILE:HA	2.04	0.40
2:L:39:HIS:HD2	2:L:58:PRO:HG3	1.87	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	221/223 (99%)	197 (89%)	21 (10%)	3 (1%)	9	33
1	B	221/223 (99%)	193 (87%)	23 (10%)	5 (2%)	5	25
1	C	221/223 (99%)	196 (89%)	22 (10%)	3 (1%)	9	33
1	D	221/223 (99%)	192 (87%)	25 (11%)	4 (2%)	6	29
1	E	221/223 (99%)	193 (87%)	25 (11%)	3 (1%)	9	33
1	F	221/223 (99%)	190 (86%)	27 (12%)	4 (2%)	6	29
2	G	51/59 (86%)	43 (84%)	6 (12%)	2 (4%)	2	16
2	H	51/59 (86%)	43 (84%)	6 (12%)	2 (4%)	2	16
2	I	51/59 (86%)	44 (86%)	5 (10%)	2 (4%)	2	16
2	J	51/59 (86%)	45 (88%)	4 (8%)	2 (4%)	2	16
2	K	51/59 (86%)	44 (86%)	5 (10%)	2 (4%)	2	16
2	L	51/59 (86%)	45 (88%)	4 (8%)	2 (4%)	2	16
All	All	1632/1692 (96%)	1425 (87%)	173 (11%)	34 (2%)	5	26

All (34) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	49	SER
1	B	49	SER
1	C	49	SER
1	D	49	SER
1	E	49	SER
1	B	115	ASN
1	E	115	ASN
1	F	49	SER
1	F	115	ASN
2	G	17	GLY
2	I	17	GLY
2	J	17	GLY
2	L	17	GLY
1	A	115	ASN
1	C	115	ASN
1	D	115	ASN
2	K	17	GLY
2	G	23	VAL
2	H	17	GLY
2	K	23	VAL
1	B	48	ASN
2	H	23	VAL

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Mol	Chain	Res	Type
2	I	23	VAL
2	J	23	VAL
1	A	73	ILE
1	D	92	PRO
2	L	23	VAL
1	C	73	ILE
1	D	73	ILE
1	E	73	ILE
1	B	73	ILE
1	F	73	ILE
1	B	92	PRO
1	F	173	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	184/184 (100%)	175 (95%)	9 (5%)	22	51
1	B	184/184 (100%)	178 (97%)	6 (3%)	33	59
1	C	184/184 (100%)	178 (97%)	6 (3%)	33	59
1	D	184/184 (100%)	176 (96%)	8 (4%)	26	54
1	E	184/184 (100%)	176 (96%)	8 (4%)	26	54
1	F	184/184 (100%)	177 (96%)	7 (4%)	29	57
2	G	45/51 (88%)	41 (91%)	4 (9%)	9	32
2	H	45/51 (88%)	40 (89%)	5 (11%)	6	22
2	I	45/51 (88%)	44 (98%)	1 (2%)	45	66
2	J	45/51 (88%)	39 (87%)	6 (13%)	4	17
2	K	45/51 (88%)	40 (89%)	5 (11%)	6	22
2	L	45/51 (88%)	39 (87%)	6 (13%)	4	17
All	All	1374/1410 (97%)	1303 (95%)	71 (5%)	21	49

All (71) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	27	VAL
1	A	50	GLN
1	A	82	PHE
1	A	84	SER
1	A	87	LYS
1	A	153	ASP
1	A	192	GLN
1	A	221	GLN
1	A	244	SER
1	B	27	VAL
1	B	50	GLN
1	B	82	PHE
1	B	153	ASP
1	B	192	GLN
1	B	221	GLN
1	C	27	VAL
1	C	50	GLN
1	C	82	PHE
1	C	153	ASP
1	C	192	GLN
1	C	221	GLN
1	D	27	VAL
1	D	50	GLN
1	D	82	PHE
1	D	84	SER
1	D	153	ASP
1	D	192	GLN
1	D	221	GLN
1	D	244	SER
1	E	27	VAL
1	E	31	VAL
1	E	50	GLN
1	E	82	PHE
1	E	84	SER
1	E	153	ASP
1	E	192	GLN
1	E	221	GLN
1	F	27	VAL
1	F	50	GLN
1	F	82	PHE
1	F	84	SER
1	F	153	ASP
1	F	192	GLN

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Mol	Chain	Res	Type
1	F	221	GLN
2	G	7	THR
2	G	8	THR
2	G	14	THR
2	G	45	ASP
2	H	8	THR
2	H	14	THR
2	H	16	SER
2	H	46	ASN
2	H	59	GLN
2	I	35	VAL
2	J	8	THR
2	J	21	CYS
2	J	31	LEU
2	J	35	VAL
2	J	36	LYS
2	J	56	ASP
2	K	8	THR
2	K	12	PRO
2	K	14	THR
2	K	42	LYS
2	K	59	GLN
2	L	8	THR
2	L	13	VAL
2	L	14	THR
2	L	25	LYS
2	L	30	ASP
2	L	59	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	30	GLN
1	A	50	GLN
1	A	210	GLN
1	B	30	GLN
1	B	50	GLN
1	C	30	GLN
1	C	50	GLN
1	C	210	GLN
1	D	30	GLN
1	D	50	GLN

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Mol	Chain	Res	Type
1	E	30	GLN
1	E	50	GLN
1	E	210	GLN
1	F	30	GLN
1	F	50	GLN
1	F	175	GLN
1	F	210	GLN
2	G	32	HIS
2	G	39	HIS
2	H	32	HIS
2	H	39	HIS
2	J	32	HIS
2	K	32	HIS
2	L	32	HIS
2	L	39	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 ⓘ

There are no oligosaccharides 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, 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	211/223 (94%)	-1.04	2 (0%) 81 65	4, 12, 41, 66	40 (18%)
1	B	211/223 (94%)	-0.65	4 (1%) 66 48	5, 15, 43, 63	40 (18%)
1	C	211/223 (94%)	-0.63	4 (1%) 66 48	5, 15, 40, 65	40 (18%)
1	D	211/223 (94%)	-1.02	0 100 100	4, 13, 39, 68	40 (18%)
1	E	211/223 (94%)	-0.71	11 (5%) 33 22	3, 14, 41, 68	40 (18%)
1	F	211/223 (94%)	-0.66	12 (5%) 29 20	4, 14, 41, 64	40 (18%)
2	G	53/59 (89%)	-1.32	0 100 100	6, 19, 39, 56	12 (22%)
2	H	38/59 (64%)	-1.08	0 100 100	6, 28, 50, 68	5 (13%)
2	I	38/59 (64%)	-0.98	0 100 100	6, 22, 51, 69	6 (15%)
2	J	53/59 (89%)	-1.25	0 100 100	5, 20, 37, 50	11 (20%)
2	K	48/59 (81%)	-0.93	0 100 100	6, 19, 38, 45	9 (18%)
2	L	49/59 (83%)	-0.93	0 100 100	7, 22, 41, 50	7 (14%)
All	All	1545/1692 (91%)	-0.84	33 (2%) 63 44	3, 15, 43, 69	290 (18%)

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	114	LEU	4.9
1	E	118	VAL	4.4
1	F	84	SER	4.2
1	E	114	LEU	4.0
1	E	110	SER	4.0
1	F	118	VAL	3.9
1	F	39	TYR	3.7
1	F	76	VAL	3.7
1	E	111	ALA	3.7
1	E	109	LYS	3.6
1	F	109	LYS	3.6

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Mol	Chain	Res	Type	RSRZ
1	C	96	SER	3.3
1	F	110	SER	3.3
1	F	127	SER	3.3
1	E	76	VAL	3.1
1	E	112	ALA	3.0
1	E	84	SER	3.0
1	A	244	SER	2.9
1	E	113	SER	2.9
1	F	112	ALA	2.9
1	E	49	SER	2.9
1	E	39	TYR	2.8
1	C	245	ASN	2.7
1	F	113	SER	2.7
1	C	109	LYS	2.3
1	B	62	GLY	2.3
1	B	109	LYS	2.3
1	F	74	ASN	2.3
1	B	39	TYR	2.2
1	B	61	SER	2.1
1	C	110	SER	2.1
1	F	85	ALA	2.0
1	A	112	ALA	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.