



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 06:33 PM GMT

PDB ID : 1BBR
Title : THE STRUCTURE OF RESIDUES 7-16 OF THE A ALPHA CHAIN
OF HUMAN FIBRINOGEN BOUND TO BOVINE THROMBIN AT 2.3
ANGSTROMS RESOLUTION
Authors : Martin, P.; Edwards, B.
Deposited on : 1992-04-27
Resolution : 2.30 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

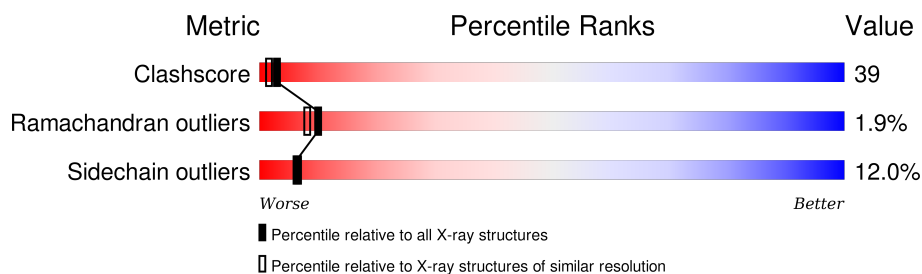
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)




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 $\leq 5\%$. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	J	49	
1	L	49	
1	M	49	
2	H	150	
3	E	109	
4	F	11	
4	G	11	

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Mol	Chain	Length	Quality of chain
4	I	11	 36% 55% 9%
5	K	259	 44% 37% 14% •
5	N	259	 42% 45% 10% •

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 8084 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 EPSILON-THROMBIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	36	Total	C	N	O	S	0	0	0
			290	181	48	60	1			
1	J	36	Total	C	N	O	S	0	0	0
			290	181	48	60	1			
1	M	36	Total	C	N	O	S	0	0	0
			290	181	48	60	1			

- Molecule 2 is a protein called EPSILON-THROMBIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	150	Total	C	N	O	S	0	0	0
			1235	793	222	215	5			

- Molecule 3 is a protein called EPSILON-THROMBIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	109	Total	C	N	O	S	0	0	0
			860	544	154	155	7			

- Molecule 4 is a protein called FIBRINOGEN ALPHA/ALPHA-E CHAIN PRECURSOR.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	F	11	Total	C	N	O	0	0	0
			75	46	13	16			
4	G	11	Total	C	N	O	0	0	0
			75	46	13	16			
4	I	11	Total	C	N	O	0	0	0
			75	46	13	16			

- Molecule 5 is a protein called EPSILON-THROMBIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	K	259	Total 2094	C 1337	N 376	O 369	S 12	0	0	0
5	N	259	Total 2094	C 1337	N 376	O 369	S 12	0	0	0

- Molecule 6 is water.

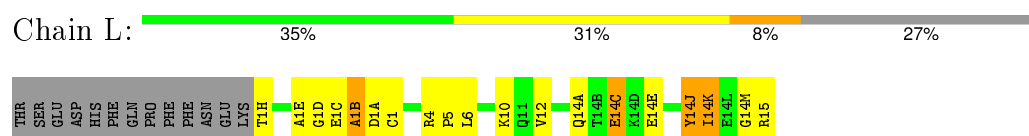
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	E	69	Total 69	O 69	0	0
6	F	10	Total 10	O 10	0	0
6	G	11	Total 11	O 11	0	0
6	H	126	Total 126	O 126	0	0
6	I	9	Total 9	O 9	0	0
6	J	23	Total 23	O 23	0	0
6	K	213	Total 213	O 213	0	0
6	L	31	Total 31	O 31	0	0
6	M	26	Total 26	O 26	0	0
6	N	188	Total 188	O 188	0	0

3 Residue-property plots

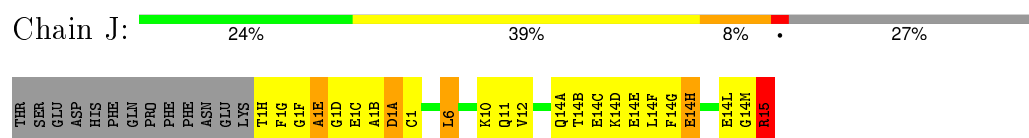
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

Note EDS was not executed.

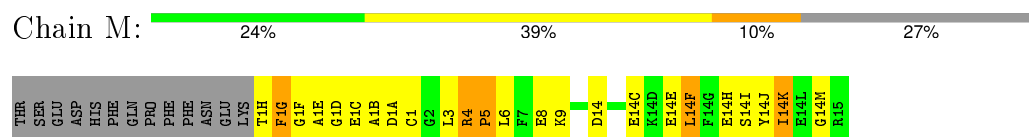
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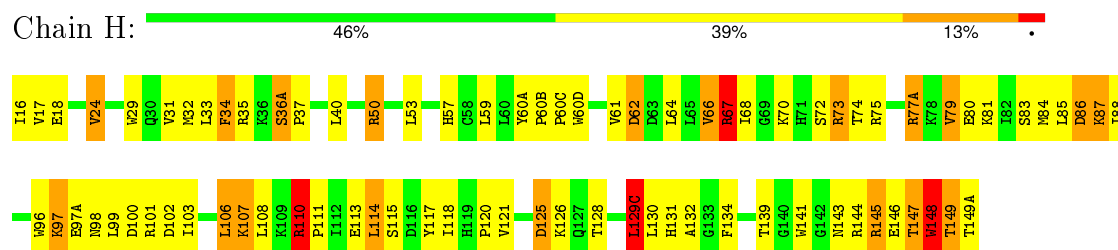
• Molecule 1: EPSILON-THROMBIN



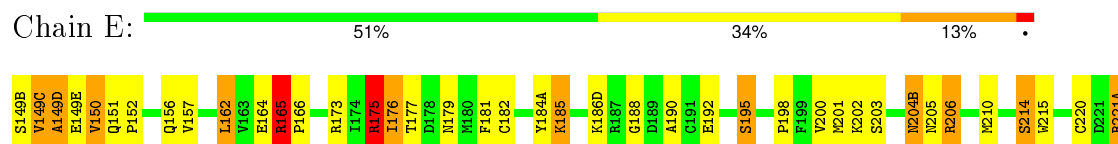
• Molecule 1: EPSILON-THROMBIN

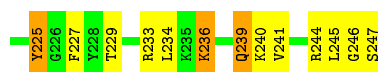


• Molecule 2: EPSILON-THROMBIN

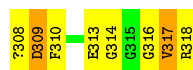


• Molecule 3: EPSILON-THROMBIN





• Molecule 4: FIBRINOGEN ALPHA/ALPHA-E CHAIN PRECURSOR



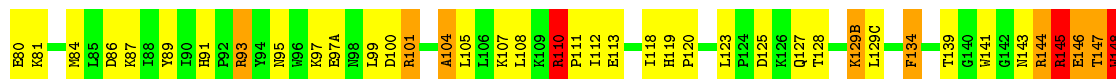
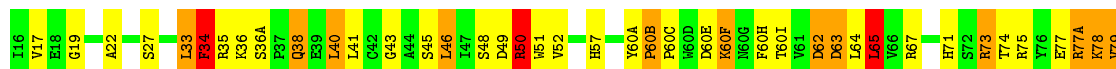
• Molecule 4: FIBRINOGEN ALPHA/ALPHA-E CHAIN PRECURSOR



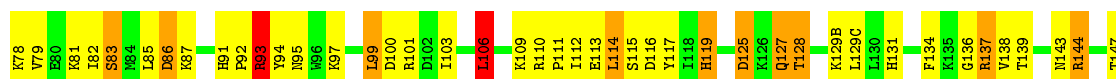
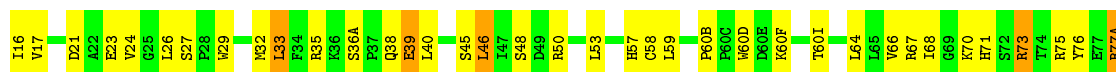
• Molecule 4: FIBRINOGEN ALPHA/ALPHA-E CHAIN PRECURSOR

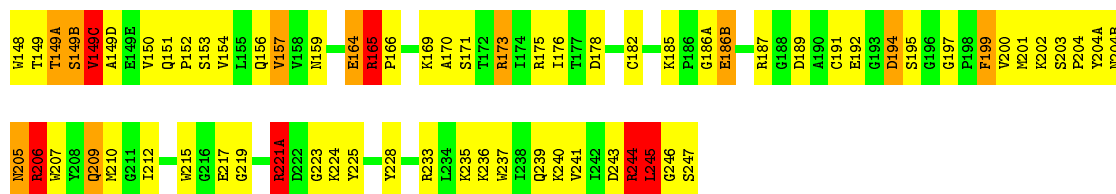


• Molecule 5: EPSILON-THROMBIN



• Molecule 5: EPSILON-THROMBIN





4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	83.02Å 89.41Å 99.30Å 90.00° 106.64° 90.00°	Depositor
Resolution (Å)	7.00 – 2.30	Depositor
% Data completeness (in resolution range)	(Not available) (7.00-2.30)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, R_{free}	0.167 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	8084	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

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	J	1.18	0/294	1.86	7/390 (1.8%)
1	L	1.07	0/294	1.64	1/390 (0.3%)
1	M	1.18	2/294 (0.7%)	1.87	5/390 (1.3%)
2	H	1.09	0/1267	1.71	17/1716 (1.0%)
3	E	1.14	0/881	1.77	16/1186 (1.3%)
4	F	1.18	0/73	2.25	3/95 (3.2%)
4	G	1.21	0/73	1.60	1/95 (1.1%)
4	I	1.24	0/73	1.95	1/95 (1.1%)
5	K	1.27	2/2148 (0.1%)	2.05	69/2905 (2.4%)
5	N	1.08	3/2148 (0.1%)	1.76	46/2905 (1.6%)
All	All	1.16	7/7545 (0.1%)	1.85	166/10167 (1.6%)

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	J	0	1
2	H	0	2
3	E	0	2
4	G	0	1
5	K	0	6
5	N	0	5
All	All	0	17

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	K	19	GLY	N-CA	5.75	1.54	1.46
5	K	80	GLU	CB-CG	-5.57	1.41	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	N	33	LEU	N-CA	5.54	1.57	1.46
1	M	14(H)	GLU	CD-OE2	-5.48	1.19	1.25
1	M	14(M)	GLY	N-CA	-5.42	1.38	1.46
5	N	219	GLY	CA-C	5.28	1.60	1.51
5	N	164	GLU	CD-OE2	-5.03	1.20	1.25

All (166) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	K	225	TYR	CB-CG-CD1	16.06	130.63	121.00
5	K	225	TYR	CB-CG-CD2	-15.70	111.58	121.00
5	K	175	ARG	NE-CZ-NH2	-13.93	113.34	120.30
5	N	75	ARG	CD-NE-CZ	12.89	141.65	123.60
5	K	60(F)	LYS	CA-CB-CG	12.84	141.65	113.40
5	K	50	ARG	NE-CZ-NH1	12.18	126.39	120.30
3	E	233	ARG	NE-CZ-NH1	11.91	126.25	120.30
5	N	206	ARG	NE-CZ-NH1	11.75	126.17	120.30
5	K	73	ARG	NE-CZ-NH1	11.66	126.13	120.30
5	K	33	LEU	CA-CB-CG	11.25	141.17	115.30
5	K	165	ARG	NE-CZ-NH2	-10.97	114.82	120.30
5	N	75	ARG	NE-CZ-NH1	10.79	125.69	120.30
5	K	221	ASP	CB-CG-OD1	10.68	127.91	118.30
1	M	4	ARG	NE-CZ-NH2	-10.61	115.00	120.30
3	E	162	LEU	CA-CB-CG	10.36	139.12	115.30
5	N	39	GLU	CA-CB-CG	10.04	135.50	113.40
2	H	67	ARG	NE-CZ-NH1	9.94	125.27	120.30
5	K	35	ARG	NE-CZ-NH1	9.84	125.22	120.30
3	E	221(A)	ARG	NE-CZ-NH1	9.74	125.17	120.30
5	N	33	LEU	CB-CA-C	9.44	128.13	110.20
1	M	4	ARG	NE-CZ-NH1	9.39	124.99	120.30
2	H	73	ARG	NE-CZ-NH1	9.19	124.90	120.30
5	K	173	ARG	NE-CZ-NH1	9.08	124.84	120.30
5	N	221(A)	ARG	NE-CZ-NH2	-9.07	115.76	120.30
1	M	14(M)	GLY	N-CA-C	9.04	135.70	113.10
5	K	50	ARG	NE-CZ-NH2	-8.92	115.84	120.30
4	F	318	ARG	NE-CZ-NH2	-8.88	115.86	120.30
3	E	206	ARG	NE-CZ-NH1	-8.88	115.86	120.30
5	N	125	ASP	CB-CG-OD1	8.79	126.21	118.30
5	K	60(A)	TYR	CB-CG-CD1	-8.55	115.87	121.00
5	K	93	ARG	NE-CZ-NH1	8.42	124.51	120.30
5	N	206	ARG	NE-CZ-NH2	-8.29	116.16	120.30
5	K	145	ARG	CA-CB-CG	8.19	131.41	113.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	K	35	ARG	NE-CZ-NH2	-8.13	116.24	120.30
5	K	189	ASP	CB-CG-OD2	8.09	125.58	118.30
5	K	101	ARG	CD-NE-CZ	-8.01	112.38	123.60
5	N	33	LEU	CA-CB-CG	7.96	133.60	115.30
5	K	144	ARG	NE-CZ-NH2	-7.95	116.32	120.30
5	K	185	LYS	CA-CB-CG	7.72	130.38	113.40
2	H	145	ARG	NE-CZ-NH1	7.60	124.10	120.30
1	J	14(C)	GLU	OE1-CD-OE2	7.56	132.38	123.30
5	N	86	ASP	CB-CG-OD1	-7.53	111.53	118.30
5	K	80	GLU	CB-CG-CD	7.50	134.44	114.20
5	N	67	ARG	NE-CZ-NH1	7.48	124.04	120.30
2	H	86	ASP	CB-CG-OD1	-7.24	111.78	118.30
5	N	244	ARG	NE-CZ-NH1	7.23	123.91	120.30
5	N	157	VAL	CB-CA-C	-7.22	97.68	111.40
5	N	164	GLU	CA-CB-CG	7.20	129.24	113.40
5	K	175	ARG	CD-NE-CZ	-7.20	113.53	123.60
5	N	194	ASP	CB-CG-OD2	7.19	124.77	118.30
5	K	186(B)	GLU	CA-C-N	7.08	130.36	116.20
5	K	49	ASP	CB-CG-OD2	7.05	124.65	118.30
5	N	189	ASP	CB-CG-OD2	7.02	124.62	118.30
3	E	184(A)	TYR	CB-CG-CD1	-7.00	116.80	121.00
1	J	14(F)	LEU	CA-CB-CG	6.98	131.35	115.30
5	K	60(A)	TYR	CB-CG-CD2	6.97	125.18	121.00
4	I	309	ASP	CB-CG-OD1	6.96	124.57	118.30
5	K	149	THR	N-CA-CB	6.93	123.46	110.30
5	K	208	TYR	CB-CG-CD2	-6.92	116.85	121.00
1	M	14	ASP	CB-CG-OD2	6.87	124.49	118.30
1	M	14(F)	LEU	CA-CB-CG	6.79	130.91	115.30
5	K	139	THR	CA-CB-CG2	6.77	121.88	112.40
5	N	101	ARG	NE-CZ-NH1	6.76	123.68	120.30
5	N	165	ARG	NE-CZ-NH1	-6.74	116.93	120.30
5	K	80	GLU	CA-CB-CG	6.69	128.11	113.40
5	K	65	LEU	CA-CB-CG	6.64	130.57	115.30
3	E	190	ALA	N-CA-CB	6.61	119.35	110.10
5	N	165	ARG	CD-NE-CZ	-6.58	114.38	123.60
5	N	93	ARG	NE-CZ-NH1	-6.58	117.01	120.30
5	K	162	LEU	CA-CB-CG	6.39	129.99	115.30
5	N	83	SER	N-CA-CB	6.33	120.00	110.50
5	N	186(B)	GLU	N-CA-C	6.30	128.02	111.00
5	K	192	GLU	OE1-CD-OE2	6.29	130.85	123.30
5	N	173	ARG	NE-CZ-NH1	-6.27	117.17	120.30
5	K	144	ARG	NE-CZ-NH1	6.27	123.43	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	N	119	HIS	CA-CB-CG	6.26	124.24	113.60
3	E	221(A)	ARG	NE-CZ-NH2	-6.25	117.18	120.30
4	F	318	ARG	NE-CZ-NH1	6.24	123.42	120.30
2	H	129(C)	LEU	CA-CB-CG	6.22	129.61	115.30
5	N	186(B)	GLU	CA-C-N	6.16	128.53	116.20
5	N	75	ARG	NE-CZ-NH2	-6.16	117.22	120.30
5	K	161	PRO	O-C-N	6.15	132.53	122.70
2	H	77(A)	ARG	NE-CZ-NH2	-6.14	117.23	120.30
5	K	221	ASP	CB-CG-OD2	-6.13	112.78	118.30
5	K	186(B)	GLU	CA-C-O	-6.10	107.29	120.10
5	K	34	PHE	N-CA-CB	-6.09	99.64	110.60
3	E	184(A)	TYR	CB-CG-CD2	6.05	124.63	121.00
5	K	191	CYS	CB-CA-C	6.04	122.49	110.40
5	N	175	ARG	NE-CZ-NH1	-6.00	117.30	120.30
2	H	79	VAL	N-CA-C	5.97	127.12	111.00
5	K	50	ARG	CD-NE-CZ	5.95	131.93	123.60
5	N	137	ARG	NE-CZ-NH1	5.93	123.27	120.30
5	K	148	TRP	CA-CB-CG	5.92	124.95	113.70
5	N	101	ARG	NE-CZ-NH2	-5.85	117.38	120.30
2	H	148	TRP	N-CA-CB	5.85	121.13	110.60
5	K	77(A)	ARG	CA-CB-CG	5.85	126.27	113.40
2	H	36(A)	SER	N-CA-CB	-5.84	101.74	110.50
2	H	33	LEU	O-C-N	5.82	132.01	122.70
5	K	146	GLU	CA-CB-CG	5.78	126.12	113.40
5	N	23	GLU	CA-CB-CG	5.76	126.08	113.40
5	N	175	ARG	CD-NE-CZ	-5.75	115.54	123.60
5	K	134	PHE	CA-CB-CG	5.75	127.69	113.90
5	K	110	ARG	CB-CA-C	-5.72	98.96	110.40
5	K	190	ALA	N-CA-CB	5.65	118.01	110.10
5	K	186(B)	GLU	N-CA-C	5.64	126.24	111.00
5	K	134	PHE	CB-CG-CD1	5.63	124.74	120.80
5	N	137	ARG	NE-CZ-NH2	-5.62	117.49	120.30
5	K	210	MET	CA-CB-CG	-5.61	103.76	113.30
5	K	204(A)	TYR	CB-CG-CD1	-5.57	117.66	121.00
2	H	34	PHE	N-CA-CB	-5.55	100.61	110.60
3	E	165	ARG	CD-NE-CZ	-5.55	115.83	123.60
5	N	100	ASP	CB-CG-OD2	5.54	123.29	118.30
5	K	228	TYR	CB-CG-CD1	5.54	124.33	121.00
5	K	73	ARG	NH1-CZ-NH2	-5.53	113.32	119.40
5	K	189	ASP	CB-CA-C	5.51	121.43	110.40
5	K	100	ASP	CB-CG-OD1	5.49	123.24	118.30
5	K	67	ARG	CD-NE-CZ	-5.48	115.93	123.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	K	65	LEU	CB-CA-C	5.45	120.56	110.20
4	G	314	GLY	N-CA-C	5.45	126.73	113.10
5	K	157	VAL	CB-CA-C	-5.44	101.06	111.40
5	N	21	ASP	CB-CG-OD1	5.43	123.19	118.30
5	N	157	VAL	CA-CB-CG2	5.43	119.05	110.90
2	H	60(A)	TYR	CB-CG-CD1	-5.42	117.75	121.00
3	E	157	VAL	CB-CA-C	-5.38	101.18	111.40
5	K	212	ILE	CA-CB-CG2	5.38	121.66	110.90
3	E	181	PHE	CB-CA-C	5.33	121.07	110.40
5	K	145	ARG	NE-CZ-NH1	5.33	122.97	120.30
1	J	14(C)	GLU	CG-CD-OE2	-5.33	107.64	118.30
2	H	125	ASP	CB-CG-OD2	5.33	123.09	118.30
5	N	209	GLN	N-CA-CB	5.30	120.13	110.60
5	K	97(A)	GLU	CG-CD-OE1	5.29	128.88	118.30
2	H	62	ASP	CB-CA-C	5.29	120.97	110.40
5	K	51	TRP	C-N-CA	5.28	134.89	121.70
5	K	234	LEU	CB-CA-C	5.25	120.18	110.20
3	E	198	PRO	C-N-CA	5.24	134.80	121.70
5	K	43	GLY	N-CA-C	-5.23	100.02	113.10
2	H	80	GLU	CA-CB-CG	5.22	124.88	113.40
2	H	18	GLU	CG-CD-OE1	-5.20	107.90	118.30
5	N	113	GLU	OE1-CD-OE2	5.20	129.54	123.30
5	K	97(A)	GLU	CA-CB-CG	5.19	124.82	113.40
5	K	104	ALA	N-CA-CB	5.19	117.37	110.10
1	J	14(E)	GLU	CA-CB-CG	5.18	124.81	113.40
5	N	64	LEU	N-CA-CB	-5.18	100.04	110.40
5	K	62	ASP	C-N-CA	5.18	134.65	121.70
5	N	225	TYR	CB-CG-CD1	-5.17	117.90	121.00
1	L	14(C)	GLU	CA-CB-CG	5.16	124.75	113.40
5	N	199	PHE	N-CA-CB	5.16	119.88	110.60
5	N	144	ARG	CD-NE-CZ	-5.15	116.39	123.60
5	K	77	GLU	CG-CD-OE2	5.14	128.58	118.30
3	E	176	ILE	CA-CB-CG2	5.13	121.17	110.90
1	J	6	LEU	CB-CA-C	5.13	119.94	110.20
5	N	206	ARG	CD-NE-CZ	5.12	130.76	123.60
5	K	192	GLU	CG-CD-OE1	-5.11	108.08	118.30
3	E	225	TYR	CB-CG-CD2	5.11	124.06	121.00
5	N	157	VAL	N-CA-CB	5.11	122.73	111.50
3	E	176	ILE	CB-CA-C	5.10	121.80	111.60
5	N	209	GLN	O-C-N	5.10	130.86	122.70
4	F	314	GLY	N-CA-C	5.10	125.85	113.10
5	K	149(E)	GLU	N-CA-CB	5.07	119.73	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
5	N	67	ARG	CD-NE-CZ	-5.07	116.50	123.60
1	J	14(E)	GLU	CB-CG-CD	5.06	127.85	114.20
2	H	35	ARG	NE-CZ-NH1	5.05	122.83	120.30
3	E	200	VAL	CA-CB-CG1	5.05	118.48	110.90
5	K	93	ARG	NH1-CZ-NH2	-5.02	113.88	119.40
1	J	14(H)	GLU	CB-CG-CD	5.01	127.72	114.20
5	N	106	LEU	CA-CB-CG	5.00	126.81	115.30

There are no chirality outliers.

All (17) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	E	165	ARG	Sidechain
3	E	175	ARG	Sidechain
4	G	318	ARG	Sidechain
2	H	110	ARG	Sidechain
2	H	67	ARG	Sidechain
1	J	15	ARG	Sidechain
5	K	110	ARG	Sidechain
5	K	165	ARG	Sidechain
5	K	175	ARG	Sidechain
5	K	233	ARG	Sidechain
5	K	50	ARG	Sidechain
5	K	77(A)	ARG	Sidechain
5	N	165	ARG	Sidechain
5	N	187	ARG	Sidechain
5	N	206	ARG	Sidechain
5	N	221(A)	ARG	Sidechain
5	N	73	ARG	Sidechain

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	J	290	0	276	37	0
1	L	290	0	276	30	0
1	M	290	0	276	47	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	H	1235	0	1252	101	0
3	E	860	0	844	87	0
4	F	75	0	69	8	0
4	G	75	0	69	6	0
4	I	75	0	69	8	0
5	K	2094	0	2097	156	0
5	N	2094	0	2097	178	0
6	E	69	0	0	15	0
6	F	10	0	0	0	0
6	G	11	0	0	1	0
6	H	126	0	0	24	0
6	I	9	0	0	6	0
6	J	23	0	0	9	0
6	K	213	0	0	53	0
6	L	31	0	0	6	0
6	M	26	0	0	18	0
6	N	188	0	0	51	0
All	All	8084	0	7325	573	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 39.

All (573) 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)
5:K:60(F):LYS:HB2	6:K:422:HOH:O	1.17	1.28
5:K:176:ILE:HG21	6:K:407:HOH:O	1.27	1.25
1:J:14(G):PHE:HB3	6:J:616:HOH:O	1.30	1.24
5:K:52:VAL:HG22	6:K:432:HOH:O	1.39	1.23
5:N:204:PRO:HB3	6:N:396:HOH:O	1.40	1.21
5:K:169:LYS:NZ	5:K:169:LYS:HB2	1.54	1.16
2:H:62:ASP:HB2	6:H:259:HOH:O	1.42	1.15
5:K:233:ARG:HD2	6:K:363:HOH:O	1.48	1.11
3:E:205:ASN:N	6:E:312:HOH:O	1.81	1.11
5:K:148:TRP:HB2	5:K:150:VAL:HG21	1.35	1.08
5:N:57:HIS:HB3	6:N:427:HOH:O	1.53	1.05
5:N:240:LYS:HG3	5:N:245:LEU:HA	1.12	1.05
5:K:160:LEU:HB3	6:K:308:HOH:O	1.58	1.03
5:K:46:LEU:HD23	6:K:432:HOH:O	1.57	1.03
1:M:14(K):ILE:CG1	6:M:37:HOH:O	2.09	1.01
1:L:15:ARG:CG	2:H:131:HIS:HB3	1.90	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:15:ARG:HG3	2:H:131:HIS:HB3	1.42	1.00
5:N:128:THR:HG22	5:N:129(C):LEU:HD22	1.43	1.00
5:K:235:LYS:HE3	6:K:423:HOH:O	1.60	0.99
1:M:14(K):ILE:HG12	6:M:37:HOH:O	1.63	0.97
2:H:144:ARG:NH1	6:H:267:HOH:O	1.98	0.97
6:H:267:HOH:O	3:E:149(E):GLU:HA	1.64	0.95
5:K:41:LEU:HB3	6:K:457:HOH:O	1.66	0.95
5:N:97:LYS:HG2	6:N:334:HOH:O	1.67	0.95
1:J:1(G):PHE:O	6:J:612:HOH:O	1.81	0.95
5:N:119:HIS:CB	6:N:389:HOH:O	2.14	0.94
5:N:149(C):VAL:HA	6:N:399:HOH:O	1.65	0.94
5:N:81:LYS:HD2	5:N:112:ILE:HD11	1.49	0.94
5:K:149(A):THR:HA	5:K:149(D):ALA:O	1.68	0.93
4:I:316:GLY:C	6:I:665:HOH:O	2.05	0.92
5:N:66:VAL:HG21	5:N:85:LEU:HD21	1.52	0.92
5:N:200:VAL:HG12	5:N:209:GLN:HA	1.49	0.92
3:E:165:ARG:HD2	3:E:165:ARG:H	1.32	0.91
3:E:177:THR:HG22	3:E:179:ASN:H	1.33	0.91
5:K:169:LYS:HZ3	5:K:169:LYS:HB2	1.22	0.90
5:N:240:LYS:HD2	5:N:245:LEU:HD22	1.54	0.90
5:K:204(B):ASN:ND2	5:K:204(B):ASN:O	2.05	0.90
5:K:144:ARG:HD3	6:K:433:HOH:O	1.72	0.89
1:M:5:PRO:HD3	6:N:389:HOH:O	1.71	0.89
1:M:5:PRO:CD	6:N:389:HOH:O	2.19	0.89
5:K:244:ARG:O	5:K:245:LEU:HB2	1.71	0.89
1:J:14(A):GLN:HG2	6:J:646:HOH:O	1.69	0.89
5:K:46:LEU:HD22	5:K:48:SER:O	1.72	0.89
3:E:246:GLY:O	3:E:247:SER:HB2	1.71	0.89
2:H:57:HIS:CD2	4:F:317:VAL:HG13	2.08	0.89
2:H:145:ARG:HD2	5:K:149(A):THR:HG21	1.53	0.88
5:K:97:LYS:HD2	6:K:361:HOH:O	1.73	0.88
5:N:147:THR:HG22	5:N:149(B):SER:HB2	1.53	0.88
5:K:148:TRP:HB2	5:K:150:VAL:CG2	2.02	0.88
5:K:164:GLU:HG2	5:K:167:VAL:HG13	1.54	0.88
1:M:3:LEU:HD22	6:N:252:HOH:O	1.74	0.87
4:I:313:GLU:HG3	6:I:675:HOH:O	1.75	0.87
2:H:97(A):GLU:HG3	4:F:308:ACE:H2	1.56	0.87
5:N:240:LYS:HG3	5:N:245:LEU:CA	2.03	0.87
5:N:215:TRP:HB2	6:I:665:HOH:O	1.73	0.86
1:J:1(H):THR:N	1:J:1(C):GLU:OE2	2.06	0.86
5:K:235:LYS:HG3	6:K:423:HOH:O	1.73	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:73:ARG:NH1	3:E:149(C):VAL:HG23	1.90	0.86
5:N:119:HIS:CG	6:N:389:HOH:O	2.27	0.86
3:E:165:ARG:N	3:E:165:ARG:HD2	1.91	0.85
2:H:102:ASP:OD2	6:H:256:HOH:O	1.93	0.85
1:M:1(E):ALA:HB3	6:M:36:HOH:O	1.77	0.85
5:N:240:LYS:CG	5:N:245:LEU:HA	2.05	0.84
5:N:50:ARG:HD3	6:N:259:HOH:O	1.78	0.83
5:N:195:SER:HB2	4:I:318:ARG:C	1.99	0.83
5:N:66:VAL:CG2	5:N:85:LEU:HD21	2.08	0.82
5:K:176:ILE:CG2	6:K:407:HOH:O	2.00	0.82
5:K:147:THR:HG22	5:K:149(C):VAL:HG11	1.63	0.81
1:J:15:ARG:NH1	6:J:696:HOH:O	2.09	0.81
5:N:24:VAL:HB	6:N:388:HOH:O	1.81	0.81
5:K:169:LYS:HZ2	5:K:169:LYS:HB2	1.46	0.81
2:H:145:ARG:HD2	5:K:149(A):THR:CG2	2.11	0.81
5:K:148:TRP:HB3	6:K:317:HOH:O	1.81	0.80
5:K:38:GLN:OE1	6:K:439:HOH:O	2.00	0.80
5:N:86:ASP:O	5:N:87:LYS:HG3	1.82	0.79
2:H:77(A):ARG:HD3	6:H:274:HOH:O	1.82	0.79
5:K:143:ASN:OD1	6:K:315:HOH:O	2.00	0.78
3:E:165:ARG:CB	6:E:306:HOH:O	2.30	0.78
5:N:81:LYS:CD	5:N:112:ILE:HD11	2.14	0.77
3:E:151:GLN:HB3	6:E:300:HOH:O	1.82	0.77
5:N:119:HIS:HB3	6:N:389:HOH:O	1.76	0.77
5:N:149(D):ALA:C	5:N:150:VAL:H	1.85	0.77
2:H:24:VAL:HG23	2:H:117:TYR:HE1	1.49	0.77
5:N:240:LYS:HD3	5:N:245:LEU:HD13	1.67	0.77
5:K:240:LYS:HD2	5:K:247:SER:O	1.84	0.77
5:N:117:TYR:HE1	6:N:388:HOH:O	1.68	0.77
1:L:15:ARG:HG2	2:H:131:HIS:HB3	1.67	0.76
5:K:62:ASP:HB2	6:K:436:HOH:O	1.84	0.76
1:M:14(K):ILE:CD1	6:M:37:HOH:O	2.32	0.76
2:H:99:LEU:HD11	4:F:317:VAL:HG22	1.68	0.76
3:E:165:ARG:HB3	6:E:305:HOH:O	1.86	0.75
2:H:145:ARG:HH21	2:H:149:THR:HG21	1.52	0.75
5:N:204(B):ASN:O	5:N:206:ARG:N	2.16	0.74
2:H:73:ARG:HD3	3:E:152:PRO:O	1.86	0.74
2:H:100:ASP:OD1	3:E:177:THR:HG21	1.86	0.74
5:K:84:MET:HG2	6:K:438:HOH:O	1.86	0.73
5:N:149(B):SER:HB2	5:N:150:VAL:HG21	1.70	0.73
6:H:256:HOH:O	3:E:214:SER:OG	2.05	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:110:ARG:NE	6:H:185:HOH:O	2.22	0.73
1:L:10:LYS:O	1:L:12:VAL:HG23	1.88	0.73
2:H:148:TRP:HD1	5:K:149(D):ALA:H	1.37	0.72
2:H:97(A):GLU:OE2	3:E:175:ARG:HD3	1.89	0.72
1:J:1(F):GLY:HA3	5:K:235:LYS:NZ	2.04	0.72
2:H:148:TRP:HD1	5:K:149(D):ALA:N	1.86	0.72
5:N:119:HIS:CD2	6:N:389:HOH:O	2.43	0.72
5:N:170:ALA:HA	6:N:431:HOH:O	1.89	0.72
3:E:165:ARG:HB3	6:E:306:HOH:O	1.89	0.72
3:E:149(E):GLU:O	3:E:150:VAL:HG12	1.89	0.72
5:K:148:TRP:CG	5:K:149:THR:N	2.55	0.72
5:N:57:HIS:CB	6:N:427:HOH:O	2.25	0.72
5:K:235:LYS:CG	6:K:423:HOH:O	2.32	0.71
5:K:38:GLN:HB2	6:K:458:HOH:O	1.90	0.71
5:K:178:ASP:O	5:K:233:ARG:HD3	1.91	0.71
5:K:164:GLU:CG	5:K:167:VAL:HG13	2.20	0.71
1:M:5:PRO:HG2	5:N:116:ASP:O	1.90	0.71
5:K:205:ASN:N	6:K:431:HOH:O	2.24	0.70
1:L:1(C):GLU:O	1:L:1(B):ALA:HB3	1.91	0.70
5:N:244:ARG:O	5:N:245:LEU:HB2	1.91	0.70
5:K:245:LEU:HD12	5:K:247:SER:OXT	1.90	0.70
5:K:148:TRP:CZ2	6:K:315:HOH:O	2.43	0.70
1:L:14(K):ILE:C	1:L:14(M):GLY:H	1.95	0.69
5:N:60(I):THR:HB	6:N:363:HOH:O	1.93	0.69
3:E:204(B):ASN:O	3:E:204(B):ASN:ND2	2.24	0.69
5:K:143:ASN:ND2	5:K:192:GLU:HG3	2.08	0.69
1:M:1(H):THR:HB	5:N:235:LYS:HZ2	1.56	0.69
3:E:165:ARG:HD3	3:E:166:PRO:HD3	1.75	0.69
3:E:240:LYS:HD3	3:E:247:SER:H	1.56	0.69
1:L:10:LYS:HD2	6:L:338:HOH:O	1.91	0.69
5:N:58:CYS:O	6:N:287:HOH:O	2.11	0.69
1:M:14(K):ILE:HD13	6:M:37:HOH:O	1.90	0.68
5:K:145:ARG:O	6:K:317:HOH:O	2.10	0.68
1:L:1(C):GLU:O	1:L:1(B):ALA:CB	2.41	0.68
3:E:165:ARG:C	6:E:306:HOH:O	2.32	0.68
2:H:149:THR:OG1	2:H:149(A):THR:N	2.27	0.68
5:N:204(B):ASN:ND2	5:N:204(B):ASN:O	2.27	0.68
1:L:14(K):ILE:C	6:L:591:HOH:O	2.32	0.68
1:M:5:PRO:O	1:M:9:LYS:HB2	1.94	0.67
4:G:317:VAL:HG13	6:G:589:HOH:O	1.93	0.67
5:N:169:LYS:NZ	6:N:338:HOH:O	2.28	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:N:137:ARG:NH1	5:N:207:TRP:CH2	2.62	0.67
3:E:165:ARG:CD	3:E:166:PRO:HD3	2.25	0.67
5:N:203:SER:O	6:N:390:HOH:O	2.13	0.67
2:H:146:GLU:OE1	3:E:221(A):ARG:NH2	2.28	0.67
5:N:149(B):SER:CB	5:N:150:VAL:HG21	2.25	0.67
5:K:149:THR:O	5:K:149(B):SER:N	2.26	0.66
3:E:245:LEU:N	3:E:245:LEU:HD22	2.11	0.66
5:K:22:ALA:HB2	5:K:157:VAL:HG22	1.78	0.66
5:N:173:ARG:NH1	5:N:173:ARG:HG3	2.08	0.66
3:E:204(B):ASN:C	6:E:312:HOH:O	2.20	0.66
5:K:33:LEU:HD22	6:K:388:HOH:O	1.94	0.66
5:N:131:HIS:HD2	5:N:134:PHE:CE2	2.14	0.66
5:K:33:LEU:HD13	6:K:388:HOH:O	1.95	0.66
1:J:1(F):GLY:HA3	5:K:235:LYS:HZ2	1.60	0.65
5:K:149(A):THR:O	5:K:149(D):ALA:N	2.29	0.65
3:E:149(C):VAL:HG22	3:E:149(D):ALA:H	1.61	0.65
5:K:148:TRP:CB	5:K:150:VAL:HG21	2.22	0.65
5:N:239:GLN:NE2	5:N:247:SER:HB2	2.11	0.65
5:K:204(B):ASN:HD22	5:K:204(B):ASN:C	1.99	0.65
1:J:14(M):GLY:HA3	5:K:134:PHE:HE1	1.62	0.65
5:K:74:THR:HA	6:K:337:HOH:O	1.96	0.65
1:J:1(H):THR:HA	6:J:613:HOH:O	1.95	0.65
2:H:75:ARG:NH2	6:H:269:HOH:O	2.27	0.64
2:H:115:SER:O	6:H:260:HOH:O	2.14	0.64
1:J:1(E):ALA:HA	5:K:125:ASP:OD2	1.98	0.64
1:M:3:LEU:CD2	6:N:252:HOH:O	2.38	0.64
5:N:243:ASP:HB3	5:N:244:ARG:HD2	1.80	0.64
2:H:61:VAL:HG22	2:H:85:LEU:HB2	1.80	0.64
5:N:60(D):TRP:NE1	6:N:326:HOH:O	2.19	0.64
5:K:105:LEU:HD11	5:K:238:ILE:HG23	1.80	0.63
5:N:203:SER:C	6:N:390:HOH:O	2.37	0.63
5:N:149(B):SER:O	5:N:149(C):VAL:HG13	1.99	0.63
5:K:204(B):ASN:C	6:K:431:HOH:O	2.36	0.63
3:E:165:ARG:CD	3:E:165:ARG:H	1.87	0.62
1:J:1(C):GLU:HG2	1:J:1:CYS:HB3	1.81	0.62
5:K:160:LEU:HD23	6:K:308:HOH:O	1.98	0.62
1:M:5:PRO:HD3	6:M:35:HOH:O	1.98	0.62
5:K:147:THR:HG23	5:K:149(C):VAL:HG21	1.79	0.62
5:N:57:HIS:CE1	5:N:195:SER:OG	2.52	0.62
5:K:73:ARG:HD3	5:K:152:PRO:O	1.98	0.62
3:E:165:ARG:CA	6:E:306:HOH:O	2.47	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:N:87:LYS:HG2	6:N:433:HOH:O	1.98	0.62
5:K:128:THR:HG23	5:K:129(C):LEU:HD22	1.82	0.62
5:K:148:TRP:CZ3	5:K:192:GLU:OE2	2.52	0.62
5:N:240:LYS:HG2	5:N:240:LYS:O	1.99	0.62
5:N:186(A):GLY:N	6:N:318:HOH:O	2.09	0.62
5:K:73:ARG:HB2	5:K:141:TRP:CD1	2.35	0.62
1:J:1(H):THR:HG23	5:K:48:SER:CB	2.30	0.61
5:N:149(A):THR:HB	6:N:435:HOH:O	2.00	0.61
3:E:177:THR:HG22	3:E:179:ASN:N	2.13	0.61
1:J:14(H):GLU:O	1:J:14(L):GLU:HG3	2.00	0.61
5:N:81:LYS:CG	5:N:112:ILE:HD11	2.31	0.61
3:E:236:LYS:NZ	3:E:239:GLN:OE1	2.32	0.61
5:K:60(F):LYS:HD2	6:K:422:HOH:O	1.95	0.61
2:H:114:LEU:O	2:H:115:SER:HB3	1.99	0.61
2:H:50:ARG:HD3	2:H:111:PRO:HD3	1.82	0.61
1:J:1(H):THR:HG23	5:K:48:SER:OG	2.01	0.60
5:N:149(D):ALA:C	5:N:150:VAL:N	2.54	0.60
5:N:165:ARG:NH1	6:N:331:HOH:O	2.34	0.60
5:N:149(C):VAL:O	5:N:151:GLN:NE2	2.35	0.60
5:N:71:HIS:NE2	5:N:154:VAL:CG2	2.64	0.60
1:M:6:LEU:O	6:M:27:HOH:O	2.16	0.60
5:N:147:THR:HG22	5:N:149(B):SER:CB	2.27	0.60
3:E:203:SER:HB3	3:E:204(B):ASN:O	2.02	0.59
2:H:97:LYS:HE3	6:H:151:HOH:O	2.01	0.59
2:H:60(D):TRP:HB3	6:H:233:HOH:O	2.00	0.59
1:L:6:LEU:HA	1:L:10:LYS:HD3	1.83	0.59
5:N:60(F):LYS:HD3	6:N:287:HOH:O	2.02	0.59
1:L:15:ARG:HG3	2:H:131:HIS:CB	2.26	0.59
5:K:62:ASP:CB	6:K:436:HOH:O	2.45	0.59
5:K:78:LYS:HE2	6:K:399:HOH:O	2.01	0.59
5:N:239:GLN:NE2	5:N:247:SER:OXT	2.35	0.59
4:I:317:VAL:N	6:I:665:HOH:O	2.31	0.59
2:H:149(A):THR:OXT	3:E:150:VAL:HG11	2.02	0.59
1:M:14(K):ILE:HG23	6:M:37:HOH:O	2.02	0.59
1:L:14(J):TYR:O	1:L:14(K):ILE:HB	2.01	0.59
5:K:246:GLY:C	6:K:417:HOH:O	2.41	0.58
5:K:87:LYS:HD2	5:K:89:TYR:CZ	2.37	0.58
1:L:14(E):GLU:OE2	3:E:186(D):LYS:NZ	2.36	0.58
5:K:247:SER:HB2	6:K:417:HOH:O	2.03	0.58
3:E:149(B):SER:O	3:E:149(C):VAL:HB	2.02	0.58
3:E:177:THR:HG22	3:E:179:ASN:HB2	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:81:LYS:HE3	6:H:239:HOH:O	2.03	0.58
5:K:36:LYS:HD3	6:K:438:HOH:O	2.03	0.58
5:K:148:TRP:HZ3	5:K:192:GLU:OE2	1.85	0.58
6:M:38:HOH:O	5:N:129(C):LEU:HG	2.04	0.58
5:N:16:ILE:N	5:N:194:ASP:OD2	2.37	0.58
2:H:145:ARG:HG2	3:E:150:VAL:HG23	1.85	0.58
5:N:165:ARG:HB3	5:N:166:PRO:HD3	1.85	0.58
5:N:46:LEU:HD22	5:N:48:SER:O	2.04	0.58
1:J:1(C):GLU:CG	1:J:1:CYS:HB3	2.35	0.57
5:K:195:SER:OG	4:G:318:ARG:C	2.42	0.57
1:J:1(B):ALA:C	5:K:206:ARG:HH12	2.08	0.57
5:N:143:ASN:OD1	5:N:192:GLU:HG3	2.05	0.57
2:H:73:ARG:HH12	3:E:149(C):VAL:HA	1.69	0.57
5:N:147:THR:O	5:N:148:TRP:CD1	2.57	0.57
2:H:32:MET:HG3	2:H:40:LEU:CD2	2.34	0.57
3:E:204(B):ASN:C	3:E:204(B):ASN:HD22	2.08	0.56
5:N:147:THR:CG2	5:N:150:VAL:HG11	2.34	0.56
1:J:1(F):GLY:O	1:J:1(E):ALA:HB2	2.04	0.56
3:E:149(C):VAL:HG13	3:E:149(D):ALA:N	2.20	0.56
5:N:24:VAL:CB	6:N:388:HOH:O	2.48	0.56
5:N:203:SER:HG	5:N:204(A):TYR:HD2	1.53	0.56
5:N:147:THR:HA	5:N:149(B):SER:OG	2.05	0.56
3:E:149(D):ALA:O	3:E:151:GLN:HG2	2.05	0.56
1:J:15:ARG:HA	6:J:680:HOH:O	2.04	0.56
5:K:60(I):THR:O	5:K:63:ASP:HB2	2.06	0.56
1:M:5:PRO:CD	6:M:35:HOH:O	2.54	0.56
2:H:32:MET:HG3	2:H:40:LEU:HD23	1.87	0.56
2:H:146:GLU:HB3	5:K:149(B):SER:HB2	1.88	0.56
5:N:136:GLY:HA3	5:N:199:PHE:CZ	2.39	0.56
1:J:1(C):GLU:O	1:J:1(B):ALA:HB3	2.05	0.56
1:M:14(K):ILE:CG2	6:M:37:HOH:O	2.54	0.56
2:H:29:TRP:CD2	2:H:121:VAL:HB	2.41	0.56
5:K:113:GLU:HG3	6:K:446:HOH:O	2.05	0.56
5:K:34:PHE:HE1	6:K:458:HOH:O	1.89	0.55
1:L:14(K):ILE:O	6:L:591:HOH:O	2.18	0.55
1:J:14(M):GLY:HA3	5:K:134:PHE:CE1	2.41	0.55
5:K:52:VAL:CG2	6:K:432:HOH:O	2.17	0.55
3:E:204(B):ASN:CA	6:E:312:HOH:O	2.53	0.55
2:H:74:THR:HG22	2:H:75:ARG:N	2.21	0.55
2:H:24:VAL:HG23	2:H:117:TYR:CE1	2.35	0.55
1:L:14(A):GLN:HB3	6:L:511:HOH:O	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:K:239:GLN:HG3	6:K:417:HOH:O	2.05	0.55
1:M:3:LEU:HD21	5:N:206:ARG:HG2	1.89	0.55
5:K:129(C):LEU:HD23	5:K:210:MET:HE3	1.87	0.55
1:L:1(D):GLY:HA2	6:L:158:HOH:O	2.06	0.55
4:I:316:GLY:O	6:I:665:HOH:O	2.18	0.55
5:K:149(A):THR:CA	5:K:149(D):ALA:O	2.50	0.54
3:E:165:ARG:N	3:E:165:ARG:CD	2.55	0.54
4:I:310:PHE:HZ	6:I:665:HOH:O	1.90	0.54
2:H:66:VAL:HG12	2:H:83:SER:OG	2.07	0.54
5:N:81:LYS:HG3	5:N:112:ILE:HD11	1.90	0.54
3:E:173:ARG:HB2	4:F:313:GLU:OE1	2.07	0.54
1:M:14(E):GLU:HB2	6:M:33:HOH:O	2.06	0.54
5:K:148:TRP:CD1	5:K:150:VAL:CG2	2.91	0.54
2:H:139:THR:HA	3:E:156:GLN:O	2.08	0.54
1:L:1:CYS:O	3:E:206:ARG:HD3	2.07	0.54
5:N:221(A):ARG:NH2	6:N:429:HOH:O	2.41	0.54
5:K:17:VAL:O	5:K:188:GLY:HA2	2.08	0.54
5:N:240:LYS:CB	5:N:246:GLY:H	2.21	0.54
5:N:29:TRP:O	5:N:45:SER:HA	2.08	0.54
1:J:1(F):GLY:HA2	5:K:123:LEU:HB2	1.88	0.54
5:K:211:GLY:HA2	5:K:229:THR:O	2.08	0.54
5:K:22:ALA:O	5:K:71:HIS:HE1	1.91	0.54
2:H:97(A):GLU:HG3	4:F:308:ACE:CH3	2.33	0.53
5:K:127:GLN:O	5:K:129(B):LYS:HD3	2.08	0.53
2:H:60(B):PRO:HB2	2:H:60(C):PRO:HD3	1.90	0.53
5:N:204:PRO:HA	6:N:390:HOH:O	2.07	0.53
2:H:97(A):GLU:O	4:F:310:PHE:HB2	2.07	0.53
3:E:221(A):ARG:HD3	6:E:311:HOH:O	2.09	0.53
1:J:1(B):ALA:HA	5:K:206:ARG:HH22	1.73	0.53
5:N:128:THR:O	5:N:129(C):LEU:HB2	2.09	0.53
6:H:256:HOH:O	3:E:214:SER:CB	2.54	0.53
1:L:1(E):ALA:HB2	3:E:206:ARG:CZ	2.39	0.53
5:N:27:SER:OG	5:N:29:TRP:NE1	2.42	0.53
3:E:177:THR:CG2	3:E:179:ASN:HB2	2.39	0.53
5:N:127:GLN:O	5:N:129(B):LYS:HD2	2.09	0.52
1:M:6:LEU:HD11	5:N:116:ASP:HB3	1.90	0.52
5:N:236:LYS:HE3	5:N:247:SER:OG	2.10	0.52
5:N:239:GLN:CD	5:N:247:SER:HB2	2.29	0.52
3:E:214:SER:HB3	3:E:215:TRP:HD1	1.74	0.52
1:J:1(H):THR:HG23	5:K:48:SER:HB3	1.92	0.52
2:H:113:GLU:HG2	6:H:239:HOH:O	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:12:VAL:HG13	6:J:517:HOH:O	2.10	0.52
1:M:8:GLU:HG2	6:N:252:HOH:O	2.09	0.52
5:N:79:VAL:HG12	5:N:117:TYR:CD2	2.43	0.52
5:N:117:TYR:CE1	6:N:388:HOH:O	2.51	0.52
2:H:17:VAL:O	3:E:188:GLY:HA2	2.09	0.52
1:J:1(C):GLU:C	1:J:1(A):ASP:H	2.14	0.52
5:N:243:ASP:C	5:N:244:ARG:HD2	2.30	0.52
5:N:81:LYS:HD2	5:N:112:ILE:CD1	2.30	0.52
5:N:114:LEU:O	5:N:115:SER:OG	2.20	0.52
2:H:149(A):THR:O	6:H:197:HOH:O	2.19	0.51
1:M:14(C):GLU:OE2	5:N:202:LYS:NZ	2.39	0.51
5:N:66:VAL:HG12	5:N:68:ILE:HD11	1.92	0.51
5:K:60(F):LYS:HG3	5:K:60(H):PHE:CE2	2.45	0.51
5:K:148:TRP:CB	6:K:317:HOH:O	2.48	0.51
3:E:236:LYS:HD2	3:E:236:LYS:N	2.20	0.51
5:N:152:PRO:HG3	6:N:422:HOH:O	2.09	0.51
2:H:36(A):SER:HA	2:H:37:PRO:C	2.31	0.51
2:H:74:THR:HG21	3:E:149(B):SER:HB2	1.92	0.51
5:N:24:VAL:CG2	6:N:388:HOH:O	2.59	0.51
5:K:38:GLN:HB2	6:K:459:HOH:O	2.11	0.51
5:N:171:SER:O	5:N:224:LYS:NZ	2.37	0.51
1:J:1(D):GLY:HA2	1:J:1:CYS:SG	2.51	0.51
5:K:97:LYS:HE2	6:K:257:HOH:O	2.10	0.51
5:N:204(B):ASN:HD22	5:N:206:ARG:HG3	1.76	0.51
5:K:86:ASP:HB3	5:K:107:LYS:HG3	1.93	0.51
5:N:93:ARG:HH11	5:N:93:ARG:HG2	1.76	0.51
2:H:97(A):GLU:CD	3:E:175:ARG:HH11	2.15	0.50
5:N:237:TRP:O	5:N:241:VAL:HG13	2.12	0.50
5:K:60(F):LYS:CB	6:K:422:HOH:O	2.02	0.50
5:K:185:LYS:HB2	5:K:186(B):GLU:OE1	2.11	0.50
3:E:149(D):ALA:HB3	3:E:151:GLN:HE21	1.76	0.50
5:K:235:LYS:CD	6:K:423:HOH:O	2.59	0.50
5:N:240:LYS:HB2	5:N:246:GLY:H	1.77	0.50
5:K:160:LEU:CG	6:K:308:HOH:O	2.58	0.50
5:N:186(A):GLY:CA	6:N:318:HOH:O	2.55	0.50
2:H:50:ARG:CD	6:H:172:HOH:O	2.60	0.50
2:H:74:THR:HG22	2:H:75:ARG:H	1.77	0.50
2:H:60(B):PRO:N	2:H:60(C):PRO:CD	2.74	0.50
3:E:221(A):ARG:CD	6:E:311:HOH:O	2.59	0.50
5:K:34:PHE:CE1	5:K:38:GLN:O	2.65	0.50
5:N:239:GLN:HB3	5:N:247:SER:HA	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:K:163:VAL:CG1	5:K:167:VAL:HG22	2.42	0.49
3:E:176:ILE:HD11	3:E:215:TRP:HZ2	1.77	0.49
3:E:239:GLN:NE2	6:E:294:HOH:O	1.99	0.49
5:N:239:GLN:NE2	5:N:247:SER:CA	2.75	0.49
5:K:127:GLN:HG3	5:K:129(B):LYS:CE	2.42	0.49
5:N:197:GLY:HA3	6:N:278:HOH:O	2.11	0.49
3:E:176:ILE:HG13	3:E:227:PHE:CE2	2.46	0.49
5:N:91:HIS:ND1	5:N:92:PRO:HD2	2.27	0.49
1:J:1(H):THR:O	1:J:1(G):PHE:CD1	2.66	0.49
5:N:204(B):ASN:O	5:N:206:ARG:HG3	2.12	0.49
5:N:144:ARG:NH2	5:N:152:PRO:HA	2.27	0.49
2:H:149(A):THR:OXT	3:E:150:VAL:CG1	2.59	0.49
5:N:57:HIS:HE1	5:N:195:SER:OG	1.94	0.49
5:N:128:THR:CG2	5:N:129(C):LEU:HD22	2.30	0.49
1:M:4:ARG:O	1:M:5:PRO:C	2.50	0.49
6:H:273:HOH:O	3:E:152:PRO:HG3	2.12	0.49
5:K:45:SER:O	5:K:52:VAL:HA	2.13	0.48
5:N:59:LEU:HD11	5:N:106:LEU:HD11	1.93	0.48
1:L:14(J):TYR:O	1:L:14(K):ILE:CB	2.61	0.48
1:J:1(H):THR:CA	6:J:613:HOH:O	2.58	0.48
1:L:1(E):ALA:HB1	3:E:206:ARG:NH1	2.28	0.48
2:H:53:LEU:HD11	2:H:103:ILE:HD11	1.95	0.48
5:K:60(B):PRO:HB2	5:K:60(C):PRO:HD3	1.94	0.48
5:N:186(A):GLY:HA3	6:N:318:HOH:O	2.13	0.48
3:E:201:MET:SD	3:E:210:MET:HG3	2.53	0.48
1:J:1(D):GLY:C	1:J:1(B):ALA:H	2.15	0.48
5:N:185:LYS:HG3	5:N:186(B):GLU:OE1	2.14	0.48
5:K:143:ASN:ND2	6:K:317:HOH:O	2.46	0.48
3:E:215:TRP:HB2	4:F:316:GLY:O	2.14	0.48
5:N:86:ASP:HB2	5:N:109:LYS:HA	1.95	0.48
1:L:1(C):GLU:OE1	2:H:120:PRO:HG2	2.14	0.48
5:N:50:ARG:HE	5:N:111:PRO:HG3	1.79	0.47
1:L:15:ARG:CZ	2:H:132:ALA:HB3	2.44	0.47
1:M:1(H):THR:HB	5:N:235:LYS:NZ	2.28	0.47
2:H:148:TRP:CD1	5:K:149(D):ALA:N	2.76	0.47
5:K:95:ASN:O	5:K:99:LEU:HA	2.14	0.47
2:H:73:ARG:HB2	2:H:141:TRP:CD1	2.50	0.47
2:H:146:GLU:HG3	3:E:220:CYS:H	1.78	0.47
2:H:68:ILE:HA	6:H:261:HOH:O	2.14	0.47
2:H:31:VAL:HG22	2:H:68:ILE:HG12	1.96	0.47
2:H:32:MET:SD	2:H:67:ARG:HD3	2.54	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:N:53:LEU:HD11	5:N:103:ILE:HD11	1.97	0.47
5:K:148:TRP:HE1	5:K:151:GLN:HE21	1.63	0.47
2:H:96:TRP:HA	2:H:99:LEU:HD23	1.96	0.47
5:N:240:LYS:CG	5:N:240:LYS:O	2.61	0.47
5:N:151:GLN:HB3	6:N:282:HOH:O	2.15	0.47
5:N:35:ARG:O	5:N:38:GLN:HA	2.15	0.47
5:N:204:PRO:CB	6:N:396:HOH:O	2.22	0.47
5:K:149(A):THR:C	5:K:149(C):VAL:N	2.67	0.47
5:N:204(B):ASN:HD22	5:N:206:ARG:CG	2.28	0.47
5:N:139:THR:HG22	5:N:156:GLN:O	2.14	0.47
5:N:131:HIS:HD2	5:N:134:PHE:HE2	1.60	0.47
5:N:221(A):ARG:NH2	6:N:329:HOH:O	2.47	0.47
1:J:1(F):GLY:O	1:J:1(E):ALA:CB	2.63	0.47
5:K:149:THR:CG2	5:K:149:THR:O	2.63	0.47
5:N:221(A):ARG:NH1	6:N:429:HOH:O	2.48	0.47
3:E:185:LYS:HG3	3:E:225:TYR:OH	2.15	0.47
1:M:14(J):TYR:OH	6:M:25:HOH:O	2.18	0.47
5:K:34:PHE:HB3	5:K:65:LEU:HD12	1.97	0.46
5:K:165:ARG:N	5:K:166:PRO:CD	2.77	0.46
5:N:76:TYR:HE1	5:N:82:ILE:HD11	1.80	0.46
5:N:95:ASN:O	5:N:99:LEU:HA	2.14	0.46
1:L:1(E):ALA:CB	3:E:206:ARG:CZ	2.93	0.46
5:K:119:HIS:HA	5:K:120:PRO:HD3	1.77	0.46
5:N:125:ASP:OD1	5:N:128:THR:OG1	2.27	0.46
5:K:247:SER:HB3	6:K:275:HOH:O	2.16	0.46
5:K:60(F):LYS:NZ	6:K:457:HOH:O	2.48	0.46
5:N:203:SER:OG	5:N:204(A):TYR:HD2	1.98	0.46
5:K:145:ARG:HE	5:K:149(C):VAL:HG11	1.80	0.46
2:H:146:GLU:OE2	5:K:149:THR:HG22	2.14	0.46
5:N:239:GLN:NE2	5:N:247:SER:HA	2.30	0.46
5:N:148:TRP:CD2	6:N:414:HOH:O	2.68	0.46
2:H:81:LYS:HD3	2:H:81:LYS:HA	1.80	0.46
3:E:229:THR:CG2	3:E:234:LEU:HD12	2.46	0.46
3:E:164:GLU:HB2	3:E:165:ARG:HD2	1.97	0.46
2:H:70:LYS:HE3	2:H:72:SER:O	2.16	0.46
5:K:127:GLN:HG2	6:K:378:HOH:O	2.16	0.46
2:H:59:LEU:HD11	2:H:106:LEU:HD11	1.98	0.46
5:N:240:LYS:CD	5:N:245:LEU:HD13	2.43	0.46
1:L:14(K):ILE:C	1:L:14(M):GLY:N	2.67	0.46
1:J:1(F):GLY:HA2	6:J:612:HOH:O	2.15	0.45
1:L:15:ARG:HG2	2:H:132:ALA:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:N:236:LYS:HG3	5:N:247:SER:HB3	1.98	0.45
5:N:178:ASP:HB3	5:N:233:ARG:NH1	2.31	0.45
5:K:148:TRP:CD1	5:K:150:VAL:HG22	2.51	0.45
1:M:1(G):PHE:HD2	1:M:1(E):ALA:HB2	1.80	0.45
1:M:1(E):ALA:O	1:M:1(D):GLY:C	2.55	0.45
5:N:24:VAL:HG23	6:N:388:HOH:O	2.15	0.45
5:N:149(A):THR:O	6:N:435:HOH:O	2.20	0.45
2:H:148:TRP:CD1	5:K:149(C):VAL:HA	2.51	0.45
3:E:246:GLY:O	3:E:247:SER:CB	2.51	0.45
5:K:128:THR:CG2	5:K:129(C):LEU:HD22	2.47	0.45
5:N:73:ARG:NH1	5:N:152:PRO:O	2.43	0.45
5:K:161:PRO:HG2	5:K:184:GLY:O	2.15	0.45
2:H:79:VAL:HG21	6:H:247:HOH:O	2.15	0.45
5:K:169:LYS:HE3	6:K:250:HOH:O	2.17	0.45
1:M:1(H):THR:HG22	1:M:1(G):PHE:O	2.16	0.45
5:N:71:HIS:CD2	5:N:154:VAL:HG23	2.52	0.45
5:N:139:THR:HA	5:N:156:GLN:O	2.16	0.45
5:N:17:VAL:HG23	5:N:191:CYS:HB2	1.99	0.45
5:K:40:LEU:HD23	5:K:40:LEU:C	2.37	0.45
5:K:148:TRP:CB	5:K:150:VAL:CG2	2.87	0.45
1:M:4:ARG:HA	1:M:5:PRO:HD2	1.80	0.45
1:M:3:LEU:CD2	5:N:206:ARG:HG2	2.46	0.45
5:N:60(B):PRO:O	5:N:60(D):TRP:N	2.49	0.45
2:H:128:THR:HG23	2:H:129(C):LEU:HD22	1.99	0.45
3:E:239:GLN:HE21	3:E:239:GLN:HB3	1.40	0.45
5:N:165:ARG:NE	6:N:375:HOH:O	2.43	0.45
5:N:114:LEU:C	5:N:115:SER:HG	2.18	0.45
1:M:1(C):GLU:CB	1:M:1:CYS:HB3	2.47	0.45
5:K:203:SER:HA	5:K:204:PRO:HD3	1.76	0.45
5:K:146:GLU:OE2	5:K:221(A):ARG:HD3	2.17	0.45
2:H:68:ILE:HG22	2:H:118:ILE:HG12	1.97	0.45
2:H:57:HIS:NE2	4:F:317:VAL:HG13	2.29	0.45
3:E:244:ARG:NE	6:E:307:HOH:O	2.25	0.45
1:M:1(H):THR:HG22	5:N:235:LYS:HZ1	1.82	0.45
2:H:147:THR:O	2:H:147:THR:HG22	2.16	0.45
1:M:8:GLU:HB3	6:N:252:HOH:O	2.17	0.44
1:J:14(M):GLY:O	1:J:15:ARG:CB	2.65	0.44
2:H:66:VAL:HG11	2:H:108:LEU:HD21	1.99	0.44
5:N:239:GLN:NE2	5:N:247:SER:CB	2.80	0.44
1:J:1(F):GLY:CA	5:K:123:LEU:HB2	2.46	0.44
3:E:149(C):VAL:O	3:E:149(D):ALA:HB2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:N:71:HIS:CD2	5:N:154:VAL:CG2	3.01	0.44
5:K:204(B):ASN:O	5:K:206:ARG:N	2.43	0.44
2:H:98:ASN:O	2:H:99:LEU:HB2	2.18	0.44
5:N:91:HIS:CG	5:N:92:PRO:HD2	2.52	0.44
1:M:1(H):THR:N	5:N:239:GLN:NE2	2.66	0.44
2:H:57:HIS:CE1	3:E:195:SER:HG	2.36	0.44
2:H:61:VAL:HG23	2:H:88:ILE:HG13	1.99	0.44
1:M:1(G):PHE:HB3	5:N:125:ASP:HB3	1.98	0.44
3:E:245:LEU:CD2	3:E:245:LEU:N	2.80	0.44
5:K:89:TYR:O	5:K:104:ALA:HA	2.18	0.44
4:G:311:LEU:HA	4:G:311:LEU:HD12	1.66	0.44
5:K:127:GLN:CD	6:K:378:HOH:O	2.56	0.44
2:H:143:ASN:ND2	3:E:192:GLU:CG	2.81	0.44
2:H:98:ASN:N	2:H:98:ASN:OD1	2.50	0.43
5:N:173:ARG:NH1	5:N:173:ARG:CG	2.72	0.43
1:M:14(F):LEU:HD21	5:N:159:ASN:OD1	2.18	0.43
2:H:87:LYS:HD2	2:H:88:ILE:H	1.82	0.43
5:K:73:ARG:NH2	6:K:336:HOH:O	2.51	0.43
5:N:223:GLY:O	6:N:416:HOH:O	2.21	0.43
1:M:1(G):PHE:N	6:M:36:HOH:O	2.50	0.43
2:H:74:THR:CG2	2:H:75:ARG:N	2.81	0.43
2:H:50:ARG:HD3	6:H:172:HOH:O	2.19	0.43
1:M:3:LEU:HD11	5:N:206:ARG:HH21	1.83	0.43
5:N:77(A):ARG:HH21	5:N:78:LYS:HD2	1.83	0.43
5:K:22:ALA:HB2	5:K:157:VAL:CG2	2.46	0.43
1:L:14(C):GLU:OE2	3:E:202:LYS:NZ	2.28	0.43
2:H:84:MET:SD	6:H:234:HOH:O	2.62	0.43
5:N:66:VAL:HG23	5:N:85:LEU:HD21	1.95	0.43
5:K:195:SER:HG	4:G:318:ARG:C	2.21	0.43
2:H:34:PHE:HE1	6:H:241:HOH:O	2.01	0.43
5:N:94:TYR:CE1	6:N:427:HOH:O	2.72	0.43
5:K:224:LYS:HD3	5:K:224:LYS:HA	1.85	0.43
1:J:14(G):PHE:CE1	5:K:202:LYS:HD3	2.54	0.43
5:K:148:TRP:CD1	5:K:149:THR:N	2.80	0.43
5:N:204(B):ASN:ND2	5:N:206:ARG:HD2	2.34	0.43
3:E:244:ARG:C	3:E:245:LEU:HD22	2.39	0.43
5:K:50:ARG:HE	5:K:111:PRO:HB3	1.83	0.43
2:H:146:GLU:OE2	5:K:149:THR:CG2	2.67	0.43
1:L:1(E):ALA:CB	3:E:206:ARG:NH1	2.82	0.43
1:M:14(I):SER:HB3	6:M:39:HOH:O	2.19	0.43
5:K:169:LYS:NZ	6:K:407:HOH:O	2.51	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:128:THR:CG2	2:H:129(C):LEU:HD22	2.49	0.42
1:M:1(C):GLU:O	1:M:1(A):ASP:N	2.51	0.42
2:H:101:ARG:NH1	6:H:153:HOH:O	2.33	0.42
3:E:244:ARG:HD3	3:E:244:ARG:HA	1.48	0.42
3:E:236:LYS:HB3	6:E:313:HOH:O	2.19	0.42
1:M:5:PRO:CG	6:M:35:HOH:O	2.67	0.42
3:E:149(C):VAL:HG22	3:E:151:GLN:O	2.20	0.42
3:E:214:SER:HB3	3:E:215:TRP:CD1	2.53	0.42
5:N:35:ARG:HD2	5:N:39:GLU:OE2	2.20	0.42
3:E:149(C):VAL:HG13	3:E:149(D):ALA:H	1.82	0.42
5:N:212:ILE:O	5:N:228:TYR:HA	2.20	0.42
5:N:138:VAL:CG2	5:N:199:PHE:HD2	2.32	0.42
2:H:32:MET:CG	2:H:40:LEU:HD23	2.48	0.42
5:K:73:ARG:HD2	6:K:434:HOH:O	2.19	0.42
5:K:101:ARG:HH11	5:K:101:ARG:HD2	1.49	0.42
5:K:165:ARG:HB3	5:K:166:PRO:HD3	2.02	0.42
1:J:14(B):THR:HB	5:K:159:ASN:HD21	1.85	0.42
4:I:311:LEU:HD12	4:I:311:LEU:HA	1.74	0.42
1:M:1(H):THR:HG22	1:M:1(G):PHE:N	2.34	0.42
3:E:165:ARG:NH1	6:E:290:HOH:O	2.53	0.42
2:H:114:LEU:HD12	2:H:118:ILE:HG22	2.02	0.42
5:N:66:VAL:HG12	5:N:68:ILE:CD1	2.49	0.42
5:K:57:HIS:CD2	4:G:317:VAL:HB	2.54	0.42
2:H:31:VAL:CG1	2:H:66:VAL:HG22	2.50	0.42
1:J:1(E):ALA:O	5:K:208:TYR:OH	2.26	0.41
5:N:217:GLU:HB3	6:N:336:HOH:O	2.20	0.41
5:K:189:ASP:OD2	4:G:318:ARG:NH2	2.52	0.41
1:M:1(C):GLU:HB3	1:M:1:CYS:HB3	2.02	0.41
5:N:32:MET:HE3	5:N:70:LYS:HD3	2.02	0.41
1:L:4:ARG:HA	1:L:5:PRO:HD3	1.91	0.41
5:N:129(C):LEU:O	5:N:134:PHE:HD2	2.03	0.41
5:K:34:PHE:HE1	5:K:38:GLN:O	2.02	0.41
2:H:50:ARG:HB2	2:H:50:ARG:HE	1.20	0.41
5:N:16:ILE:CD1	5:N:138:VAL:HG12	2.50	0.41
5:K:79:VAL:HG11	6:K:351:HOH:O	2.20	0.41
5:N:71:HIS:CE1	5:N:154:VAL:HG22	2.56	0.41
5:K:233:ARG:HB3	5:K:233:ARG:HE	1.29	0.41
1:M:1(F):GLY:HA2	6:M:31:HOH:O	2.21	0.41
2:H:86:ASP:HB3	2:H:107:LYS:HG3	2.01	0.41
5:N:240:LYS:CD	5:N:245:LEU:HD22	2.36	0.41
5:N:173:ARG:HH11	5:N:173:ARG:CG	2.33	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:1(H):THR:O	2:H:125:ASP:HB3	2.21	0.41
2:H:16:ILE:O	2:H:144:ARG:HA	2.21	0.41
5:N:131:HIS:CD2	5:N:134:PHE:CE2	3.01	0.41
2:H:143:ASN:HD22	3:E:192:GLU:CD	2.21	0.41
6:H:267:HOH:O	3:E:149(E):GLU:CA	2.41	0.41
5:N:195:SER:HB2	4:I:318:ARG:O	2.19	0.41
5:N:240:LYS:HD2	5:N:245:LEU:CD2	2.36	0.41
1:M:1(H):THR:OG1	5:N:239:GLN:NE2	2.54	0.41
1:L:14(A):GLN:CB	6:L:511:HOH:O	2.66	0.41
5:N:76:TYR:CE2	5:N:77(A):ARG:HG2	2.55	0.41
2:H:130:LEU:HA	3:E:162:LEU:HD21	2.02	0.41
5:N:137:ARG:NH1	5:N:207:TRP:HH2	2.13	0.40
5:K:75:ARG:NH1	5:K:75:ARG:HG3	2.35	0.40
5:K:108:LEU:HD13	5:K:112:ILE:CG1	2.51	0.40
1:M:1(H):THR:O	5:N:235:LYS:CE	2.68	0.40
5:K:81:LYS:HG2	5:K:118:ILE:CD1	2.51	0.40
5:K:91:HIS:CE1	5:K:93:ARG:HB2	2.56	0.40
2:H:134:PHE:CD1	2:H:134:PHE:N	2.88	0.40
5:N:201:MET:SD	5:N:210:MET:HG3	2.61	0.40
5:N:57:HIS:CA	6:N:427:HOH:O	2.62	0.40
1:J:1(C):GLU:C	1:J:1(A):ASP:N	2.73	0.40
1:M:5:PRO:HG3	6:M:35:HOH:O	2.21	0.40
5:N:192:GLU:HG2	5:N:192:GLU:H	1.75	0.40
5:N:93:ARG:HH11	5:N:93:ARG:CG	2.33	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	J	34/49 (69%)	28 (82%)	5 (15%)	1 (3%)	6 3

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	L	34/49 (69%)	27 (79%)	4 (12%)	3 (9%)	1	0
1	M	34/49 (69%)	26 (76%)	6 (18%)	2 (6%)	2	1
2	H	148/150 (99%)	135 (91%)	13 (9%)	0	100	100
3	E	107/109 (98%)	97 (91%)	7 (6%)	3 (3%)	6	4
4	F	9/11 (82%)	8 (89%)	0	1 (11%)	0	0
4	G	9/11 (82%)	9 (100%)	0	0	100	100
4	I	9/11 (82%)	8 (89%)	1 (11%)	0	100	100
5	K	257/259 (99%)	235 (91%)	19 (7%)	3 (1%)	16	16
5	N	257/259 (99%)	229 (89%)	24 (9%)	4 (2%)	12	11
All	All	898/957 (94%)	802 (89%)	79 (9%)	17 (2%)	10	8

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	L	1(B)	ALA
1	L	14(K)	ILE
3	E	149(C)	VAL
3	E	150	VAL
4	F	309	ASP
1	J	1(E)	ALA
5	K	149(A)	THR
5	K	205	ASN
5	K	245	LEU
5	N	205	ASN
5	N	245	LEU
3	E	149(D)	ALA
1	M	1(B)	ALA
5	N	149(A)	THR
5	N	149(C)	VAL
1	L	14(J)	TYR
1	M	5	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	J	30/43 (70%)	24 (80%)	6 (20%)	1	1
1	L	30/43 (70%)	29 (97%)	1 (3%)	45	61
1	M	30/43 (70%)	28 (93%)	2 (7%)	20	26
2	H	134/134 (100%)	119 (89%)	15 (11%)	7	8
3	E	92/92 (100%)	82 (89%)	10 (11%)	8	9
4	F	6/6 (100%)	4 (67%)	2 (33%)	0	0
4	G	6/6 (100%)	5 (83%)	1 (17%)	3	2
4	I	6/6 (100%)	5 (83%)	1 (17%)	3	2
5	K	226/226 (100%)	195 (86%)	31 (14%)	4	4
5	N	226/226 (100%)	201 (89%)	25 (11%)	8	8
All	All	786/825 (95%)	692 (88%)	94 (12%)	6	6

All (94) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	1(A)	ASP
2	H	24	VAL
2	H	50	ARG
2	H	64	LEU
2	H	66	VAL
2	H	87	LYS
2	H	97	LYS
2	H	106	LEU
2	H	107	LYS
2	H	110	ARG
2	H	114	LEU
2	H	126	LYS
2	H	129(C)	LEU
2	H	147	THR
2	H	148	TRP
2	H	149	THR
3	E	165	ARG
3	E	175	ARG
3	E	182	CYS
3	E	185	LYS
3	E	195	SER
3	E	204(B)	ASN
3	E	214	SER

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Mol	Chain	Res	Type
3	E	236	LYS
3	E	239	GLN
3	E	241	VAL
4	F	309	ASP
4	F	317	VAL
1	J	1(A)	ASP
1	J	6	LEU
1	J	10	LYS
1	J	11	GLN
1	J	14(D)	LYS
1	J	15	ARG
5	K	27	SER
5	K	34	PHE
5	K	36(A)	SER
5	K	38	GLN
5	K	40	LEU
5	K	46	LEU
5	K	60(B)	PRO
5	K	60(E)	ASP
5	K	63	ASP
5	K	64	LEU
5	K	65	LEU
5	K	78	LYS
5	K	79	VAL
5	K	110	ARG
5	K	129(B)	LYS
5	K	145	ARG
5	K	147	THR
5	K	148	TRP
5	K	149	THR
5	K	149(E)	GLU
5	K	153	SER
5	K	154	VAL
5	K	157	VAL
5	K	160	LEU
5	K	169	LYS
5	K	185	LYS
5	K	192	GLU
5	K	204(B)	ASN
5	K	221(A)	ARG
5	K	241	VAL
5	K	247	SER

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Mol	Chain	Res	Type
4	G	311	LEU
1	M	1(G)	PHE
1	M	14(K)	ILE
5	N	26	LEU
5	N	33	LEU
5	N	36(A)	SER
5	N	40	LEU
5	N	46	LEU
5	N	77(A)	ARG
5	N	83	SER
5	N	93	ARG
5	N	99	LEU
5	N	106	LEU
5	N	110	ARG
5	N	114	LEU
5	N	127	GLN
5	N	128	THR
5	N	149	THR
5	N	149(B)	SER
5	N	149(C)	VAL
5	N	153	SER
5	N	157	VAL
5	N	164	GLU
5	N	176	ILE
5	N	182	CYS
5	N	205	ASN
5	N	244	ARG
5	N	245	LEU
4	I	309	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	L	13	GLN
2	H	60(G)	ASN
2	H	143	ASN
3	E	151	GLN
3	E	204(B)	ASN
1	J	14(A)	GLN
5	K	71	HIS
5	K	204(B)	ASN
1	M	13	GLN

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Mol	Chain	Res	Type
5	N	38	GLN
5	N	127	GLN
5	N	131	HIS
5	N	204(B)	ASN
5	N	205	ASN
5	N	239	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.