



# Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 10:28 AM GMT

PDB ID : 1A2C  
Title : Structure of thrombin inhibited by AERUGINOSIN298-A from a BLUE-GREEN ALGA  
Authors : Rios-Steiner, J.L.; Murakami, M.; Tulinsky, A.  
Deposited on : 1997-12-26  
Resolution : 2.10 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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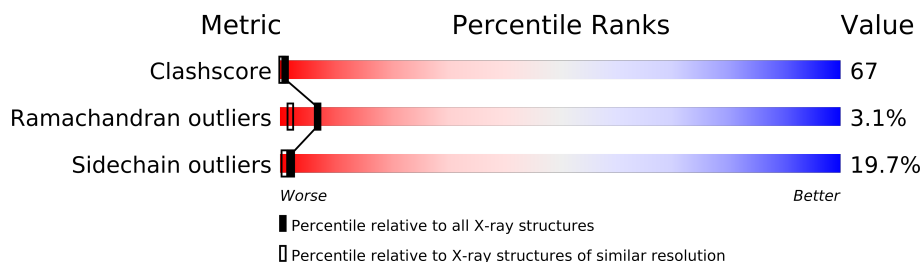
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 21963  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.10 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	79885	3649 (2.10-2.10)
Ramachandran outliers	78287	3610 (2.10-2.10)
Sidechain outliers	78261	3611 (2.10-2.10)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	L	36	
2	H	259	
3	I	12	
4	J	4	

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 2629 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Thrombin light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	36	Total	C	N	O	S	0	0	0
			281	174	45	61	1			

- Molecule 2 is a protein called Thrombin heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	252	Total	C	N	O	S	0	0	0
			2039	1299	360	366	14			

- Molecule 3 is a protein called Hirudin variant-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	I	10	Total	C	N	O	S	0	0	0
			89	56	10	22	1			

- Molecule 4 is a protein called Aeruginosin 298-A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	J	4	Total	C	N	O	0	0	0
			43	30	6	7			

- Molecule 5 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	H	1	Total	Na	0	0
			1	1		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	H	138	Total	O	0	0
			138	138		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	I	6	Total 6	O 6	0	0
6	J	6	Total 6	O 6	0	0
6	L	26	Total 26	O 26	0	0

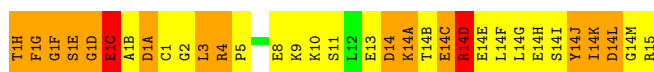
### 3 Residue-property plots

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.

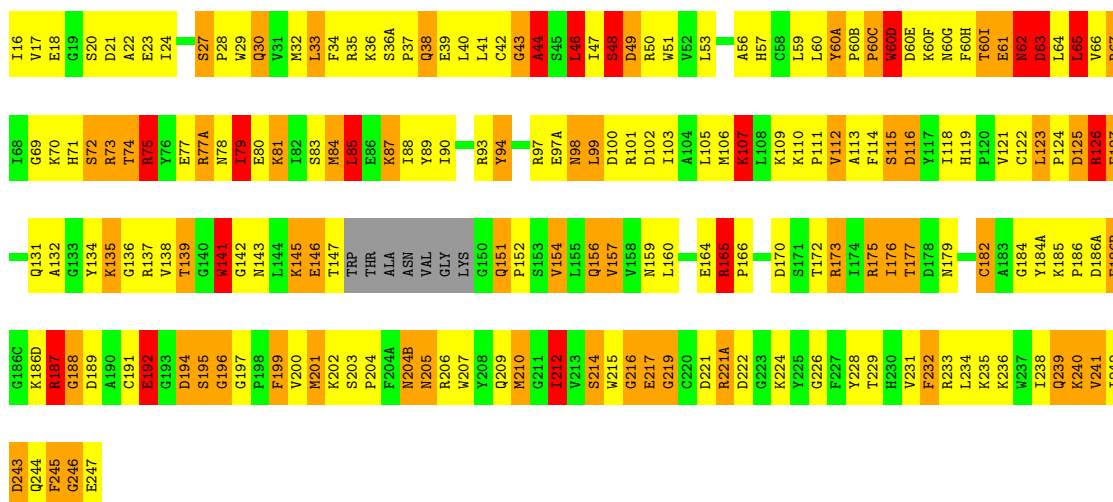
- Molecule 1: Thrombin light chain

Chain L: 



- Molecule 2: Thrombin heavy chain

Chain H: 



- Molecule 3: Hirudin variant-2

Chain I: 



- Molecule 4: Aeruginosin 298-A

Chain J: 



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	71.97Å 72.48Å 72.24Å 90.00° 100.93° 90.00°	Depositor
Resolution (Å)	7.00 – 2.10	Depositor
% Data completeness (in resolution range)	70.0 (7.00-2.10)	Depositor
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	PROLSQ, X-PLOR	Depositor
R, $R_{free}$	0.150 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2629	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	29.0	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: NA, TYS, 34H, OAR, PRJ

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	L	1.85	2/284 (0.7%)	2.66	18/377 (4.8%)
2	H	1.16	1/2091 (0.0%)	2.39	109/2823 (3.9%)
3	I	1.00	0/73	2.41	4/96 (4.2%)
4	J	0.53	0/7	3.36	1/8 (12.5%)
All	All	1.25	3/2455 (0.1%)	2.43	132/3304 (4.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	L	0	3
2	H	0	21
All	All	0	24

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L	14(L)	ASP	C-N	23.18	1.74	1.33
1	L	14(J)	TYR	C-N	-9.23	1.12	1.34
2	H	216	GLY	C-N	6.85	1.49	1.34

All (132) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	206	ARG	NE-CZ-NH1	18.54	129.57	120.30
2	H	126	ARG	NE-CZ-NH2	16.13	128.36	120.30
1	L	14(L)	ASP	O-C-N	-15.15	97.45	123.20
2	H	206	ARG	NE-CZ-NH2	-14.95	112.83	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	97	ARG	NE-CZ-NH2	13.61	127.11	120.30
2	H	101	ARG	NE-CZ-NH2	-12.67	113.97	120.30
1	L	1(A)	ASP	CB-CG-OD1	-12.53	107.02	118.30
2	H	243	ASP	CB-CG-OD1	12.27	129.34	118.30
2	H	194	ASP	CB-CG-OD1	-12.10	107.41	118.30
2	H	97	ARG	NE-CZ-NH1	-12.07	114.27	120.30
1	L	1(A)	ASP	CB-CG-OD2	11.53	128.67	118.30
1	L	4	ARG	NE-CZ-NH2	10.93	125.76	120.30
2	H	137	ARG	NE-CZ-NH1	-10.87	114.87	120.30
2	H	146	GLU	OE1-CD-OE2	10.86	136.33	123.30
2	H	173	ARG	NE-CZ-NH2	10.82	125.71	120.30
1	L	14(L)	ASP	CA-C-N	-10.62	94.96	116.20
2	H	194	ASP	CB-CG-OD2	10.14	127.42	118.30
2	H	233	ARG	CD-NE-CZ	10.13	137.78	123.60
1	L	14	ASP	CB-CG-OD1	-10.11	109.20	118.30
2	H	73	ARG	NE-CZ-NH2	10.06	125.33	120.30
2	H	221(A)	ARG	NE-CZ-NH1	-9.38	115.61	120.30
2	H	73	ARG	NH1-CZ-NH2	-8.95	109.56	119.40
2	H	73	ARG	NE-CZ-NH1	8.93	124.76	120.30
2	H	49	ASP	CB-CG-OD1	-8.86	110.33	118.30
2	H	137	ARG	NE-CZ-NH2	8.82	124.71	120.30
2	H	60(E)	ASP	CB-CG-OD1	-8.66	110.51	118.30
1	L	14	ASP	CB-CG-OD2	8.62	126.05	118.30
2	H	141	TRP	O-C-N	-8.18	109.30	123.20
2	H	165	ARG	CA-CB-CG	8.17	131.37	113.40
2	H	97	ARG	CD-NE-CZ	-7.98	112.43	123.60
4	J	2	LEU	CB-CA-C	7.92	125.24	110.20
1	L	4	ARG	NH1-CZ-NH2	-7.78	110.85	119.40
2	H	75	ARG	NE-CZ-NH2	7.71	124.15	120.30
1	L	14(D)	ARG	NE-CZ-NH2	7.54	124.07	120.30
2	H	137	ARG	O-C-N	7.43	134.59	122.70
2	H	176	ILE	CA-CB-CG2	7.40	125.69	110.90
2	H	49	ASP	CB-CG-OD2	7.35	124.92	118.30
1	L	10	LYS	O-C-N	7.34	134.44	122.70
2	H	200	VAL	CA-CB-CG1	7.33	121.90	110.90
2	H	123	LEU	CA-CB-CG	7.33	132.15	115.30
2	H	24	ILE	C-N-CA	7.30	137.64	122.30
2	H	125	ASP	CB-CG-OD2	7.17	124.76	118.30
2	H	132	ALA	O-C-N	7.08	135.24	123.20
2	H	186(B)	GLU	CG-CD-OE2	7.08	132.45	118.30
2	H	173	ARG	CD-NE-CZ	-6.94	113.89	123.60
2	H	94	TYR	CB-CG-CD2	-6.84	116.90	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	143	ASN	O-C-N	6.82	133.62	122.70
1	L	14(J)	TYR	CA-C-N	-6.81	102.22	117.20
1	L	13	GLU	CB-CA-C	-6.75	96.90	110.40
2	H	201	MET	CA-CB-CG	-6.71	101.89	113.30
2	H	186(B)	GLU	CG-CD-OE1	-6.60	105.09	118.30
2	H	38	GLN	O-C-N	6.56	133.19	122.70
2	H	33	LEU	N-CA-CB	-6.55	97.30	110.40
2	H	137	ARG	CA-C-O	-6.54	106.37	120.10
2	H	173	ARG	NE-CZ-NH1	-6.47	117.06	120.30
2	H	30	GLN	CA-CB-CG	6.46	127.62	113.40
2	H	60(A)	TYR	CA-CB-CG	-6.33	101.38	113.40
2	H	77(A)	ARG	CA-C-O	-6.32	106.82	120.10
3	I	362	GLU	CB-CG-CD	6.31	131.24	114.20
2	H	126	ARG	NH1-CZ-NH2	-6.28	112.49	119.40
2	H	199	PHE	O-C-N	-6.25	112.71	122.70
2	H	145	LYS	N-CA-CB	6.19	121.74	110.60
2	H	27	SER	N-CA-CB	-6.18	101.23	110.50
2	H	77(A)	ARG	NE-CZ-NH1	-6.14	117.23	120.30
2	H	63	ASP	O-C-N	6.13	132.51	122.70
2	H	210	MET	CG-SD-CE	-6.11	90.43	100.20
2	H	165	ARG	CD-NE-CZ	-6.09	115.07	123.60
2	H	60(E)	ASP	N-CA-CB	-6.09	99.65	110.60
2	H	210	MET	CA-CB-CG	-6.08	102.97	113.30
2	H	126	ARG	CG-CD-NE	6.05	124.50	111.80
2	H	142	GLY	CA-C-O	6.00	131.40	120.60
1	L	2	GLY	N-CA-C	5.95	127.98	113.10
2	H	138	VAL	CA-CB-CG1	5.85	119.67	110.90
2	H	175	ARG	C-N-CA	5.83	136.27	121.70
2	H	105	LEU	O-C-N	5.82	132.02	122.70
1	L	11	SER	CB-CA-C	5.82	121.15	110.10
2	H	233	ARG	NE-CZ-NH1	5.81	123.20	120.30
2	H	143	ASN	CA-C-O	-5.78	107.96	120.10
3	I	359	ILE	O-C-N	5.78	132.07	121.10
1	L	10	LYS	CD-CE-NZ	-5.76	98.45	111.70
3	I	362	GLU	CG-CD-OE1	5.73	129.76	118.30
2	H	62	ASN	CB-CG-OD1	-5.71	110.18	121.60
2	H	44	ALA	CB-CA-C	5.71	118.66	110.10
2	H	62	ASN	OD1-CG-ND2	5.69	134.98	121.90
2	H	60(D)	TRP	N-CA-C	-5.66	95.72	111.00
2	H	74	THR	CA-CB-OG1	-5.65	97.14	109.00
2	H	93	ARG	NE-CZ-NH1	5.64	123.12	120.30
2	H	165	ARG	NE-CZ-NH1	-5.59	117.50	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	135	LYS	C-N-CA	5.59	134.04	122.30
1	L	14(C)	GLU	CB-CA-C	-5.58	99.25	110.40
2	H	77(A)	ARG	CD-NE-CZ	-5.51	115.88	123.60
2	H	116	ASP	O-C-N	5.51	131.52	122.70
2	H	60(A)	TYR	CB-CG-CD1	-5.51	117.69	121.00
2	H	186	PRO	O-C-N	5.50	131.50	122.70
2	H	200	VAL	CG1-CB-CG2	-5.45	102.17	110.90
2	H	46	LEU	CA-CB-CG	5.45	127.83	115.30
2	H	173	ARG	N-CA-CB	5.44	120.39	110.60
2	H	187	ARG	NE-CZ-NH2	5.42	123.01	120.30
2	H	60(D)	TRP	N-CA-CB	5.41	120.34	110.60
2	H	170	ASP	CB-CG-OD2	5.40	123.16	118.30
2	H	243	ASP	CA-C-N	-5.37	105.39	117.20
2	H	156	GLN	CG-CD-OE1	-5.34	110.92	121.60
2	H	186(B)	GLU	O-C-N	-5.33	114.13	123.20
2	H	75	ARG	CA-CB-CG	-5.33	101.68	113.40
2	H	179	ASN	CB-CG-OD1	-5.32	110.96	121.60
2	H	246	GLY	N-CA-C	5.32	126.41	113.10
2	H	46	LEU	CB-CG-CD2	5.30	120.02	111.00
2	H	157	VAL	CA-CB-CG2	5.26	118.79	110.90
2	H	212	ILE	CA-CB-CG1	5.26	121.00	111.00
2	H	48	SER	CB-CA-C	5.23	120.04	110.10
2	H	85	LEU	CA-C-N	-5.22	105.72	117.20
2	H	113	ALA	O-C-N	5.22	131.05	122.70
2	H	67	ARG	CB-CG-CD	-5.21	98.05	111.60
2	H	77	GLU	CG-CD-OE2	5.19	128.68	118.30
2	H	154	VAL	N-CA-CB	-5.14	100.18	111.50
3	I	357	GLU	CG-CD-OE2	-5.14	108.02	118.30
2	H	154	VAL	CA-CB-CG1	5.11	118.57	110.90
2	H	139	THR	CA-C-N	-5.10	105.99	116.20
2	H	196	GLY	O-C-N	-5.05	114.61	123.20
2	H	232	PHE	O-C-N	-5.05	114.62	122.70
2	H	98	ASN	OD1-CG-ND2	5.05	133.52	121.90
2	H	123	LEU	CB-CG-CD2	-5.05	102.41	111.00
2	H	77(A)	ARG	NE-CZ-NH2	5.05	122.82	120.30
2	H	192	GLU	CB-CA-C	-5.04	100.31	110.40
2	H	116	ASP	CA-CB-CG	5.03	124.47	113.40
2	H	243	ASP	CA-CB-CG	5.03	124.46	113.40
2	H	177	THR	CA-CB-CG2	5.02	119.42	112.40
1	L	4	ARG	CG-CD-NE	5.02	122.33	111.80
1	L	1(A)	ASP	CA-CB-CG	-5.01	102.37	113.40
2	H	187	ARG	C-N-CA	-5.01	111.78	122.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	188	GLY	N-CA-C	-5.00	100.59	113.10
2	H	243	ASP	CA-C-O	5.00	130.61	120.10

There are no chirality outliers.

All (24) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	H	107	LYS	Mainchain
2	H	134	TYR	Mainchain
2	H	141	TRP	Mainchain
2	H	151	GLN	Mainchain
2	H	164	GLU	Mainchain
2	H	172	THR	Mainchain
2	H	192	GLU	Mainchain
2	H	196	GLY	Mainchain
2	H	197	GLY	Mainchain
2	H	212	ILE	Mainchain
2	H	29	TRP	Mainchain
2	H	43	GLY	Mainchain
2	H	44	ALA	Mainchain
2	H	47	ILE	Mainchain
2	H	60(C)	PRO	Mainchain
2	H	60(D)	TRP	Mainchain
2	H	65	LEU	Mainchain
2	H	72	SER	Mainchain
2	H	75	ARG	Sidechain
2	H	79	ILE	Mainchain
2	H	99	LEU	Mainchain
1	L	14(D)	ARG	Mainchain
1	L	3	LEU	Mainchain
1	L	5	PRO	Mainchain

## 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	L	281	0	265	78	2
2	H	2039	0	2010	251	2
3	I	89	0	67	20	1
4	J	43	0	45	24	0
5	H	1	0	0	0	0
6	H	138	0	0	13	1
6	I	6	0	0	1	0
6	J	6	0	0	1	0
6	L	26	0	0	0	0
All	All	2629	0	2387	326	3

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 67.

All (326) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:1(C):GLU:CG	1:L:1(B):ALA:H	1.21	1.46
1:L:14(L):ASP:C	1:L:14(M):GLY:N	1.74	1.37
2:H:201:MET:CE	2:H:210:MET:HG3	1.55	1.33
1:L:1(C):GLU:HG3	1:L:1(B):ALA:N	1.33	1.20
1:L:1(E):SER:HA	2:H:123:LEU:O	1.43	1.14
1:L:14(D):ARG:HD3	1:L:14(E):GLU:N	1.62	1.13
2:H:195:SER:CB	4:J:4:OAR:HC2	1.79	1.13
2:H:195:SER:HB2	4:J:4:OAR:C	1.80	1.10
2:H:50:ARG:HG3	2:H:247:GLU:CG	1.81	1.09
2:H:110:LYS:HG3	2:H:111:PRO:HD2	1.23	1.08
1:L:14(D):ARG:HH11	1:L:14(E):GLU:HB2	0.91	1.08
1:L:14(D):ARG:NH1	1:L:14(E):GLU:HB2	1.69	1.07
1:L:14(D):ARG:HD3	1:L:14(E):GLU:H	0.94	1.06
2:H:69:GLY:O	2:H:79:ILE:HD11	1.55	1.05
2:H:50:ARG:HG3	2:H:247:GLU:HG3	1.32	1.05
2:H:195:SER:HB2	4:J:4:OAR:HC2	1.33	1.03
1:L:14(D):ARG:CD	1:L:14(E):GLU:H	1.72	1.01
2:H:201:MET:HE3	2:H:210:MET:CG	1.91	1.01
2:H:17:VAL:O	2:H:188:GLY:HA2	1.61	1.01
2:H:201:MET:CE	2:H:210:MET:CG	2.38	1.00
1:L:1(H):THR:O	2:H:123:LEU:HD12	1.64	0.97
2:H:50:ARG:HG3	2:H:247:GLU:CD	1.86	0.96
2:H:21:ASP:HB3	2:H:154:VAL:CG1	1.97	0.95
2:H:50:ARG:HH21	2:H:107:LYS:CD	1.80	0.94
1:L:14(A):LYS:HG3	2:H:23:GLU:OE2	1.67	0.94
2:H:201:MET:HE3	2:H:210:MET:HG3	0.95	0.93
2:H:50:ARG:CG	2:H:247:GLU:HG3	1.98	0.93

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:14(A):LYS:HE2	2:H:23:GLU:OE2	1.70	0.92
1:L:1(C):GLU:HB3	1:L:1:CYS:HB3	1.53	0.91
2:H:75:ARG:HD3	3:I:357:GLU:OE1	1.70	0.90
2:H:50:ARG:HH21	2:H:107:LYS:CE	1.87	0.88
2:H:103:ILE:HG21	2:H:234:LEU:HD12	1.55	0.87
3:I:360:PRO:HG2	3:I:363:TYS:CD2	2.05	0.87
1:L:14(D):ARG:CD	1:L:14(E):GLU:N	2.34	0.86
2:H:110:LYS:HG3	2:H:111:PRO:CD	2.06	0.85
2:H:49:ASP:O	2:H:112:VAL:HG23	1.75	0.85
3:I:360:PRO:HG2	3:I:363:TYS:HD2	1.57	0.85
2:H:22:ALA:HB2	2:H:157:VAL:CG1	2.08	0.84
2:H:124:PRO:O	2:H:235:LYS:NZ	2.09	0.84
2:H:60(B):PRO:N	2:H:60(C):PRO:HD2	1.92	0.84
2:H:204(B):ASN:C	2:H:204(B):ASN:HD22	1.78	0.83
2:H:242:ILE:O	2:H:246:GLY:HA3	1.79	0.83
1:L:1(G):PHE:CD2	1:L:1(F):GLY:N	2.46	0.83
1:L:14(L):ASP:CA	1:L:14(M):GLY:N	2.41	0.83
2:H:165:ARG:HB2	2:H:166:PRO:HD3	1.61	0.83
1:L:14(D):ARG:HH11	1:L:14(E):GLU:CB	1.84	0.82
2:H:60(A):TYR:C	2:H:60(C):PRO:HD2	2.00	0.82
2:H:60(D):TRP:CZ2	4:J:3:PRJ:H13	2.15	0.82
1:L:1(C):GLU:CG	1:L:1(B):ALA:N	2.04	0.81
2:H:191:CYS:O	2:H:194:ASP:HB2	1.79	0.81
2:H:195:SER:OG	4:J:4:OAR:HC2	1.79	0.81
2:H:50:ARG:CB	2:H:247:GLU:HG3	2.11	0.80
2:H:60(B):PRO:N	2:H:60(C):PRO:CD	2.45	0.80
2:H:87:LYS:HE3	2:H:88:ILE:H	1.46	0.80
2:H:219:GLY:N	4:J:1:34H:O4	2.13	0.80
1:L:14(G):LEU:O	1:L:14(L):ASP:HA	1.81	0.79
2:H:49:ASP:HB3	2:H:114:PHE:CZ	2.17	0.79
2:H:35:ARG:O	2:H:38:GLN:HA	1.83	0.79
2:H:217:GLU:HB2	2:H:224:LYS:HD3	1.62	0.79
2:H:103:ILE:HG21	2:H:234:LEU:CD1	2.13	0.79
2:H:36:LYS:O	2:H:38:GLN:HG3	1.83	0.79
2:H:21:ASP:HB3	2:H:154:VAL:HG11	1.64	0.78
2:H:50:ARG:HH21	2:H:107:LYS:HE3	1.47	0.78
2:H:56:ALA:CB	2:H:90:ILE:HG23	2.14	0.78
2:H:60(I):THR:HG23	2:H:63:ASP:CG	2.05	0.77
2:H:107:LYS:NZ	2:H:107:LYS:HB2	1.99	0.77
2:H:67:ARG:HD3	2:H:70:LYS:HD2	1.67	0.77
2:H:78:ASN:N	6:H:453:HOH:O	1.95	0.76
2:H:22:ALA:HB2	2:H:157:VAL:HG11	1.67	0.75

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:H:217:GLU:HG3	2:H:224:LYS:HD3	1.69	0.75
2:H:240:LYS:O	2:H:244:GLN:HB2	1.86	0.74
2:H:67:ARG:CD	2:H:70:LYS:HD2	2.17	0.74
2:H:201:MET:HE1	2:H:210:MET:HG3	1.68	0.74
1:L:14(D):ARG:O	1:L:14(H):GLU:HG3	1.88	0.74
1:L:1(E):SER:CA	2:H:123:LEU:O	2.30	0.73
2:H:65:LEU:HD11	2:H:84:MET:CE	2.18	0.73
2:H:217:GLU:OE1	4:J:2:LEU:HD21	1.88	0.73
1:L:1(A):ASP:OD2	1:L:9:LYS:HE3	1.88	0.73
2:H:203:SER:HB3	2:H:204(B):ASN:HD21	1.54	0.73
2:H:32:MET:HG3	2:H:40:LEU:HD13	1.71	0.73
2:H:156:GLN:C	2:H:157:VAL:HG13	2.08	0.73
4:J:4:OAR:HG3	6:J:462:HOH:O	1.87	0.73
2:H:89:TYR:CE2	2:H:245:PHE:CE1	2.77	0.73
2:H:69:GLY:O	2:H:79:ILE:CD1	2.36	0.72
2:H:37:PRO:O	2:H:39:GLU:HG2	1.90	0.71
1:L:14(I):SER:C	1:L:14(K):ILE:N	2.44	0.71
2:H:184(A):TYR:O	6:H:503:HOH:O	2.09	0.71
1:L:1(D):GLY:CA	6:H:529:HOH:O	2.39	0.71
2:H:165:ARG:N	2:H:166:PRO:HD2	2.05	0.70
1:L:1(D):GLY:HA3	6:H:529:HOH:O	1.91	0.70
2:H:32:MET:HG3	2:H:40:LEU:CD1	2.22	0.70
2:H:217:GLU:HG3	2:H:224:LYS:CE	2.22	0.70
1:L:1(G):PHE:CD1	1:L:1(G):PHE:N	2.59	0.70
1:L:8:GLU:OE2	2:H:202:LYS:HE3	1.90	0.70
2:H:50:ARG:HB2	2:H:247:GLU:HG3	1.73	0.69
2:H:217:GLU:CG	2:H:224:LYS:HD3	2.22	0.69
2:H:74:THR:O	6:H:615:HOH:O	2.10	0.69
2:H:217:GLU:HG3	2:H:224:LYS:HE3	1.73	0.69
1:L:1(C):GLU:HG3	1:L:1(B):ALA:H	0.53	0.69
1:L:14(D):ARG:CG	1:L:14(E):GLU:N	2.55	0.69
2:H:60(D):TRP:CH2	4:J:3:PRJ:H13	2.26	0.69
2:H:61:GLU:OE1	2:H:87:LYS:HA	1.93	0.69
3:I:360:PRO:HG2	3:I:363:TYS:CE2	2.23	0.69
2:H:107:LYS:O	2:H:107:LYS:HG3	1.94	0.68
1:L:14(D):ARG:NH1	1:L:14(E):GLU:CB	2.51	0.68
2:H:221(A):ARG:HH22	4:J:1:34H:H5	1.58	0.68
2:H:221(A):ARG:NH2	4:J:1:34H:H5	2.07	0.68
2:H:98:ASN:ND2	2:H:175:ARG:O	2.18	0.68
1:L:1(H):THR:O	2:H:123:LEU:CD1	2.40	0.68
2:H:50:ARG:NH2	2:H:107:LYS:CD	2.54	0.68
3:I:355:ASP:HB3	6:I:553:HOH:O	1.92	0.68

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:1(H):THR:HB	1:L:1(G):PHE:CD1	2.29	0.67
2:H:85:LEU:HD13	2:H:106:MET:HE2	1.77	0.67
1:L:14(L):ASP:O	1:L:14(M):GLY:N	2.27	0.67
2:H:156:GLN:C	2:H:157:VAL:CG1	2.64	0.66
2:H:217:GLU:CB	2:H:224:LYS:HD3	2.25	0.66
2:H:79:ILE:HD11	6:H:500:HOH:O	1.94	0.66
2:H:60(I):THR:HG23	2:H:63:ASP:OD1	1.95	0.66
2:H:60(A):TYR:CE2	4:J:3:PRJ:H12	2.31	0.66
2:H:147:THR:HG22	6:H:521:HOH:O	1.96	0.65
2:H:204(B):ASN:C	2:H:204(B):ASN:ND2	2.48	0.65
3:I:357:GLU:HG2	3:I:358:GLU:N	2.10	0.65
4:J:2:LEU:HD23	4:J:2:LEU:N	2.12	0.65
1:L:1(G):PHE:O	1:L:1(F):GLY:C	2.35	0.65
1:L:14(B):THR:O	1:L:14(D):ARG:HD3	1.97	0.65
2:H:182:CYS:HA	2:H:226:GLY:O	1.96	0.65
2:H:56:ALA:HB1	2:H:90:ILE:HG23	1.77	0.65
2:H:56:ALA:HB2	2:H:90:ILE:HG23	1.78	0.65
1:L:14(J):TYR:C	1:L:14(K):ILE:HG13	2.15	0.64
2:H:203:SER:HB3	2:H:204(B):ASN:ND2	2.12	0.64
1:L:4:ARG:NH2	1:L:14(C):GLU:OE2	2.31	0.64
2:H:59:LEU:HD22	2:H:88:ILE:HD13	1.80	0.64
2:H:49:ASP:N	2:H:49:ASP:OD1	2.27	0.64
2:H:201:MET:HE1	2:H:210:MET:CG	2.25	0.64
2:H:50:ARG:NH2	2:H:107:LYS:HE3	2.12	0.63
2:H:165:ARG:NH2	2:H:177:THR:O	2.32	0.63
2:H:50:ARG:NH2	2:H:107:LYS:HD2	2.14	0.63
1:L:14(G):LEU:O	1:L:14(L):ASP:CA	2.46	0.62
2:H:79:ILE:CD1	6:H:500:HOH:O	2.47	0.62
2:H:217:GLU:HG3	2:H:224:LYS:CD	2.28	0.62
1:L:1(D):GLY:N	2:H:123:LEU:H	1.97	0.62
1:L:1(G):PHE:HD2	1:L:1(F):GLY:N	1.97	0.61
1:L:3:LEU:O	2:H:119:HIS:CD2	2.54	0.61
2:H:30:GLN:OE1	2:H:139:THR:OG1	2.18	0.61
1:L:14(F):LEU:HD12	1:L:14(F):LEU:N	2.15	0.61
2:H:216:GLY:O	4:J:2:LEU:N	2.35	0.60
3:I:361:GLU:C	3:I:363:TYS:N	2.52	0.60
2:H:125:ASP:O	2:H:127:GLU:N	2.35	0.60
2:H:81:LYS:HE3	6:H:468:HOH:O	2.00	0.60
2:H:49:ASP:O	2:H:112:VAL:CG2	2.48	0.60
2:H:201:MET:CE	2:H:210:MET:CB	2.80	0.60
3:I:360:PRO:O	3:I:363:TYS:N	2.35	0.60
2:H:125:ASP:O	2:H:126:ARG:C	2.40	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:H:115:SER:OG	2:H:116:ASP:N	2.30	0.60
2:H:165:ARG:HB2	2:H:166:PRO:CD	2.32	0.60
2:H:65:LEU:HD11	2:H:84:MET:HE1	1.84	0.60
2:H:22:ALA:CB	2:H:157:VAL:HG11	2.32	0.58
4:J:2:LEU:CD2	4:J:2:LEU:N	2.65	0.58
2:H:107:LYS:HB2	2:H:107:LYS:HZ2	1.66	0.58
2:H:217:GLU:O	2:H:219:GLY:O	2.21	0.58
1:L:1(C):GLU:HG3	1:L:1(B):ALA:CA	2.26	0.58
2:H:195:SER:CB	4:J:4:OAR:C	2.54	0.58
2:H:60(F):LYS:HD3	2:H:60(H):PHE:CE2	2.38	0.58
2:H:242:ILE:O	2:H:246:GLY:CA	2.49	0.58
2:H:102:ASP:OD2	2:H:214:SER:OG	2.23	0.57
1:L:1(G):PHE:H	1:L:1(G):PHE:HD1	1.46	0.57
2:H:165:ARG:N	2:H:166:PRO:CD	2.68	0.57
1:L:14(F):LEU:CD1	1:L:14(F):LEU:N	2.67	0.57
2:H:217:GLU:HB2	2:H:224:LYS:CD	2.34	0.56
2:H:165:ARG:CB	2:H:166:PRO:HD3	2.31	0.56
2:H:241:VAL:HB	2:H:245:PHE:CE1	2.41	0.56
1:L:14(A):LYS:CE	2:H:23:GLU:OE2	2.51	0.56
2:H:60:LEU:HD13	2:H:60(G):ASN:OD1	2.05	0.56
2:H:85:LEU:HD13	2:H:106:MET:CE	2.36	0.55
2:H:146:GLU:HG2	2:H:146:GLU:O	2.05	0.55
1:L:1(E):SER:H	2:H:235:LYS:HZ1	1.53	0.55
2:H:94:TYR:HE1	2:H:99:LEU:HD22	1.72	0.55
1:L:1(C):GLU:HG2	1:L:1(A):ASP:H	1.71	0.55
2:H:201:MET:HB2	2:H:210:MET:HE2	1.88	0.55
2:H:165:ARG:CB	2:H:166:PRO:CD	2.85	0.54
2:H:51:TRP:CZ3	2:H:107:LYS:HB3	2.43	0.54
2:H:67:ARG:HD2	2:H:70:LYS:CD	2.37	0.54
2:H:67:ARG:HH11	2:H:70:LYS:HD2	1.71	0.54
2:H:110:LYS:CG	2:H:111:PRO:HD2	2.17	0.54
1:L:14(F):LEU:H	1:L:14(F):LEU:CD1	2.21	0.54
2:H:135:LYS:HA	2:H:160:LEU:O	2.08	0.54
2:H:46:LEU:HD22	2:H:48:SER:O	2.07	0.54
3:I:360:PRO:CG	3:I:363:TYS:HD2	2.36	0.53
2:H:81:LYS:HD3	2:H:118:ILE:CD1	2.38	0.53
1:L:14(B):THR:O	1:L:14(D):ARG:CD	2.57	0.53
1:L:1(D):GLY:HA3	2:H:122:CYS:HA	1.91	0.53
2:H:103:ILE:CG2	2:H:234:LEU:HD12	2.32	0.53
2:H:38:GLN:NE2	3:I:359:ILE:HG23	2.23	0.53
2:H:242:ILE:O	2:H:246:GLY:N	2.41	0.53
2:H:65:LEU:HD11	2:H:84:MET:HE2	1.87	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:H:49:ASP:OD2	2:H:111:PRO:HB3	2.09	0.53
1:L:1(C):GLU:HG3	1:L:1(B):ALA:CB	2.39	0.53
1:L:1(E):SER:H	2:H:235:LYS:NZ	2.08	0.52
1:L:1(C):GLU:N	6:H:529:HOH:O	2.38	0.52
1:L:14(A):LYS:CG	2:H:23:GLU:OE2	2.51	0.52
2:H:146:GLU:CG	2:H:146:GLU:O	2.58	0.52
1:L:14(B):THR:O	1:L:14(E):GLU:N	2.40	0.52
1:L:4:ARG:HG2	2:H:28:PRO:CG	2.40	0.52
2:H:136:GLY:HA3	2:H:199:PHE:CZ	2.45	0.52
2:H:202:LYS:HE2	2:H:205:ASN:O	2.10	0.52
2:H:67:ARG:HD2	2:H:70:LYS:HD2	1.92	0.52
2:H:195:SER:HG	4:J:4:OAR:HC2	1.76	0.51
1:L:14(A):LYS:HE2	2:H:23:GLU:CG	2.40	0.51
2:H:204(B):ASN:N	2:H:204(B):ASN:ND2	2.54	0.51
2:H:42:CYS:HB3	2:H:195:SER:O	2.10	0.51
2:H:210:MET:O	2:H:231:VAL:HB	2.11	0.51
2:H:51:TRP:CH2	2:H:107:LYS:HB3	2.44	0.51
2:H:21:ASP:HB3	2:H:154:VAL:HG12	1.85	0.51
2:H:204(B):ASN:ND2	2:H:204(B):ASN:H	2.08	0.51
2:H:241:VAL:HA	2:H:244:GLN:HB2	1.93	0.51
2:H:43:GLY:O	2:H:44:ALA:HB2	2.10	0.51
3:I:360:PRO:O	3:I:363:TYS:HB3	2.10	0.51
3:I:357:GLU:CG	3:I:358:GLU:N	2.74	0.51
1:L:1(D):GLY:CA	2:H:123:LEU:H	2.25	0.50
2:H:202:LYS:HD2	2:H:207:TRP:CE2	2.46	0.50
2:H:73:ARG:CZ	2:H:151:GLN:HB3	2.42	0.50
1:L:14(M):GLY:O	1:L:15:ARG:OXT	2.30	0.49
2:H:71:HIS:CD2	2:H:154:VAL:HG22	2.47	0.49
1:L:14(F):LEU:HD11	2:H:159:ASN:CG	2.33	0.49
2:H:139:THR:HG22	2:H:157:VAL:HG12	1.94	0.49
2:H:75:ARG:CD	3:I:357:GLU:OE1	2.50	0.49
2:H:184:GLY:O	6:H:464:HOH:O	2.20	0.49
1:L:1(C):GLU:HG2	1:L:1(A):ASP:N	2.27	0.49
2:H:176:ILE:HD11	2:H:215:TRP:CH2	2.48	0.49
3:I:363:TYS:O1	3:I:363:TYS:HE2	2.13	0.48
3:I:360:PRO:HG2	3:I:363:TYS:HE2	1.96	0.48
2:H:60(I):THR:O	2:H:63:ASP:HB2	2.14	0.48
2:H:87:LYS:HB3	2:H:89:TYR:CE1	2.48	0.48
4:J:2:LEU:CB	4:J:3:PRJ:HD2	2.43	0.48
2:H:22:ALA:HB2	2:H:157:VAL:HG13	1.93	0.48
2:H:126:ARG:HA	2:H:232:PHE:CZ	2.49	0.48
1:L:14(D):ARG:NH1	1:L:14(E):GLU:CG	2.77	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:H:60(B):PRO:CD	2:H:60(C):PRO:CD	2.92	0.48
1:L:14(D):ARG:HG2	1:L:14(E):GLU:N	2.26	0.47
2:H:65:LEU:CD1	2:H:84:MET:HE2	2.44	0.47
2:H:21:ASP:CB	2:H:154:VAL:CG1	2.83	0.47
2:H:189:ASP:OD1	4:J:4:OAR:NH1	2.45	0.47
2:H:235:LYS:O	2:H:239:GLN:N	2.44	0.47
2:H:56:ALA:HB1	2:H:90:ILE:CG2	2.43	0.47
2:H:195:SER:HB2	4:J:4:OAR:HC1	1.85	0.47
2:H:36:LYS:HG3	2:H:65:LEU:HD22	1.96	0.47
2:H:85:LEU:HD22	2:H:106:MET:HB3	1.96	0.47
2:H:81:LYS:NZ	2:H:118:ILE:HD12	2.29	0.47
2:H:60(G):ASN:ND2	6:H:550:HOH:O	2.48	0.47
2:H:21:ASP:CB	2:H:154:VAL:HG11	2.42	0.46
2:H:74:THR:HB	3:I:356:PHE:HA	1.96	0.46
1:L:14(B):THR:HB	1:L:14(D):ARG:NH1	2.30	0.46
2:H:204(B):ASN:HD22	2:H:205:ASN:N	2.12	0.46
1:L:14:ASP:C	1:L:14:ASP:OD1	2.53	0.46
2:H:131:GLN:HB3	2:H:131:GLN:HE21	1.49	0.46
1:L:1(A):ASP:OD2	1:L:9:LYS:CE	2.61	0.46
2:H:89:TYR:CZ	2:H:245:PHE:CE1	3.04	0.46
2:H:70:LYS:NZ	2:H:80:GLU:OE1	2.45	0.46
2:H:41:LEU:HD13	2:H:60(H):PHE:CE2	2.51	0.46
2:H:73:ARG:NE	2:H:152:PRO:O	2.32	0.46
2:H:60(B):PRO:CD	2:H:60(C):PRO:HD2	2.46	0.45
2:H:34:PHE:HE2	2:H:38:GLN:HG2	1.81	0.45
2:H:77(A):ARG:HG3	2:H:77(A):ARG:O	2.17	0.45
2:H:103:ILE:HD12	2:H:212:ILE:HD12	1.97	0.45
1:L:1(A):ASP:O	2:H:119:HIS:NE2	2.42	0.45
2:H:49:ASP:HB2	2:H:112:VAL:O	2.16	0.45
4:J:1:34H:C8	4:J:2:LEU:CD2	2.95	0.45
2:H:216:GLY:O	4:J:2:LEU:CA	2.65	0.45
2:H:204(B):ASN:N	2:H:204(B):ASN:HD22	2.03	0.45
2:H:38:GLN:NE2	3:I:359:ILE:CG2	2.80	0.45
2:H:32:MET:HB2	2:H:141:TRP:CZ3	2.51	0.45
1:L:14(K):ILE:O	1:L:14(L):ASP:HB2	2.16	0.44
3:I:363:TYS:CE2	3:I:363:TYS:O1	2.65	0.44
2:H:17:VAL:O	2:H:18:GLU:HB2	2.17	0.44
1:L:14(A):LYS:HE2	2:H:23:GLU:HG3	2.00	0.44
4:J:2:LEU:HB3	4:J:3:PRJ:HD2	2.00	0.44
3:I:358:GLU:CD	3:I:358:GLU:H	2.20	0.44
1:L:14(C):GLU:O	1:L:14(D):ARG:C	2.56	0.44
2:H:57:HIS:CE1	2:H:195:SER:OG	2.71	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:H:64:LEU:O	6:H:460:HOH:O	2.21	0.44
2:H:70:LYS:HE3	2:H:70:LYS:HB3	1.44	0.44
2:H:89:TYR:CE2	2:H:245:PHE:CZ	3.06	0.43
2:H:125:ASP:OD1	2:H:127:GLU:HG2	2.18	0.43
2:H:103:ILE:CG2	2:H:234:LEU:CD1	2.92	0.43
2:H:61:GLU:HG2	2:H:61:GLU:H	1.26	0.43
2:H:173:ARG:HH11	2:H:173:ARG:HD2	1.52	0.43
1:L:14(M):GLY:C	1:L:15:ARG:OXT	2.56	0.43
2:H:165:ARG:HD2	2:H:165:ARG:HH11	1.50	0.43
2:H:32:MET:CG	2:H:40:LEU:HD13	2.47	0.43
2:H:16:ILE:N	2:H:194:ASP:OD2	2.52	0.42
1:L:14(A):LYS:HE2	2:H:23:GLU:CD	2.37	0.42
2:H:212:ILE:O	2:H:228:TYR:HB3	2.18	0.42
2:H:61:GLU:OE1	2:H:88:ILE:N	2.53	0.42
2:H:62:ASN:HD22	2:H:62:ASN:C	2.23	0.42
2:H:77(A):ARG:O	2:H:77(A):ARG:CG	2.67	0.42
2:H:103:ILE:HD11	2:H:238:ILE:HD11	2.00	0.42
2:H:38:GLN:OE1	3:I:364:LEU:HD11	2.20	0.42
2:H:191:CYS:O	2:H:192:GLU:C	2.57	0.42
2:H:100:ASP:CG	2:H:177:THR:HG21	2.40	0.42
1:L:14(J):TYR:HD2	2:H:204:PRO:HG3	1.85	0.41
2:H:65:LEU:CD1	2:H:84:MET:CE	2.92	0.41
2:H:67:ARG:HD2	2:H:70:LYS:HD3	2.00	0.41
2:H:61:GLU:OE1	2:H:87:LYS:CA	2.64	0.41
2:H:70:LYS:CE	2:H:72:SER:O	2.68	0.41
2:H:77(A):ARG:HH11	2:H:77(A):ARG:HD2	1.50	0.41
2:H:187:ARG:HD3	2:H:221:ASP:OD2	2.21	0.41
2:H:60:LEU:HA	2:H:60(F):LYS:O	2.20	0.41
2:H:73:ARG:NE	2:H:151:GLN:HB3	2.35	0.41
2:H:97(A):GLU:OE1	2:H:175:ARG:NH2	2.52	0.41
2:H:121:VAL:HG11	2:H:209:GLN:HB2	2.02	0.41
2:H:185:LYS:O	2:H:186(B):GLU:N	2.53	0.41
1:L:1(G):PHE:C	1:L:1(G):PHE:CD2	2.94	0.41
2:H:98:ASN:N	2:H:98:ASN:OD1	2.47	0.41
1:L:1(D):GLY:H	2:H:123:LEU:H	1.66	0.41
1:L:1(H):THR:HB	1:L:1(G):PHE:CE1	2.55	0.41
2:H:49:ASP:HB3	2:H:114:PHE:HZ	1.81	0.41
2:H:53:LEU:HD11	2:H:103:ILE:HG13	2.02	0.41
2:H:60(A):TYR:CZ	2:H:60(C):PRO:HG2	2.56	0.41
2:H:195:SER:OG	4:J:4:OAR:C	2.60	0.41
2:H:50:ARG:HD3	2:H:111:PRO:HD3	2.03	0.41
2:H:56:ALA:CB	2:H:90:ILE:CG2	2.93	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:14(J):TYR:N	1:L:14(J):TYR:CD1	2.87	0.40
2:H:35:ARG:HB3	2:H:39:GLU:HG3	2.04	0.40
2:H:85:LEU:CD1	2:H:106:MET:CE	2.99	0.40
2:H:85:LEU:CD1	2:H:106:MET:HE1	2.52	0.40
2:H:21:ASP:CB	2:H:154:VAL:HG12	2.51	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:14(L):ASP:C	2:H:173:ARG:NH2[4.556]	1.86	0.34
1:L:14(L):ASP:O	2:H:173:ARG:NH2[4.556]	2.09	0.11
3:I:358:GLU:OE1	6:H:574:HOH:O[2.555]	2.18	0.02

## 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	L	34/36 (94%)	19 (56%)	10 (29%)	5 (15%)	0	0
2	H	248/259 (96%)	223 (90%)	21 (8%)	4 (2%)	14	7
3	I	7/12 (58%)	7 (100%)	0	0	100	100
All	All	289/307 (94%)	249 (86%)	31 (11%)	9 (3%)	7	2

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	L	1(G)	PHE
1	L	1(F)	GLY
1	L	1(D)	GLY
2	H	219	GLY
1	L	1(E)	SER
1	L	1(C)	GLU
2	H	192	GLU
2	H	126	ARG

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Mol	Chain	Res	Type
2	H	44	ALA

### 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	L	30/31 (97%)	25 (83%)	5 (17%)	3	1
2	H	220/225 (98%)	177 (80%)	43 (20%)	2	1
3	I	8/10 (80%)	6 (75%)	2 (25%)	1	0
4	J	1/1 (100%)	0	1 (100%)	0	0
All	All	259/267 (97%)	208 (80%)	51 (20%)	2	1

All (51) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	1(H)	THR
1	L	1(C)	GLU
1	L	14(A)	LYS
1	L	14(D)	ARG
1	L	14(K)	ILE
2	H	20	SER
2	H	27	SER
2	H	33	LEU
2	H	36(A)	SER
2	H	46	LEU
2	H	48	SER
2	H	60(I)	THR
2	H	61	GLU
2	H	62	ASN
2	H	63	ASP
2	H	65	LEU
2	H	66	VAL
2	H	79	ILE
2	H	81	LYS
2	H	83	SER
2	H	84	MET

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Mol	Chain	Res	Type
2	H	85	LEU
2	H	87	LYS
2	H	107	LYS
2	H	109	LYS
2	H	112	VAL
2	H	115	SER
2	H	127	GLU
2	H	145	LYS
2	H	165	ARG
2	H	182	CYS
2	H	186(A)	ASP
2	H	186(D)	LYS
2	H	187	ARG
2	H	192	GLU
2	H	195	SER
2	H	204(B)	ASN
2	H	205	ASN
2	H	214	SER
2	H	217	GLU
2	H	222	ASP
2	H	229	THR
2	H	236	LYS
2	H	239	GLN
2	H	240	LYS
2	H	241	VAL
2	H	243	ASP
2	H	245	PHE
3	I	358	GLU
3	I	359	ILE
4	J	2	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
2	H	62	ASN
2	H	131	GLN
2	H	156	GLN
2	H	204(B)	ASN
2	H	205	ASN
2	H	244	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

3 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
3	TYS	I	363	3	16,16,17	5.48	4 (25%)	20,22,24	2.40	6 (30%)
4	PRJ	J	3	4	13,13,14	5.41	6 (46%)	16,18,20	3.67	8 (50%)
4	OAR	J	4	4	10,10,10	1.31	1 (10%)	11,11,11	2.70	4 (36%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	TYS	I	363	3	-	0/9/11/13	0/1/1/1
4	PRJ	J	3	4	-	0/0/23/25	0/0/2/2
4	OAR	J	4	4	-	0/9/9/9	0/0/0/0

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	I	363	TYS	O-C	21.02	1.25	1.11
4	J	3	PRJ	O-C	17.82	1.23	1.11
4	J	3	PRJ	C14-CD	5.33	1.62	1.53
3	I	363	TYS	OH-CZ	-4.26	1.37	1.42
4	J	3	PRJ	C14-C13	3.25	1.58	1.51
3	I	363	TYS	OH-S	2.96	1.69	1.63
3	I	363	TYS	CA-C	2.73	1.53	1.48
4	J	3	PRJ	CD-N	-2.69	1.43	1.48
4	J	3	PRJ	C11-C12	2.51	1.59	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	J	3	PRJ	CG-CD	2.26	1.56	1.53
4	J	4	OAR	CA-N1	-2.07	1.41	1.47

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	J	3	PRJ	C-CA-N	9.05	124.16	111.32
4	J	3	PRJ	CB-CG-CD	-6.77	94.27	100.42
3	I	363	TYS	C-CA-N	6.69	120.51	113.83
4	J	4	OAR	CB-CA-C	-6.11	104.06	112.49
4	J	3	PRJ	C11-CG-CD	6.05	121.57	113.39
3	I	363	TYS	OH-S-O2	-5.71	91.14	107.64
4	J	4	OAR	CG-CB-CA	-4.05	95.62	116.13
4	J	3	PRJ	CG-CD-N	3.32	108.37	102.58
4	J	3	PRJ	C14-C13-C12	3.24	114.67	110.54
4	J	4	OAR	CB-CG-CD	-3.21	103.72	111.94
4	J	3	PRJ	C14-CD-CG	-3.10	106.03	113.01
3	I	363	TYS	O2-S-O1	2.75	124.16	112.89
3	I	363	TYS	OH-CZ-CE2	-2.73	114.17	118.70
4	J	4	OAR	CB-CA-N1	2.50	115.31	108.68
4	J	3	PRJ	C11-C12-C13	-2.37	107.14	111.55
3	I	363	TYS	OH-CZ-CE1	2.28	122.49	118.70
4	J	3	PRJ	C14-CD-N	-2.12	108.33	118.38
3	I	363	TYS	CD1-CE1-CZ	-2.03	117.03	119.76

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.



There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 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 ⓘ

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.