



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 20, 2020 – 09:40 PM BST

PDB ID : 5IMH
Title : D31P mutant of C69-family cysteine dipeptidase from *Lactobacillus farciminis*
Authors : Kono, R.; Watanabe, K.
Deposited on : 2016-03-06
Resolution : 2.47 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

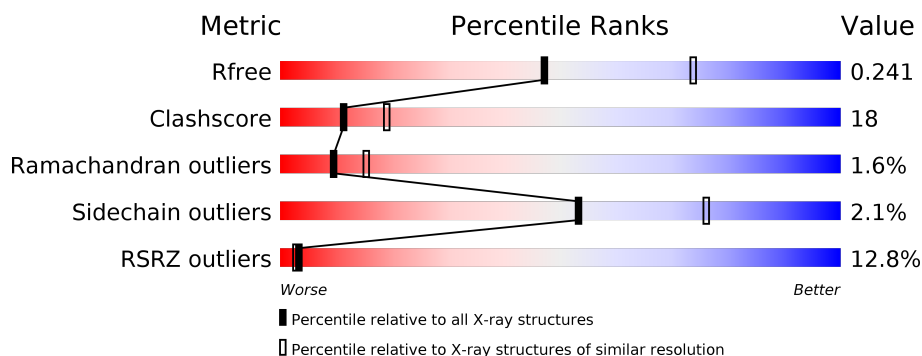
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.47 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5857 (2.50-2.46)
Clashscore	141614	6594 (2.50-2.46)
Ramachandran outliers	138981	6469 (2.50-2.46)
Sidechain outliers	138945	6471 (2.50-2.46)
RSRZ outliers	127900	5738 (2.50-2.46)

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 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	469	<div> <div>11%</div> <div> <div></div> <div>73%</div> <div>22%</div> <div>• •</div> </div> </div>
1	B	469	<div> <div>14%</div> <div> <div></div> <div>73%</div> <div>23%</div> <div>• •</div> </div> </div>
1	C	469	<div> <div>13%</div> <div> <div></div> <div>73%</div> <div>23%</div> <div>• •</div> </div> </div>
1	D	469	<div> <div>13%</div> <div> <div></div> <div>75%</div> <div>21%</div> <div>•</div> </div> </div>
1	E	469	<div> <div>13%</div> <div> <div></div> <div>74%</div> <div>19%</div> <div>5% •</div> </div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 19121 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 Dipeptidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	467	Total	C	N	O	S	0	0	0
			3706	2323	631	740	12			
1	B	467	Total	C	N	O	S	0	0	0
			3706	2323	631	740	12			
1	C	467	Total	C	N	O	S	0	0	0
			3706	2323	631	740	12			
1	D	467	Total	C	N	O	S	0	0	0
			3706	2323	631	740	12			
1	E	467	Total	C	N	O	S	0	0	0
			3706	2323	631	740	12			

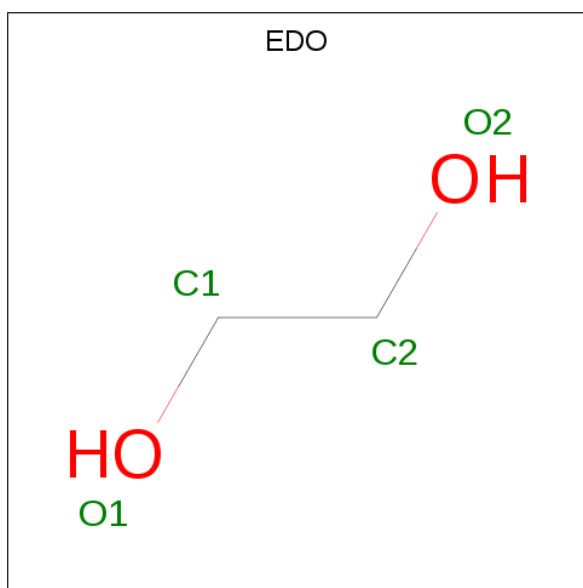
There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	31	PRO	ASP	engineered mutation	UNP A0A0R1IQH8
B	31	PRO	ASP	engineered mutation	UNP A0A0R1IQH8
C	31	PRO	ASP	engineered mutation	UNP A0A0R1IQH8
D	31	PRO	ASP	engineered mutation	UNP A0A0R1IQH8
E	31	PRO	ASP	engineered mutation	UNP A0A0R1IQH8

- Molecule 2 is COBALT (II) ION (three-letter code: CO) (formula: Co).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Co	0	0
			1	1		
2	A	2	Total	Co	0	0
			2	2		
2	D	1	Total	Co	0	0
			1	1		
2	C	2	Total	Co	0	0
			2	2		
2	E	1	Total	Co	0	0
			1	1		

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



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

- Molecule 4 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



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

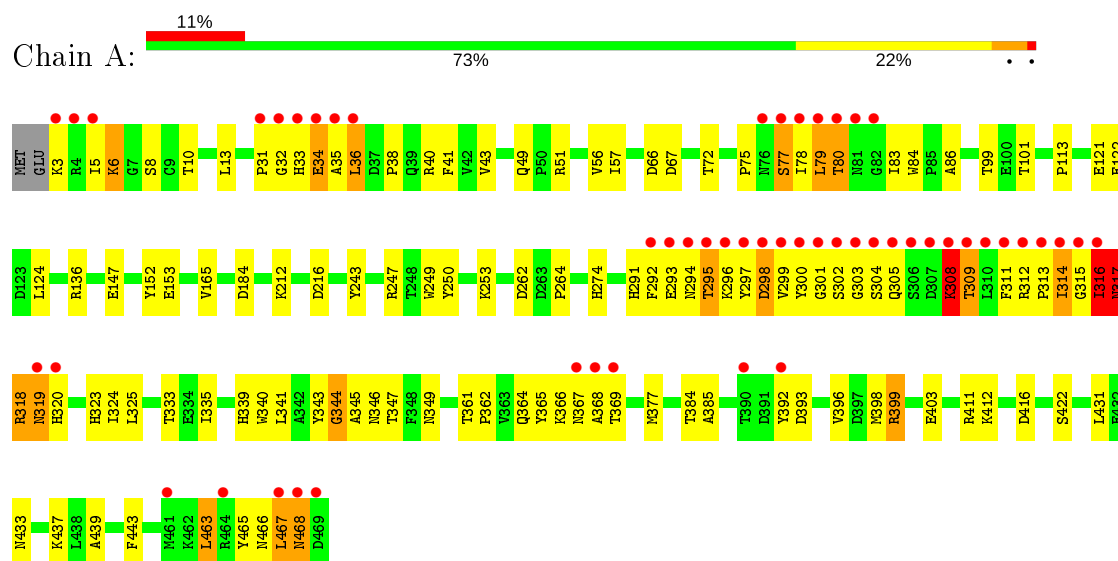
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	159	Total	O	0	0
			159	159		
5	B	114	Total	O	0	0
			114	114		
5	C	107	Total	O	0	0
			107	107		
5	D	97	Total	O	0	0
			97	97		
5	E	83	Total	O	0	0
			83	83		

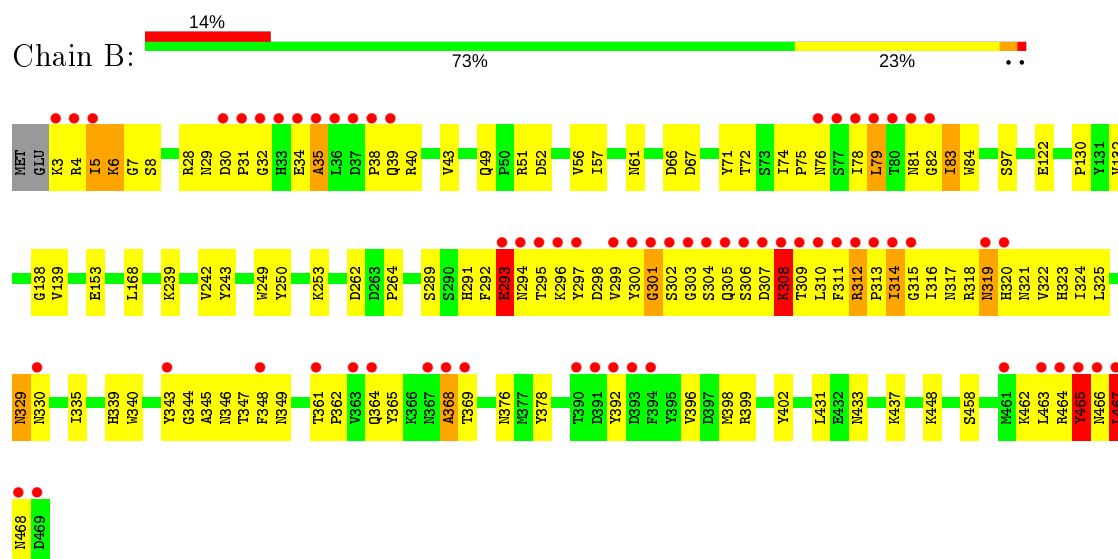
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

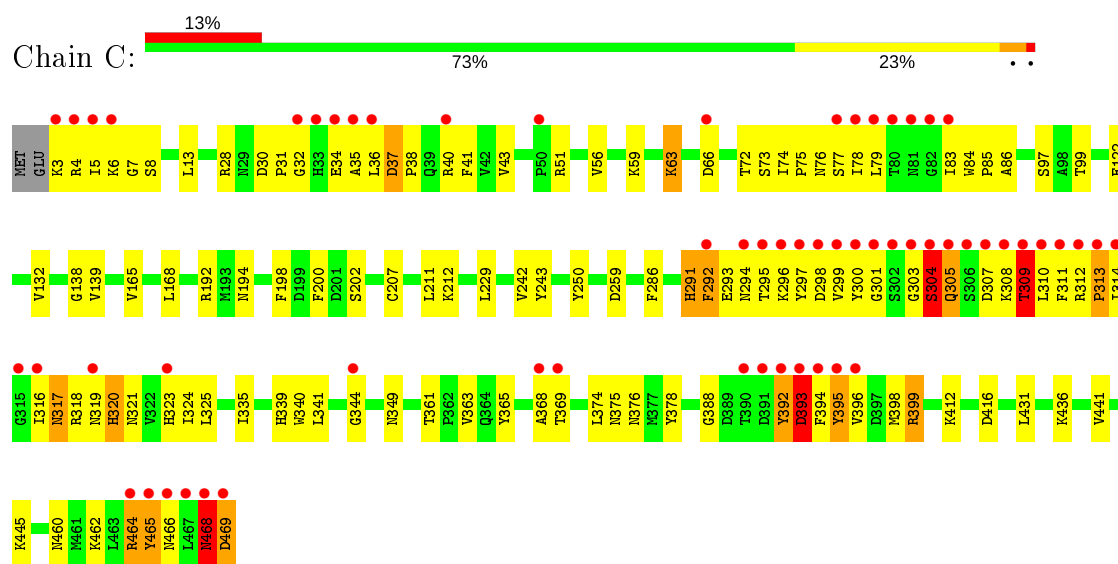
• Molecule 1: Dipeptidase



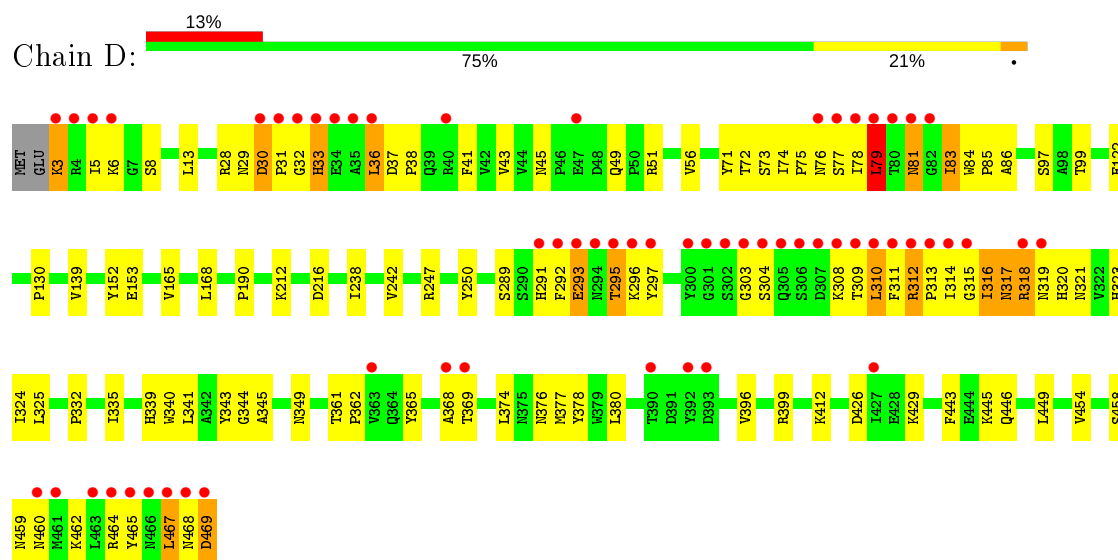
• Molecule 1: Dipeptidase



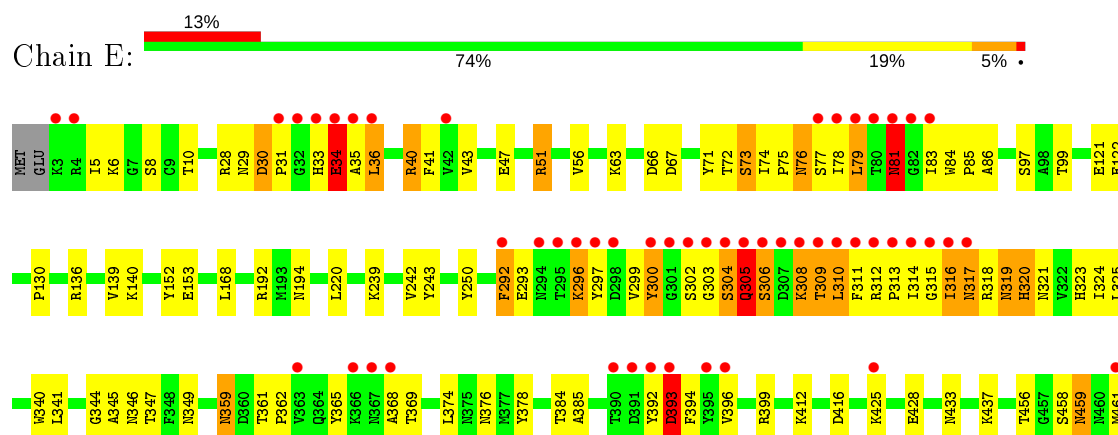
• Molecule 1: Dipeptidase



• Molecule 1: Dipeptidase



• Molecule 1: Dipeptidase



K462	
L463	
R464	
Y465	
H466	
L467	
M468	
P469	

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	192.34Å 137.09Å 101.30Å 90.00° 100.75° 90.00°	Depositor
Resolution (Å)	47.24 – 2.47 47.24 – 2.47	Depositor EDS
% Data completeness (in resolution range)	99.5 (47.24-2.47) 99.5 (47.24-2.47)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.96 (at 2.48Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.188 , 0.240 0.191 , 0.241	Depositor DCC
R_{free} test set	4624 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	36.9	Xtriage
Anisotropy	0.520	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 50.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	19121	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.48% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CO, EDO, ACT

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	0.54	0/3789	0.81	7/5157 (0.1%)
1	B	0.54	0/3789	0.86	8/5157 (0.2%)
1	C	0.54	0/3789	0.84	6/5157 (0.1%)
1	D	0.49	0/3789	0.81	11/5157 (0.2%)
1	E	0.55	2/3789 (0.1%)	0.93	18/5157 (0.3%)
All	All	0.53	2/18945 (0.0%)	0.85	50/25785 (0.2%)

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	A	0	3
1	B	0	3
1	C	0	7
1	D	0	3
1	E	0	12
All	All	0	28

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	462	LYS	CD-CE	-6.61	1.34	1.51
1	E	462	LYS	CE-NZ	-5.15	1.36	1.49

All (50) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	36	LEU	CA-CB-CG	15.10	150.02	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	36	LEU	CB-CG-CD2	12.90	132.94	111.00
1	E	36	LEU	CB-CG-CD1	-10.64	92.92	111.00
1	E	462	LYS	CD-CE-NZ	-10.10	88.47	111.70
1	E	308	LYS	CA-CB-CG	-8.96	93.68	113.40
1	D	36	LEU	CA-CB-CG	8.57	135.01	115.30
1	B	308	LYS	CD-CE-NZ	-8.48	92.19	111.70
1	A	36	LEU	CA-CB-CG	8.46	134.75	115.30
1	D	317	ASN	CB-CA-C	7.68	125.77	110.40
1	D	317	ASN	N-CA-CB	-7.43	97.22	110.60
1	B	79	LEU	CB-CG-CD2	-7.34	98.52	111.00
1	D	467	LEU	CA-CB-CG	7.22	131.90	115.30
1	D	317	ASN	C-N-CA	7.09	139.42	121.70
1	B	79	LEU	CA-CB-CG	7.08	131.59	115.30
1	C	468	ASN	N-CA-C	6.92	129.68	111.00
1	C	7	GLY	N-CA-C	6.83	130.16	113.10
1	A	308	LYS	N-CA-C	6.76	129.25	111.00
1	E	79	LEU	CB-CG-CD1	-6.71	99.60	111.00
1	B	301	GLY	N-CA-C	6.70	129.85	113.10
1	B	329	ASN	N-CA-C	-6.62	93.13	111.00
1	A	468	ASN	N-CA-C	6.40	128.28	111.00
1	E	308	LYS	CB-CG-CD	6.34	128.09	111.60
1	D	317	ASN	CA-C-N	6.32	131.10	117.20
1	E	308	LYS	CD-CE-NZ	-6.21	97.43	111.70
1	E	462	LYS	CB-CG-CD	-6.09	95.77	111.60
1	E	30	ASP	CB-CG-OD1	5.88	123.59	118.30
1	C	304	SER	N-CA-C	5.86	126.81	111.00
1	D	79	LEU	CA-CB-CG	5.84	128.74	115.30
1	B	302	SER	N-CA-C	5.82	126.70	111.00
1	A	34	GLU	N-CA-C	-5.76	95.44	111.00
1	B	467	LEU	N-CA-C	5.74	126.49	111.00
1	E	81	ASN	N-CA-C	5.70	126.39	111.00
1	E	79	LEU	CA-CB-CG	5.68	128.37	115.30
1	E	5	ILE	CG1-CB-CG2	-5.67	98.93	111.40
1	E	310	LEU	CA-CB-CG	5.62	128.23	115.30
1	E	310	LEU	CB-CG-CD2	-5.57	101.54	111.00
1	D	30	ASP	CB-CG-OD1	5.50	123.25	118.30
1	D	469	ASP	CB-CG-OD1	5.46	123.21	118.30
1	D	312	ARG	NE-CZ-NH1	5.38	122.99	120.30
1	A	344	GLY	N-CA-C	-5.38	99.66	113.10
1	B	368	ALA	C-N-CA	5.36	135.10	121.70
1	A	294	ASN	N-CA-C	-5.36	96.53	111.00
1	E	303	GLY	N-CA-C	5.28	126.30	113.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	76	ASN	N-CA-C	5.27	125.24	111.00
1	D	312	ARG	NE-CZ-NH2	-5.13	117.74	120.30
1	C	393	ASP	CA-C-N	-5.06	106.06	117.20
1	E	465	TYR	CA-CB-CG	5.04	122.98	113.40
1	C	393	ASP	N-CA-C	5.03	124.58	111.00
1	C	395	TYR	N-CA-C	5.01	124.54	111.00
1	A	317	ASN	N-CA-C	5.00	124.51	111.00

There are no chirality outliers.

All (28) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	298	ASP	Peptide
1	A	316	ILE	Peptide
1	A	318	ARG	Peptide
1	B	293	GLU	Peptide
1	B	308	LYS	Peptide
1	B	465	TYR	Peptide
1	C	293	GLU	Peptide
1	C	304	SER	Peptide
1	C	309	THR	Peptide
1	C	392	TYR	Peptide
1	C	393	ASP	Peptide
1	C	464	ARG	Peptide
1	C	468	ASN	Peptide
1	D	293	GLU	Peptide
1	D	316	ILE	Peptide
1	D	81	ASN	Peptide
1	E	293	GLU	Peptide
1	E	304	SER	Peptide
1	E	305	GLN	Peptide
1	E	306	SER	Peptide
1	E	309	THR	Peptide
1	E	316	ILE	Peptide
1	E	317	ASN	Peptide
1	E	34	GLU	Peptide
1	E	393	ASP	Peptide
1	E	464	ARG	Peptide
1	E	81	ASN	Peptide
1	E	83	ILE	Peptide

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	3706	0	3539	129	0
1	B	3706	0	3539	155	0
1	C	3706	0	3539	145	0
1	D	3706	0	3539	109	0
1	E	3706	0	3539	120	0
2	A	2	0	0	0	0
2	B	1	0	0	0	0
2	C	2	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
3	A	12	0	18	3	0
3	C	8	0	12	2	0
4	B	4	0	3	0	0
5	A	159	0	0	8	0
5	B	114	0	0	4	0
5	C	107	0	0	5	0
5	D	97	0	0	6	0
5	E	83	0	0	1	0
All	All	19121	0	17728	646	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 18.

All (646) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:297:TYR:HB3	1:E:308:LYS:HD2	1.21	1.13
1:B:317:ASN:H	1:B:318:ARG:HA	1.19	1.02
1:C:34:GLU:HG2	1:C:35:ALA:H	1.25	1.00
1:E:317:ASN:H	1:E:318:ARG:HB2	1.27	0.95
1:B:318:ARG:NH1	1:B:346:ASN:O	2.01	0.92
1:B:79:LEU:HD21	1:B:84:TRP:HD1	1.34	0.92
1:E:368:ALA:HA	1:E:369:THR:HG22	1.51	0.91
1:C:363:VAL:H	1:C:436:LYS:HZ2	1.13	0.90
1:E:308:LYS:HZ1	1:E:311:PHE:HB2	1.36	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:318:ARG:HD2	1:C:319:ASN:HB2	1.54	0.90
1:B:368:ALA:HA	1:B:369:THR:HG22	1.55	0.89
1:C:291:HIS:CE1	1:C:316:ILE:HB	2.10	0.87
1:E:308:LYS:NZ	1:E:311:PHE:HB2	1.88	0.87
1:E:77:SER:OG	1:E:78:ILE:N	2.09	0.86
1:D:6:LYS:NZ	1:D:153:GLU:OE2	2.09	0.86
1:C:319:ASN:OD1	1:C:320:HIS:N	2.09	0.85
1:E:318:ARG:HD2	1:E:319:ASN:H	1.41	0.85
1:E:292:PHE:HD1	1:E:296:LYS:HZ1	1.23	0.85
1:B:309:THR:OG1	1:B:311:PHE:N	2.10	0.84
1:A:398:MET:HE3	1:C:3:LYS:HE3	1.61	0.83
1:E:30:ASP:N	1:E:318:ARG:HH12	1.77	0.82
1:E:359:ASN:N	1:E:359:ASN:HD22	1.75	0.82
1:D:32:GLY:N	1:D:319:ASN:OD1	2.13	0.82
1:B:317:ASN:N	1:B:318:ARG:HA	1.95	0.81
1:E:297:TYR:HB3	1:E:308:LYS:CD	2.07	0.81
1:D:396:VAL:HG22	1:D:399:ARG:NH2	1.96	0.81
1:A:317:ASN:HD22	1:A:318:ARG:N	1.78	0.81
1:A:77:SER:OG	1:A:78:ILE:N	2.13	0.80
1:C:298:ASP:H	1:C:308:LYS:HE2	1.45	0.80
1:C:396:VAL:HA	1:C:399:ARG:HB3	1.63	0.80
1:D:468:ASN:OD1	1:D:469:ASP:N	2.15	0.80
1:B:30:ASP:HB3	1:B:321:ASN:HB2	1.63	0.80
1:D:49:GLN:O	1:D:51:ARG:NH1	2.16	0.79
1:E:309:THR:OG1	1:E:310:LEU:HB2	1.83	0.79
1:D:312:ARG:NH1	1:D:313:PRO:O	2.16	0.79
1:D:78:ILE:HA	1:D:81:ASN:HD21	1.47	0.79
1:E:299:VAL:HG21	1:E:313:PRO:HG3	1.64	0.78
1:B:299:VAL:HG21	1:B:313:PRO:HG3	1.65	0.78
1:D:3:LYS:NZ	5:D:602:HOH:O	2.17	0.78
1:B:4:ARG:HG2	1:B:5:ILE:N	1.99	0.77
1:C:291:HIS:NE2	1:C:313:PRO:HB3	1.99	0.77
1:E:306:SER:HA	1:E:309:THR:HG22	1.65	0.77
1:A:317:ASN:C	1:A:317:ASN:HD22	1.88	0.77
1:C:363:VAL:H	1:C:436:LYS:NZ	1.83	0.77
1:D:78:ILE:HA	1:D:81:ASN:ND2	2.00	0.77
1:B:293:GLU:OE2	1:B:298:ASP:HB2	1.85	0.77
1:D:317:ASN:OD1	1:D:318:ARG:HB2	1.85	0.77
1:A:313:PRO:HB2	1:A:316:ILE:O	1.83	0.76
1:B:344:GLY:H	1:B:349:ASN:HA	1.48	0.76
1:C:393:ASP:OD2	1:C:396:VAL:HG22	1.86	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:297:TYR:CE1	1:A:311:PHE:HB2	2.21	0.76
1:C:51:ARG:NH1	1:C:66:ASP:O	2.19	0.76
1:C:34:GLU:OE1	1:C:77:SER:OG	2.02	0.76
1:E:296:LYS:HG2	1:E:297:TYR:H	1.51	0.76
1:E:33:HIS:HB2	1:E:78:ILE:HG22	1.68	0.75
1:D:242:VAL:HB	1:D:310:LEU:O	1.86	0.75
1:C:51:ARG:NH1	1:C:66:ASP:OD1	2.20	0.74
1:B:466:ASN:O	1:B:467:LEU:HG	1.88	0.74
1:C:298:ASP:OD1	1:C:299:VAL:N	2.19	0.74
1:B:330:ASN:ND2	5:B:602:HOH:O	2.20	0.74
1:C:36:LEU:HB3	1:C:38:PRO:HD2	1.70	0.74
1:A:344:GLY:H	1:A:349:ASN:HA	1.53	0.74
1:A:298:ASP:HB2	1:A:300:TYR:CD1	2.23	0.73
1:A:79:LEU:HD22	1:A:84:TRP:NE1	2.03	0.73
1:B:298:ASP:OD1	1:B:299:VAL:N	2.18	0.73
1:C:8:SER:O	1:C:31:PRO:HG3	1.89	0.73
1:B:298:ASP:CG	1:B:299:VAL:H	1.91	0.72
1:D:6:LYS:O	5:D:601:HOH:O	2.07	0.72
1:C:393:ASP:HB2	1:C:396:VAL:N	2.05	0.71
1:A:43:VAL:HG22	1:A:72:THR:HG22	1.72	0.71
1:B:466:ASN:C	1:B:467:LEU:HG	2.09	0.71
1:E:344:GLY:H	1:E:349:ASN:HA	1.56	0.71
1:A:79:LEU:HD22	1:A:84:TRP:HE1	1.56	0.71
3:C:504:EDO:O1	5:C:601:HOH:O	2.09	0.71
1:B:61:ASN:OD1	5:B:601:HOH:O	2.09	0.70
1:C:303:GLY:HA2	1:C:304:SER:O	1.92	0.70
1:A:56:VAL:HB	1:A:122:GLU:HG3	1.74	0.70
1:C:291:HIS:CE1	1:C:313:PRO:HB3	2.27	0.70
1:C:34:GLU:HG2	1:C:35:ALA:N	2.04	0.69
1:A:8:SER:HB3	1:A:312:ARG:HH21	1.58	0.69
1:E:297:TYR:CB	1:E:308:LYS:HD2	2.13	0.69
1:E:34:GLU:HG2	1:E:35:ALA:HB2	1.75	0.69
1:D:84:TRP:CE3	1:D:122:GLU:HA	2.28	0.69
1:B:31:PRO:HA	1:B:319:ASN:ND2	2.08	0.69
1:C:316:ILE:HG12	1:C:320:HIS:CE1	2.27	0.69
1:A:291:HIS:CD2	1:A:316:ILE:HG12	2.28	0.68
1:A:3:LYS:N	1:B:448:LYS:HZ3	1.90	0.68
1:B:368:ALA:HA	1:B:369:THR:CG2	2.22	0.68
1:C:344:GLY:H	1:C:349:ASN:HA	1.57	0.68
1:B:344:GLY:N	1:B:349:ASN:HA	2.08	0.68
1:B:56:VAL:HG13	1:B:81:ASN:HB3	1.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:368:ALA:HA	1:E:369:THR:CG2	2.21	0.68
1:B:347:THR:HG21	1:B:392:TYR:HE1	1.58	0.68
1:B:79:LEU:HD21	1:B:84:TRP:CD1	2.25	0.68
1:A:317:ASN:H	1:A:318:ARG:HA	1.58	0.67
1:A:31:PRO:HA	1:A:319:ASN:HB2	1.76	0.67
1:A:6:LYS:HA	1:A:33:HIS:NE2	2.09	0.67
1:E:122:GLU:OE2	1:E:152:TYR:OH	2.09	0.67
1:B:323:HIS:CE1	1:B:325:LEU:HD21	2.29	0.67
1:B:32:GLY:N	1:B:319:ASN:HD22	1.92	0.67
1:A:184:ASP:OD1	3:A:504:EDO:H21	1.95	0.67
1:A:302:SER:HB3	1:C:309:THR:HG21	1.77	0.67
1:D:368:ALA:HA	1:D:369:THR:OG1	1.94	0.67
1:B:52:ASP:OD1	5:B:601:HOH:O	2.12	0.67
1:C:292:PHE:HB3	1:C:296:LYS:HZ2	1.60	0.66
1:C:34:GLU:OE1	1:C:78:ILE:N	2.27	0.66
1:A:398:MET:SD	1:C:3:LYS:NZ	2.66	0.66
1:C:318:ARG:CD	1:C:319:ASN:HB2	2.25	0.66
1:B:464:ARG:C	1:B:466:ASN:H	1.98	0.66
1:B:347:THR:HG21	1:B:392:TYR:CE1	2.31	0.66
1:B:299:VAL:HA	1:B:300:TYR:CD1	2.31	0.65
1:A:317:ASN:C	1:A:317:ASN:ND2	2.48	0.65
1:A:422:SER:O	5:A:602:HOH:O	2.15	0.65
1:C:56:VAL:HB	1:C:122:GLU:HG3	1.77	0.65
1:B:7:GLY:HA3	1:B:31:PRO:HB3	1.79	0.65
1:D:459:ASN:HA	1:D:462:LYS:HD3	1.79	0.65
1:A:316:ILE:HA	1:A:318:ARG:HG3	1.79	0.64
1:B:299:VAL:CG2	1:B:313:PRO:HG3	2.27	0.64
1:E:40:ARG:HH22	1:E:369:THR:HG21	1.62	0.64
1:B:305:GLN:HA	1:B:308:LYS:HG3	1.79	0.64
1:C:296:LYS:HG3	1:C:297:TYR:H	1.63	0.64
1:A:298:ASP:HB2	1:A:300:TYR:HD1	1.61	0.64
1:B:305:GLN:HA	1:B:308:LYS:CD	2.28	0.64
1:E:323:HIS:CE1	1:E:325:LEU:HD21	2.33	0.64
1:C:300:TYR:OH	1:C:304:SER:O	2.16	0.64
1:E:318:ARG:NH2	1:E:319:ASN:O	2.31	0.64
1:A:79:LEU:CD1	1:A:83:ILE:HA	2.26	0.64
1:D:33:HIS:NE2	1:D:77:SER:HB2	2.13	0.64
1:A:300:TYR:CG	1:A:301:GLY:N	2.67	0.63
1:A:323:HIS:CE1	1:A:325:LEU:HD21	2.33	0.63
1:E:296:LYS:HG2	1:E:297:TYR:N	2.12	0.63
1:A:298:ASP:HB3	1:A:300:TYR:HA	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:30:ASP:C	1:E:318:ARG:HH22	2.02	0.63
1:B:34:GLU:HB3	1:B:78:ILE:HD13	1.79	0.63
1:A:298:ASP:CB	1:A:300:TYR:HA	2.29	0.63
1:B:313:PRO:HB2	1:B:316:ILE:O	1.99	0.63
1:C:318:ARG:HD2	1:C:319:ASN:CB	2.27	0.63
1:D:5:ILE:O	1:D:6:LYS:HG2	1.99	0.62
1:B:293:GLU:HG3	1:B:298:ASP:CG	2.20	0.62
1:C:307:ASP:O	1:C:308:LYS:HG3	1.99	0.62
1:E:242:VAL:HB	1:E:310:LEU:O	1.99	0.62
1:C:392:TYR:O	1:C:393:ASP:HB3	2.00	0.62
1:A:297:TYR:HA	1:A:308:LYS:HE3	1.81	0.62
1:B:4:ARG:HG2	1:B:5:ILE:H	1.63	0.62
1:D:49:GLN:HE21	1:D:71:TYR:HE1	1.45	0.62
1:B:323:HIS:NE2	1:B:325:LEU:HD21	2.15	0.61
1:E:433:ASN:OD1	1:E:437:LYS:NZ	2.33	0.61
1:A:466:ASN:O	1:A:467:LEU:HB3	2.00	0.61
1:A:368:ALA:HA	1:A:369:THR:OG1	2.01	0.61
1:C:84:TRP:CE3	1:C:122:GLU:HA	2.36	0.61
1:C:41:PHE:HB3	1:C:341:LEU:HD22	1.81	0.61
1:B:306:SER:C	1:B:308:LYS:H	2.04	0.61
1:D:33:HIS:CD2	1:D:77:SER:HB2	2.36	0.61
1:E:462:LYS:O	1:E:465:TYR:HB2	2.00	0.61
1:C:294:ASN:O	1:C:296:LYS:N	2.34	0.61
1:E:317:ASN:H	1:E:318:ARG:CB	2.07	0.61
1:C:300:TYR:CD2	1:C:301:GLY:N	2.69	0.60
1:A:250:TYR:CE1	1:A:292:PHE:HA	2.37	0.60
1:E:396:VAL:HA	1:E:399:ARG:HB3	1.82	0.60
1:B:329:ASN:O	1:B:330:ASN:HB3	1.99	0.60
1:B:347:THR:O	1:B:399:ARG:NE	2.34	0.60
1:C:43:VAL:HG22	1:C:72:THR:HG22	1.83	0.60
1:D:377:MET:HG2	1:D:443:PHE:HD2	1.65	0.60
1:B:294:ASN:O	1:B:296:LYS:N	2.31	0.60
1:B:75:PRO:O	1:B:76:ASN:ND2	2.34	0.60
1:B:29:ASN:HD21	1:B:314:ILE:HG23	1.66	0.60
1:E:56:VAL:HB	1:E:122:GLU:HG3	1.84	0.60
1:C:399:ARG:NH1	5:C:602:HOH:O	2.15	0.60
1:C:393:ASP:CA	1:C:395:TYR:H	2.15	0.59
1:E:299:VAL:N	1:E:300:TYR:HA	2.15	0.59
1:C:291:HIS:ND1	1:C:299:VAL:HG21	2.17	0.59
1:C:298:ASP:H	1:C:308:LYS:CE	2.13	0.59
1:E:344:GLY:N	1:E:349:ASN:HA	2.18	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:28:ARG:HE	1:D:323:HIS:HD1	1.48	0.59
1:D:73:SER:HB3	1:D:85:PRO:HB3	1.85	0.59
1:E:359:ASN:N	1:E:359:ASN:ND2	2.50	0.59
1:C:368:ALA:HA	1:C:369:THR:OG1	2.03	0.58
1:E:6:LYS:HG3	1:E:33:HIS:NE2	2.18	0.58
1:C:316:ILE:HG12	1:C:320:HIS:HE1	1.65	0.58
1:C:63:LYS:HD2	1:C:63:LYS:H	1.69	0.58
1:D:312:ARG:HH22	1:D:318:ARG:CD	2.16	0.58
1:B:301:GLY:H	1:B:305:GLN:HE22	1.51	0.58
1:B:299:VAL:HG21	1:B:313:PRO:CG	2.32	0.58
1:C:34:GLU:CG	1:C:35:ALA:H	2.07	0.58
1:A:291:HIS:HD2	1:A:316:ILE:HG12	1.69	0.58
1:B:32:GLY:H	1:B:319:ASN:HD22	1.51	0.58
1:D:56:VAL:HB	1:D:122:GLU:HG3	1.86	0.58
1:E:317:ASN:N	1:E:318:ARG:HB2	2.10	0.58
1:C:398:MET:HB2	1:D:3:LYS:HE3	1.86	0.58
1:E:359:ASN:HD21	1:E:428:GLU:HG3	1.69	0.58
1:C:292:PHE:HB3	1:C:296:LYS:NZ	2.18	0.57
1:D:75:PRO:HB3	1:D:83:ILE:HG13	1.86	0.57
1:B:305:GLN:HA	1:B:308:LYS:CG	2.35	0.57
1:B:305:GLN:OE1	1:B:308:LYS:HB2	2.04	0.57
1:B:242:VAL:HB	1:B:310:LEU:O	2.04	0.57
1:B:49:GLN:O	1:B:51:ARG:NH1	2.37	0.57
1:C:292:PHE:HB2	1:C:297:TYR:O	2.05	0.57
1:C:375:ASN:ND2	5:C:609:HOH:O	2.37	0.57
1:D:323:HIS:CE1	1:D:325:LEU:HD21	2.40	0.57
1:C:74:ILE:HG13	1:C:323:HIS:CE1	2.40	0.57
1:A:40:ARG:NH2	1:A:367:ASN:O	2.38	0.57
1:D:317:ASN:OD1	1:D:318:ARG:CB	2.52	0.57
1:A:121:GLU:HA	1:A:124:LEU:HG	1.87	0.57
1:B:29:ASN:HD21	1:B:314:ILE:HD12	1.69	0.57
1:B:34:GLU:OE2	1:B:35:ALA:HB3	2.05	0.57
1:E:29:ASN:HD21	1:E:314:ILE:HG13	1.69	0.57
1:C:304:SER:OG	1:C:307:ASP:HB2	2.05	0.57
1:E:306:SER:OG	1:E:306:SER:O	2.23	0.57
1:B:56:VAL:HB	1:B:122:GLU:HG3	1.87	0.56
1:C:388:GLY:O	1:C:392:TYR:HA	2.04	0.56
1:B:303:GLY:H	1:B:308:LYS:NZ	2.02	0.56
1:B:316:ILE:HD12	1:B:318:ARG:HH21	1.70	0.56
1:E:79:LEU:HD11	1:E:84:TRP:NE1	2.20	0.56
1:C:393:ASP:HB2	1:C:396:VAL:H	1.69	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:40:ARG:HA	1:C:365:TYR:HD2	1.71	0.56
1:C:300:TYR:OH	1:C:305:GLN:HB2	2.05	0.56
1:E:242:VAL:O	1:E:311:PHE:HA	2.05	0.56
1:E:73:SER:HB2	1:E:85:PRO:HB3	1.87	0.56
1:B:43:VAL:HG22	1:B:72:THR:HG22	1.87	0.56
1:D:122:GLU:OE2	1:D:152:TYR:OH	2.23	0.56
1:D:29:ASN:HD21	1:D:314:ILE:HG13	1.70	0.56
1:D:297:TYR:OH	1:D:311:PHE:O	2.21	0.56
1:B:291:HIS:ND1	1:B:316:ILE:HG12	2.21	0.56
1:B:79:LEU:CD2	1:B:84:TRP:HD1	2.13	0.56
1:C:393:ASP:HB3	1:C:396:VAL:HG13	1.88	0.56
1:C:3:LYS:C	1:C:4:ARG:HG3	2.26	0.56
1:E:43:VAL:HG22	1:E:72:THR:HG22	1.86	0.56
1:D:247:ARG:HD3	1:D:314:ILE:HB	1.88	0.55
1:A:300:TYR:OH	1:A:303:GLY:N	2.40	0.55
1:A:31:PRO:HA	1:A:319:ASN:CB	2.35	0.55
1:D:317:ASN:OD1	1:D:319:ASN:N	2.38	0.55
1:A:36:LEU:HD12	1:A:38:PRO:CD	2.37	0.55
1:E:459:ASN:HA	1:E:462:LYS:HD2	1.89	0.55
1:A:75:PRO:HB3	1:A:83:ILE:HG22	1.87	0.55
1:B:75:PRO:HB3	1:B:83:ILE:HG12	1.87	0.55
1:D:295:THR:HG22	1:D:296:LYS:N	2.22	0.55
1:B:291:HIS:HB3	1:B:299:VAL:HB	1.88	0.55
1:C:363:VAL:N	1:C:436:LYS:HZ2	1.95	0.55
1:A:40:ARG:HA	1:A:365:TYR:HD2	1.72	0.55
1:C:323:HIS:CE1	1:C:325:LEU:HD21	2.41	0.55
1:A:6:LYS:HA	1:A:33:HIS:CE1	2.42	0.54
1:B:29:ASN:ND2	1:B:314:ILE:HG23	2.22	0.54
1:D:344:GLY:H	1:D:349:ASN:HA	1.72	0.54
1:D:36:LEU:HD12	1:D:38:PRO:HD3	1.89	0.54
1:E:361:THR:CG2	1:E:365:TYR:HB2	2.37	0.54
1:C:393:ASP:HB2	1:C:395:TYR:N	2.23	0.54
1:B:34:GLU:HB3	1:B:78:ILE:CD1	2.38	0.54
1:D:462:LYS:O	1:D:465:TYR:CZ	2.60	0.54
1:D:153:GLU:OE2	5:D:603:HOH:O	2.19	0.54
1:C:242:VAL:HG12	1:C:311:PHE:HE1	1.73	0.54
1:C:344:GLY:N	1:C:349:ASN:HA	2.23	0.54
1:A:398:MET:CE	1:C:3:LYS:HE3	2.34	0.54
1:C:73:SER:O	1:C:74:ILE:HD13	2.07	0.54
1:A:292:PHE:HB2	1:A:297:TYR:HD2	1.72	0.53
1:B:346:ASN:CG	1:B:347:THR:H	2.11	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:299:VAL:HA	1:E:300:TYR:HB3	1.89	0.53
1:D:295:THR:HG22	1:D:296:LYS:HG2	1.90	0.53
1:D:312:ARG:HG3	1:D:312:ARG:HH11	1.73	0.53
1:B:361:THR:HG23	1:B:362:PRO:HD2	1.90	0.53
1:C:316:ILE:CG1	1:C:320:HIS:HE1	2.21	0.53
1:A:323:HIS:NE2	1:A:325:LEU:HD21	2.23	0.53
1:E:79:LEU:HD11	1:E:84:TRP:HE1	1.73	0.53
1:A:6:LYS:NZ	1:A:121:GLU:OE1	2.40	0.53
1:B:297:TYR:CD1	1:B:307:ASP:O	2.62	0.53
1:D:28:ARG:NH1	1:D:30:ASP:HB2	2.24	0.53
1:D:78:ILE:O	1:D:79:LEU:HD23	2.09	0.53
1:E:250:TYR:CE1	1:E:292:PHE:HA	2.43	0.53
1:D:45:ASN:ND2	5:D:611:HOH:O	2.41	0.53
1:E:394:PHE:CZ	1:E:456:THR:HG22	2.44	0.53
1:A:325:LEU:HD22	1:A:339:HIS:HD2	1.74	0.52
1:B:51:ARG:HD3	5:B:649:HOH:O	2.09	0.52
1:C:323:HIS:NE2	1:C:325:LEU:HD21	2.24	0.52
1:A:333:THR:HG23	5:A:718:HOH:O	2.09	0.52
1:B:462:LYS:HG3	1:B:463:LEU:HD12	1.90	0.52
1:E:33:HIS:CB	1:E:78:ILE:HG22	2.39	0.52
1:A:317:ASN:N	1:A:318:ARG:HA	2.23	0.52
1:C:291:HIS:NE2	1:C:316:ILE:HB	2.23	0.52
1:C:412:LYS:HE3	1:C:416:ASP:OD2	2.08	0.52
1:E:79:LEU:HD12	1:E:81:ASN:OD1	2.09	0.52
1:E:396:VAL:HG13	1:E:399:ARG:HD3	1.92	0.52
1:B:29:ASN:ND2	1:B:314:ILE:HD12	2.24	0.52
1:C:34:GLU:HB3	1:C:77:SER:OG	2.10	0.52
1:C:398:MET:HE3	1:D:3:LYS:HG2	1.92	0.52
1:A:8:SER:HB2	1:A:243:TYR:OH	2.09	0.52
1:A:304:SER:OG	1:A:305:GLN:N	2.43	0.51
1:B:39:GLN:NE2	1:B:40:ARG:O	2.43	0.51
1:C:464:ARG:CA	1:C:466:ASN:H	2.22	0.51
1:D:296:LYS:O	1:D:304:SER:HB3	2.09	0.51
1:D:41:PHE:HB3	1:D:341:LEU:HD22	1.92	0.51
1:B:462:LYS:CG	1:B:463:LEU:HD12	2.40	0.51
1:B:79:LEU:HD13	1:B:82:GLY:O	2.10	0.51
1:B:6:LYS:NZ	1:B:153:GLU:OE2	2.36	0.51
1:C:363:VAL:HG13	1:C:436:LYS:HZ1	1.75	0.51
1:A:324:ILE:HB	1:A:340:TRP:HB2	1.92	0.51
1:B:325:LEU:HD22	1:B:339:HIS:CD2	2.45	0.51
1:A:297:TYR:HA	1:A:308:LYS:CE	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:412:LYS:NZ	5:D:613:HOH:O	2.43	0.51
1:D:73:SER:O	1:D:74:ILE:HD13	2.11	0.51
1:B:293:GLU:OE1	1:B:294:ASN:HA	2.10	0.51
1:B:51:ARG:NE	1:B:66:ASP:OD1	2.41	0.51
1:D:315:GLY:O	1:D:320:HIS:ND1	2.44	0.51
1:E:324:ILE:HB	1:E:340:TRP:HB2	1.92	0.51
1:A:300:TYR:CD1	1:A:308:LYS:HD3	2.46	0.51
1:C:192:ARG:O	1:C:194:ASN:ND2	2.43	0.51
1:C:464:ARG:HA	1:C:466:ASN:H	1.76	0.51
1:B:348:PHE:HA	1:B:399:ARG:CZ	2.40	0.51
1:C:300:TYR:CD1	1:C:308:LYS:HD2	2.45	0.51
1:E:40:ARG:HG3	1:E:365:TYR:HB3	1.93	0.51
1:B:291:HIS:CE1	1:B:316:ILE:HD11	2.47	0.51
1:D:242:VAL:HG11	1:D:310:LEU:HD13	1.93	0.51
1:A:6:LYS:HE2	1:A:101:THR:OG1	2.12	0.50
1:B:250:TYR:CE1	1:B:292:PHE:HA	2.46	0.50
1:C:72:THR:OG1	1:C:339:HIS:NE2	2.37	0.50
1:B:84:TRP:CE3	1:B:122:GLU:HA	2.46	0.50
1:C:393:ASP:HA	1:C:395:TYR:H	1.76	0.50
1:D:37:ASP:OD2	1:D:345:ALA:HB2	2.11	0.50
1:A:377:MET:HG2	1:A:443:PHE:HD1	1.75	0.50
1:A:344:GLY:N	1:A:349:ASN:HA	2.22	0.50
1:B:320:HIS:CE1	1:B:349:ASN:HD21	2.28	0.50
1:D:212:LYS:NZ	1:D:216:ASP:OD2	2.44	0.50
1:A:41:PHE:HB3	1:A:341:LEU:HD22	1.94	0.50
1:A:361:THR:HG23	1:A:362:PRO:HD2	1.94	0.50
1:E:192:ARG:O	1:E:194:ASN:ND2	2.45	0.50
1:E:320:HIS:N	1:E:320:HIS:CD2	2.79	0.50
1:A:291:HIS:HB3	1:A:316:ILE:HG12	1.92	0.50
1:A:67:ASP:N	1:A:67:ASP:OD1	2.45	0.50
1:B:3:LYS:HG3	1:B:4:ARG:H	1.76	0.50
1:E:296:LYS:HZ3	1:E:297:TYR:HD2	1.58	0.50
1:E:8:SER:HB2	1:E:312:ARG:HH12	1.76	0.50
1:A:13:LEU:HB3	1:A:165:VAL:HG11	1.94	0.50
1:B:139:VAL:HG13	1:B:168:LEU:HD12	1.94	0.50
1:D:250:TYR:CE1	1:D:292:PHE:HA	2.47	0.50
1:E:461:MET:O	1:E:464:ARG:HG2	2.11	0.50
1:C:291:HIS:ND1	1:C:299:VAL:CG2	2.75	0.49
1:E:41:PHE:HB3	1:E:341:LEU:HD22	1.94	0.49
1:B:31:PRO:HA	1:B:319:ASN:HD22	1.77	0.49
1:B:464:ARG:C	1:B:466:ASN:N	2.63	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:259:ASP:OD2	3:C:504:EDO:H11	2.11	0.49
1:E:29:ASN:C	1:E:318:ARG:HH12	2.15	0.49
1:E:359:ASN:HD22	1:E:359:ASN:H	1.53	0.49
1:A:291:HIS:HD2	1:A:316:ILE:HG21	1.78	0.49
1:A:49:GLN:O	1:A:51:ARG:NH1	2.45	0.49
1:A:78:ILE:HD12	1:A:79:LEU:H	1.77	0.49
1:B:28:ARG:HD3	1:B:97:SER:OG	2.12	0.49
1:C:299:VAL:O	1:C:299:VAL:HG23	2.12	0.49
1:D:303:GLY:HA3	1:E:306:SER:OG	2.12	0.49
1:D:28:ARG:HD3	1:D:97:SER:OG	2.13	0.49
1:E:465:TYR:CZ	1:E:467:LEU:O	2.65	0.49
1:B:51:ARG:HD2	1:B:66:ASP:HA	1.94	0.49
1:E:86:ALA:HB1	1:E:99:THR:CG2	2.43	0.49
1:A:377:MET:HE2	1:A:439:ALA:O	2.13	0.49
1:D:6:LYS:HZ1	1:D:153:GLU:CD	2.10	0.49
1:E:6:LYS:NZ	1:E:121:GLU:OE2	2.45	0.49
1:E:346:ASN:HB2	1:E:385:ALA:HB1	1.95	0.49
1:D:5:ILE:H	1:D:5:ILE:HD12	1.78	0.49
1:D:324:ILE:HB	1:D:340:TRP:HB2	1.96	0.48
1:E:136:ARG:O	1:E:140:LYS:HG3	2.12	0.48
1:E:318:ARG:HD2	1:E:319:ASN:N	2.21	0.48
1:E:463:LEU:HA	1:E:465:TYR:CB	2.43	0.48
1:B:299:VAL:HG11	1:B:313:PRO:HG3	1.94	0.48
1:B:299:VAL:CG1	1:B:313:PRO:HG3	2.43	0.48
1:D:289:SER:C	1:D:315:GLY:H	2.17	0.48
1:E:74:ILE:HD13	1:E:323:HIS:CE1	2.48	0.48
1:A:325:LEU:HD22	1:A:339:HIS:CD2	2.48	0.48
1:E:299:VAL:HA	1:E:300:TYR:CB	2.42	0.48
1:A:399:ARG:NH2	1:A:403:GLU:OE1	2.46	0.48
1:B:4:ARG:HG2	1:B:5:ILE:HG12	1.96	0.48
1:B:5:ILE:O	1:B:6:LYS:HB2	2.12	0.48
1:D:315:GLY:HA3	1:D:320:HIS:CE1	2.48	0.48
1:E:292:PHE:HB3	1:E:296:LYS:NZ	2.29	0.48
1:E:323:HIS:NE2	1:E:325:LEU:HD21	2.29	0.48
1:A:274:HIS:NE2	3:A:504:EDO:H11	2.28	0.48
1:A:318:ARG:CD	1:A:320:HIS:HB2	2.43	0.48
1:C:307:ASP:C	1:C:308:LYS:HG3	2.31	0.48
1:C:291:HIS:CD2	1:C:314:ILE:H	2.32	0.48
1:C:37:ASP:N	1:C:38:PRO:CD	2.76	0.48
1:D:291:HIS:HB2	1:D:313:PRO:HB3	1.95	0.48
1:E:76:ASN:HB3	1:E:77:SER:H	1.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:212:LYS:NZ	1:A:216:ASP:OD2	2.45	0.48
1:B:313:PRO:CB	1:B:316:ILE:HB	2.44	0.48
1:D:152:TYR:CE1	1:D:153:GLU:HG3	2.50	0.47
1:B:30:ASP:CB	1:B:321:ASN:HB2	2.41	0.47
1:E:359:ASN:N	1:E:428:GLU:OE2	2.40	0.47
1:A:34:GLU:CD	1:A:35:ALA:H	2.18	0.47
1:A:392:TYR:O	1:A:396:VAL:HG23	2.14	0.47
1:B:297:TYR:CE1	1:B:307:ASP:O	2.67	0.47
1:C:392:TYR:CG	1:C:392:TYR:O	2.67	0.47
1:C:8:SER:HB2	1:C:243:TYR:OH	2.14	0.47
1:D:317:ASN:ND2	1:D:320:HIS:HA	2.30	0.47
1:A:333:THR:HG22	5:A:722:HOH:O	2.15	0.47
1:C:291:HIS:CD2	1:C:316:ILE:HG13	2.50	0.47
1:C:335:ILE:HG22	1:C:431:LEU:HD21	1.96	0.47
1:C:76:ASN:ND2	1:C:84:TRP:CH2	2.83	0.47
1:A:292:PHE:HB2	1:A:297:TYR:CD2	2.50	0.47
1:E:139:VAL:HG13	1:E:168:LEU:HD12	1.95	0.47
1:E:28:ARG:HD3	1:E:97:SER:OG	2.15	0.47
1:A:412:LYS:HE3	1:A:416:ASP:OD2	2.15	0.47
1:B:38:PRO:HB3	1:B:378:TYR:CD1	2.49	0.47
1:C:291:HIS:CD2	1:C:314:ILE:N	2.82	0.47
1:E:319:ASN:N	1:E:319:ASN:OD1	2.47	0.47
1:D:380:LEU:HG	1:D:446:GLN:HG3	1.96	0.47
1:D:72:THR:OG1	1:D:339:HIS:HE1	1.97	0.47
1:E:361:THR:HG23	1:E:362:PRO:HD2	1.97	0.47
1:A:86:ALA:HB1	1:A:99:THR:CG2	2.45	0.47
1:B:304:SER:C	1:B:308:LYS:HD2	2.35	0.47
1:D:312:ARG:HH22	1:D:318:ARG:HD3	1.78	0.47
1:A:113:PRO:HD2	5:A:687:HOH:O	2.15	0.47
1:A:79:LEU:HD13	1:A:83:ILE:HA	1.96	0.47
1:B:67:ASP:OD1	1:B:67:ASP:N	2.47	0.47
1:C:40:ARG:HA	1:C:365:TYR:CD2	2.50	0.47
1:C:37:ASP:HB3	1:C:378:TYR:HE1	1.80	0.47
1:C:28:ARG:HD2	1:C:99:THR:OG1	2.15	0.47
1:B:71:TYR:CE1	1:B:130:PRO:HG3	2.50	0.47
1:B:30:ASP:O	1:B:319:ASN:ND2	2.48	0.47
1:C:5:ILE:O	1:C:6:LYS:HG2	2.15	0.47
1:A:136:ARG:NE	5:A:605:HOH:O	2.37	0.46
1:B:72:THR:OG1	1:B:339:HIS:HE1	1.98	0.46
1:C:28:ARG:HD3	1:C:97:SER:OG	2.15	0.46
1:D:293:GLU:O	1:D:293:GLU:HG2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:72:THR:OG1	1:A:339:HIS:HE1	1.99	0.46
1:B:465:TYR:HD2	1:B:466:ASN:C	2.19	0.46
1:D:36:LEU:HD12	1:D:38:PRO:CD	2.45	0.46
1:C:300:TYR:CE1	1:C:308:LYS:HD2	2.50	0.46
1:C:469:ASP:C	1:C:469:ASP:OD1	2.53	0.46
1:B:5:ILE:HG22	1:B:6:LYS:N	2.31	0.46
1:A:51:ARG:HD2	1:A:66:ASP:HA	1.96	0.46
1:B:335:ILE:HG22	1:B:431:LEU:HD11	1.98	0.46
1:D:139:VAL:HG13	1:D:168:LEU:HD12	1.97	0.46
1:E:67:ASP:OD1	1:E:67:ASP:N	2.48	0.46
1:C:74:ILE:HG13	1:C:323:HIS:NE2	2.30	0.46
1:D:315:GLY:O	1:D:317:ASN:HB2	2.16	0.46
1:A:300:TYR:CD2	1:A:301:GLY:N	2.84	0.46
1:A:300:TYR:CZ	1:A:304:SER:O	2.69	0.46
1:A:364:GLN:HG2	1:A:377:MET:CE	2.46	0.46
1:E:359:ASN:ND2	1:E:428:GLU:HG3	2.31	0.46
1:B:289:SER:OG	1:B:320:HIS:NE2	2.48	0.46
1:B:39:GLN:NE2	1:B:74:ILE:HG23	2.31	0.46
1:B:262:ASP:O	1:B:264:PRO:HD3	2.16	0.46
1:B:303:GLY:N	1:B:308:LYS:NZ	2.64	0.46
1:B:312:ARG:HA	1:B:313:PRO:HD2	1.39	0.46
1:B:5:ILE:HD13	1:B:5:ILE:H	1.81	0.46
1:B:8:SER:O	1:B:31:PRO:HD3	2.16	0.46
1:D:86:ALA:HB1	1:D:99:THR:CG2	2.46	0.46
1:E:8:SER:N	1:E:31:PRO:HG2	2.31	0.46
1:A:152:TYR:CE1	1:A:153:GLU:HG3	2.51	0.45
1:A:300:TYR:OH	1:A:304:SER:O	2.34	0.45
1:C:207:CYS:HB2	1:C:211:LEU:HD22	1.97	0.45
1:C:324:ILE:HB	1:C:340:TRP:HB2	1.97	0.45
1:B:301:GLY:H	1:B:305:GLN:NE2	2.15	0.45
1:B:320:HIS:CD2	1:B:322:VAL:HG23	2.51	0.45
1:C:393:ASP:CB	1:C:396:VAL:HG13	2.46	0.45
1:D:323:HIS:NE2	1:D:325:LEU:HD21	2.31	0.45
1:A:361:THR:HG21	1:A:365:TYR:HB2	1.97	0.45
1:B:314:ILE:HA	1:B:315:GLY:HA2	1.60	0.45
1:C:34:GLU:CD	1:C:78:ILE:HB	2.36	0.45
1:C:363:VAL:HG22	1:C:436:LYS:NZ	2.31	0.45
1:A:433:ASN:OD1	1:A:437:LYS:NZ	2.48	0.45
1:E:239:LYS:HA	1:E:239:LYS:HD2	1.84	0.45
1:A:308:LYS:O	1:A:309:THR:OG1	2.33	0.45
1:A:344:GLY:HA2	1:A:345:ALA:HA	1.78	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:346:ASN:CG	1:A:347:THR:H	2.19	0.45
1:C:465:TYR:OH	1:C:468:ASN:OD1	2.18	0.45
1:B:4:ARG:CG	1:B:5:ILE:N	2.77	0.45
1:C:307:ASP:O	1:C:308:LYS:CG	2.65	0.45
1:C:318:ARG:HH21	1:C:319:ASN:N	2.14	0.45
1:E:300:TYR:CE1	1:E:305:GLN:CD	2.90	0.45
1:D:315:GLY:HA3	1:D:320:HIS:HE1	1.82	0.45
1:D:43:VAL:HG22	1:D:72:THR:HG22	1.99	0.45
1:E:152:TYR:CE2	1:E:153:GLU:HG3	2.51	0.45
1:B:458:SER:O	1:B:462:LYS:HB3	2.17	0.45
1:D:312:ARG:HA	1:D:313:PRO:HD2	1.80	0.45
1:D:29:ASN:HA	1:D:321:ASN:O	2.17	0.45
1:D:361:THR:CG2	1:D:365:TYR:HB2	2.47	0.45
1:A:318:ARG:HH22	1:A:347:THR:HG22	1.82	0.44
1:A:293:GLU:HG2	1:A:293:GLU:O	2.18	0.44
1:A:298:ASP:HB2	1:A:300:TYR:HA	1.99	0.44
1:B:28:ARG:HE	1:B:323:HIS:HD1	1.65	0.44
1:B:362:PRO:HB2	1:B:364:GLN:HG2	1.99	0.44
1:E:314:ILE:HA	1:E:315:GLY:HA2	1.58	0.44
1:A:335:ILE:HG22	1:A:431:LEU:HD21	1.99	0.44
1:A:78:ILE:C	1:A:79:LEU:HG	2.33	0.44
1:D:426:ASP:OD2	1:D:429:LYS:HD3	2.17	0.44
1:E:10:THR:OG1	1:E:314:ILE:HG12	2.18	0.44
1:A:247:ARG:HG2	1:A:314:ILE:HG12	1.99	0.44
1:C:291:HIS:HE2	1:C:313:PRO:HB3	1.80	0.44
1:E:361:THR:HG22	1:E:365:TYR:HB2	2.00	0.44
1:E:376:ASN:OD1	1:E:378:TYR:HB3	2.17	0.44
1:A:8:SER:CB	1:A:312:ARG:HH21	2.27	0.44
1:C:291:HIS:O	1:C:292:PHE:HB2	2.17	0.44
1:E:51:ARG:HD2	1:E:66:ASP:HA	2.00	0.44
1:A:305:GLN:HA	1:A:308:LYS:HB2	1.99	0.44
1:A:314:ILE:HA	1:A:315:GLY:HA2	1.66	0.44
1:B:132:VAL:HG11	1:B:138:GLY:HA2	1.99	0.44
1:B:317:ASN:OD1	1:B:319:ASN:OD1	2.36	0.44
1:B:316:ILE:HD12	1:B:318:ARG:NH2	2.32	0.44
1:A:10:THR:OG1	1:A:314:ILE:HG21	2.18	0.44
1:A:305:GLN:HG2	1:A:305:GLN:O	2.18	0.44
1:A:411:ARG:HH11	3:A:503:EDO:H21	1.83	0.44
1:B:324:ILE:HB	1:B:340:TRP:HB2	1.99	0.44
1:E:374:LEU:HD23	1:E:374:LEU:HA	1.78	0.44
1:E:412:LYS:HE3	1:E:416:ASP:OD2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:312:ARG:HA	1:A:313:PRO:HD2	1.59	0.44
1:B:299:VAL:HA	1:B:300:TYR:CG	2.53	0.44
1:B:347:THR:O	1:B:399:ARG:CZ	2.65	0.44
1:C:300:TYR:CE1	1:C:305:GLN:HG3	2.52	0.44
1:C:393:ASP:HB2	1:C:395:TYR:H	1.81	0.44
1:A:8:SER:O	1:A:31:PRO:HD3	2.18	0.43
1:B:399:ARG:HH11	1:B:402:TYR:HD2	1.66	0.43
1:E:6:LYS:HG2	1:E:6:LYS:HZ2	1.67	0.43
1:C:286:PHE:HZ	1:D:238:ILE:HD11	1.82	0.43
1:D:293:GLU:OE1	1:D:293:GLU:N	2.51	0.43
1:E:309:THR:OG1	1:E:310:LEU:N	2.51	0.43
1:B:344:GLY:HA2	1:B:345:ALA:HA	1.79	0.43
1:B:465:TYR:HD2	1:B:466:ASN:O	2.01	0.43
1:C:139:VAL:HG13	1:C:168:LEU:HD12	2.00	0.43
1:D:76:ASN:ND2	1:D:86:ALA:HB2	2.33	0.43
1:C:393:ASP:CB	1:C:396:VAL:N	2.80	0.43
1:D:71:TYR:CE1	1:D:130:PRO:HG3	2.54	0.43
1:D:332:PRO:HD2	1:D:335:ILE:HD11	1.99	0.43
1:E:71:TYR:CE1	1:E:130:PRO:HG3	2.52	0.43
1:B:249:TRP:CZ2	1:B:253:LYS:HG3	2.53	0.43
1:C:464:ARG:C	1:C:466:ASN:H	2.21	0.43
1:D:374:LEU:HA	1:D:374:LEU:HD23	1.74	0.43
1:E:392:TYR:O	1:E:392:TYR:CD1	2.72	0.43
1:A:147:GLU:HG2	5:A:628:HOH:O	2.19	0.43
1:D:445:LYS:NZ	5:D:623:HOH:O	2.51	0.43
1:E:242:VAL:HA	1:E:311:PHE:CD1	2.54	0.43
1:B:239:LYS:HE2	1:B:243:TYR:CG	2.54	0.43
1:B:361:THR:HG21	1:B:365:TYR:HB2	2.00	0.43
1:D:317:ASN:ND2	1:D:318:ARG:NH2	2.67	0.43
1:D:343:TYR:HA	1:D:344:GLY:HA3	1.84	0.43
1:D:465:TYR:N	1:D:465:TYR:CD1	2.81	0.43
1:A:84:TRP:CE3	1:A:122:GLU:HA	2.54	0.43
1:C:32:GLY:O	1:C:318:ARG:NH2	2.50	0.43
1:C:361:THR:CG2	1:C:365:TYR:HB2	2.49	0.43
1:D:291:HIS:ND1	1:D:316:ILE:HG12	2.34	0.43
1:D:361:THR:HG23	1:D:362:PRO:HD2	2.00	0.43
1:B:307:ASP:C	1:B:308:LYS:HG2	2.39	0.42
1:C:202:SER:O	5:C:603:HOH:O	2.22	0.42
1:C:464:ARG:C	1:C:466:ASN:N	2.72	0.42
1:A:5:ILE:HG23	1:A:33:HIS:CD2	2.54	0.42
1:A:346:ASN:HB2	1:A:385:ALA:HB1	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:59:LYS:NZ	5:C:622:HOH:O	2.52	0.42
1:D:460:ASN:C	1:D:462:LYS:N	2.72	0.42
1:D:83:ILE:HG23	1:D:83:ILE:O	2.19	0.42
1:B:4:ARG:CG	1:B:5:ILE:HG12	2.49	0.42
1:D:314:ILE:HA	1:D:315:GLY:HA2	1.62	0.42
1:A:249:TRP:CZ2	1:A:253:LYS:HG3	2.54	0.42
1:A:32:GLY:H	1:A:319:ASN:CB	2.32	0.42
1:D:242:VAL:HG12	1:D:311:PHE:HE1	1.85	0.42
1:A:6:LYS:HD2	1:A:121:GLU:OE2	2.20	0.42
1:A:292:PHE:HB2	1:A:297:TYR:O	2.20	0.42
1:C:200:PHE:CD2	1:C:212:LYS:HD2	2.54	0.42
1:C:78:ILE:O	1:C:79:LEU:HD12	2.18	0.42
1:A:393:ASP:HA	1:A:396:VAL:HG23	2.01	0.42
1:A:463:LEU:HA	1:A:465:TYR:O	2.19	0.42
1:C:376:ASN:OD1	1:C:378:TYR:HB3	2.20	0.42
1:A:398:MET:SD	1:C:3:LYS:CE	3.08	0.42
1:E:296:LYS:CG	1:E:297:TYR:N	2.77	0.42
1:B:291:HIS:ND1	1:B:316:ILE:CG1	2.82	0.42
1:B:313:PRO:HB2	1:B:316:ILE:HB	2.00	0.42
1:B:72:THR:OG1	1:B:339:HIS:CE1	2.73	0.42
1:C:296:LYS:HG3	1:C:297:TYR:N	2.33	0.42
1:C:317:ASN:HA	1:C:318:ARG:HA	1.40	0.42
1:D:317:ASN:OD1	1:D:319:ASN:C	2.58	0.42
1:A:318:ARG:HH22	1:A:347:THR:CG2	2.33	0.42
1:B:325:LEU:HD22	1:B:339:HIS:HD2	1.83	0.42
1:B:361:THR:CG2	1:B:365:TYR:HB2	2.50	0.42
1:B:399:ARG:NH1	1:B:402:TYR:CD2	2.88	0.42
1:C:198:PHE:HB2	1:C:229:LEU:HG	2.02	0.42
1:E:300:TYR:HE1	1:E:305:GLN:NE2	2.18	0.42
1:E:312:ARG:HA	1:E:313:PRO:HD2	1.72	0.42
1:B:84:TRP:CD2	1:B:122:GLU:HA	2.54	0.42
5:A:604:HOH:O	1:C:3:LYS:N	2.52	0.42
1:D:454:VAL:O	1:D:458:SER:HB3	2.20	0.42
1:E:362:PRO:HB2	1:E:365:TYR:HD1	1.84	0.42
1:A:361:THR:CG2	1:A:365:TYR:HB2	2.50	0.41
1:D:462:LYS:O	1:D:464:ARG:N	2.53	0.41
1:E:30:ASP:HB3	1:E:321:ASN:HB2	2.00	0.41
1:E:344:GLY:HA2	1:E:345:ALA:HA	1.77	0.41
1:B:303:GLY:HA2	1:B:304:SER:HA	1.76	0.41
1:C:86:ALA:HB1	1:C:99:THR:CG2	2.50	0.41
1:B:306:SER:OG	1:E:302:SER:OG	2.28	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:34:GLU:HG2	1:E:35:ALA:N	2.35	0.41
1:B:299:VAL:HG12	1:B:299:VAL:O	2.19	0.41
1:B:346:ASN:CG	1:B:347:THR:N	2.74	0.41
1:C:73:SER:OG	1:C:85:PRO:HB3	2.19	0.41
1:D:313:PRO:HB2	1:D:316:ILE:O	2.21	0.41
1:E:34:GLU:HG2	1:E:35:ALA:CB	2.48	0.41
1:B:376:ASN:OD1	1:B:378:TYR:HB3	2.20	0.41
1:D:376:ASN:OD1	1:D:378:TYR:HB3	2.20	0.41
1:A:32:GLY:H	1:A:319:ASN:CG	2.24	0.41
1:B:78:ILE:C	1:B:79:LEU:HD12	2.41	0.41
1:C:291:HIS:CD2	1:C:316:ILE:H	2.39	0.41
1:C:394:PHE:CE1	1:C:460:ASN:ND2	2.89	0.41
1:E:84:TRP:CE3	1:E:122:GLU:HA	2.55	0.41
1:A:299:VAL:O	1:A:299:VAL:HG12	2.20	0.41
1:C:250:TYR:CE1	1:C:292:PHE:HA	2.56	0.41
1:C:312:ARG:HA	1:C:313:PRO:HD2	1.30	0.41
1:C:132:VAL:HG11	1:C:138:GLY:HA2	2.02	0.41
1:C:13:LEU:HB3	1:C:165:VAL:HG11	2.03	0.41
1:C:374:LEU:HA	1:C:374:LEU:HD23	1.78	0.41
1:D:29:ASN:ND2	1:D:314:ILE:HG13	2.36	0.41
1:D:344:GLY:N	1:D:349:ASN:HA	2.35	0.41
1:C:30:ASP:HB3	1:C:321:ASN:HB2	2.03	0.41
1:C:393:ASP:CG	1:C:396:VAL:HG13	2.41	0.41
1:C:462:LYS:HE3	1:C:462:LYS:HB2	1.70	0.41
1:D:8:SER:N	1:D:31:PRO:HG3	2.36	0.41
1:D:446:GLN:OE1	1:D:449:LEU:HD23	2.21	0.41
1:E:347:THR:HG21	1:E:392:TYR:CE1	2.56	0.41
1:E:40:ARG:HD2	1:E:365:TYR:HA	2.02	0.41
1:B:305:GLN:HA	1:B:308:LYS:HD3	2.03	0.41
1:B:343:TYR:HA	1:B:344:GLY:HA3	1.84	0.41
1:B:83:ILE:HG23	1:B:83:ILE:O	2.21	0.41
1:E:465:TYR:OH	1:E:468:ASN:HA	2.21	0.41
1:B:4:ARG:NH1	1:B:57:ILE:HG21	2.35	0.41
1:B:4:ARG:CG	1:B:5:ILE:H	2.30	0.41
1:C:74:ILE:CG1	1:C:323:HIS:CE1	3.03	0.41
1:C:441:VAL:O	1:C:445:LYS:HB2	2.21	0.41
1:D:312:ARG:HH22	1:D:318:ARG:HD2	1.85	0.41
1:E:220:LEU:HA	1:E:220:LEU:HD23	1.91	0.41
1:E:458:SER:O	1:E:462:LYS:HD2	2.21	0.41
1:E:8:SER:HB2	1:E:243:TYR:OH	2.21	0.41
1:A:343:TYR:HA	1:A:344:GLY:HA3	1.89	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:291:HIS:NE2	1:C:313:PRO:CB	2.77	0.40
1:E:317:ASN:N	1:E:318:ARG:CB	2.79	0.40
1:E:78:ILE:HA	1:E:78:ILE:HD12	1.95	0.40
1:A:262:ASP:O	1:A:264:PRO:HD3	2.22	0.40
1:A:295:THR:CG2	1:C:310:LEU:HD21	2.51	0.40
1:A:3:LYS:HE2	1:B:398:MET:HA	2.02	0.40
1:B:299:VAL:N	1:B:300:TYR:HA	2.36	0.40
1:D:152:TYR:CD1	1:D:153:GLU:HG3	2.55	0.40
1:D:309:THR:HB	1:D:310:LEU:H	1.70	0.40
1:D:462:LYS:HG3	1:D:465:TYR:OH	2.21	0.40
1:A:51:ARG:HD3	5:A:639:HOH:O	2.20	0.40
1:A:86:ALA:HB1	1:A:99:THR:HG21	2.03	0.40
1:D:13:LEU:HB3	1:D:165:VAL:HG11	2.03	0.40
1:E:362:PRO:HD3	5:E:653:HOH:O	2.22	0.40
1:A:57:ILE:HD13	1:A:80:THR:HG22	2.04	0.40
1:B:297:TYR:HD1	1:B:307:ASP:O	2.03	0.40
1:B:433:ASN:OD1	1:B:437:LYS:NZ	2.55	0.40
1:C:316:ILE:CG1	1:C:320:HIS:CE1	3.00	0.40
1:D:72:THR:OG1	1:D:339:HIS:CE1	2.74	0.40
1:B:291:HIS:O	1:B:292:PHE:HB2	2.22	0.40
1:E:296:LYS:HZ2	1:E:297:TYR:HB2	1.86	0.40
1:E:393:ASP:HA	1:E:396:VAL:HG23	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	465/469 (99%)	418 (90%)	41 (9%)	6 (1%)	12	19
1	B	465/469 (99%)	410 (88%)	46 (10%)	9 (2%)	8	12
1	C	465/469 (99%)	414 (89%)	40 (9%)	11 (2%)	6	8

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	465/469 (99%)	416 (90%)	44 (10%)	5 (1%)	14	23
1	E	465/469 (99%)	410 (88%)	48 (10%)	7 (2%)	10	16
All	All	2325/2345 (99%)	2068 (89%)	219 (9%)	38 (2%)	9	15

All (38) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	6	LYS
1	A	77	SER
1	A	468	ASN
1	B	5	ILE
1	B	6	LYS
1	B	295	THR
1	B	465	TYR
1	C	295	THR
1	C	304	SER
1	C	309	THR
1	C	317	ASN
1	C	468	ASN
1	D	295	THR
1	E	296	LYS
1	E	304	SER
1	E	305	GLN
1	A	296	LYS
1	A	309	THR
1	B	35	ALA
1	B	319	ASN
1	B	468	ASN
1	C	465	TYR
1	D	318	ARG
1	A	467	LEU
1	C	305	GLN
1	E	34	GLU
1	D	79	LEU
1	E	467	LEU
1	B	467	LEU
1	C	292	PHE
1	C	313	PRO
1	E	292	PHE
1	C	37	ASP
1	C	75	PRO

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Mol	Chain	Res	Type
1	B	83	ILE
1	E	75	PRO
1	D	83	ILE
1	D	190	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	413/415 (100%)	401 (97%)	12 (3%)	42	66
1	B	413/415 (100%)	409 (99%)	4 (1%)	76	89
1	C	413/415 (100%)	406 (98%)	7 (2%)	60	81
1	D	413/415 (100%)	408 (99%)	5 (1%)	71	87
1	E	413/415 (100%)	398 (96%)	15 (4%)	35	58
All	All	2065/2075 (100%)	2022 (98%)	43 (2%)	53	76

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	79	LEU
1	A	80	THR
1	A	295	THR
1	A	308	LYS
1	A	314	ILE
1	A	316	ILE
1	A	317	ASN
1	A	319	ASN
1	A	366	LYS
1	A	384	THR
1	A	399	ARG
1	A	463	LEU
1	B	293	GLU
1	B	312	ARG
1	B	314	ILE

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Mol	Chain	Res	Type
1	B	396	VAL
1	C	63	LYS
1	C	83	ILE
1	C	291	HIS
1	C	320	HIS
1	C	393	ASP
1	C	399	ARG
1	C	469	ASP
1	D	3	LYS
1	D	33	HIS
1	D	308	LYS
1	D	310	LEU
1	D	467	LEU
1	E	36	LEU
1	E	40	ARG
1	E	47	GLU
1	E	51	ARG
1	E	63	LYS
1	E	73	SER
1	E	300	TYR
1	E	316	ILE
1	E	319	ASN
1	E	320	HIS
1	E	359	ASN
1	E	384	THR
1	E	393	ASP
1	E	425	LYS
1	E	459	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	291	HIS
1	A	294	ASN
1	A	317	ASN
1	A	339	HIS
1	A	367	ASN
1	B	33	HIS
1	B	49	GLN
1	B	76	ASN
1	B	319	ASN
1	B	330	ASN

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Mol	Chain	Res	Type
1	B	339	HIS
1	C	81	ASN
1	C	320	HIS
1	D	49	GLN
1	D	81	ASN
1	D	339	HIS
1	D	367	ASN
1	D	460	ASN
1	E	76	ASN
1	E	359	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 7 are monoatomic - leaving 6 for Mogul analysis.

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	EDO	C	503	-	3,3,3	0.57	0	2,2,2	0.17	0
3	EDO	A	503	-	3,3,3	0.49	0	2,2,2	0.17	0
3	EDO	C	504	-	3,3,3	0.74	0	2,2,2	0.32	0
3	EDO	A	504	-	3,3,3	0.50	0	2,2,2	0.27	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	EDO	A	505	-	3,3,3	0.71	0	2,2,2	0.34	0
4	ACT	B	502	-	1,3,3	2.17	1 (100%)	0,3,3	0.00	-

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	EDO	A	504	-	-	0/1/1/1	-
3	EDO	A	505	-	-	0/1/1/1	-
3	EDO	A	503	-	-	1/1/1/1	-
3	EDO	C	504	-	-	1/1/1/1	-
3	EDO	C	503	-	-	1/1/1/1	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	502	ACT	CH3-C	2.17	1.51	1.48

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	504	EDO	O1-C1-C2-O2
3	A	503	EDO	O1-C1-C2-O2
3	C	503	EDO	O1-C1-C2-O2

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	503	EDO	1	0
3	C	504	EDO	2	0
3	A	504	EDO	2	0

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	467/469 (99%)	0.39	53 (11%) 5 4	21, 35, 100, 125	0
1	B	467/469 (99%)	0.56	66 (14%) 2 2	24, 38, 108, 130	0
1	C	467/469 (99%)	0.63	61 (13%) 3 2	25, 42, 106, 128	0
1	D	467/469 (99%)	0.61	61 (13%) 3 2	29, 45, 109, 129	0
1	E	467/469 (99%)	0.58	59 (12%) 3 3	27, 45, 105, 131	0
All	All	2335/2345 (99%)	0.55	300 (12%) 3 3	21, 42, 106, 131	0

All (300) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	32	GLY	16.6
1	B	32	GLY	16.1
1	C	35	ALA	13.9
1	A	468	ASN	13.8
1	D	79	LEU	13.6
1	D	32	GLY	13.5
1	C	468	ASN	13.4
1	B	310	LEU	13.0
1	B	309	THR	12.8
1	A	310	LEU	12.8
1	B	303	GLY	12.7
1	E	35	ALA	12.6
1	D	469	ASP	12.2
1	D	468	ASN	12.0
1	C	300	TYR	12.0
1	E	82	GLY	11.7
1	A	469	ASP	11.5
1	D	33	HIS	11.3
1	E	467	LEU	11.1
1	D	300	TYR	10.8

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Mol	Chain	Res	Type	RSRZ
1	E	33	HIS	10.8
1	E	303	GLY	10.7
1	D	304	SER	10.5
1	D	82	GLY	10.2
1	B	468	ASN	10.1
1	A	303	GLY	9.7
1	C	301	GLY	9.7
1	C	467	LEU	9.6
1	B	469	ASP	9.6
1	A	33	HIS	9.5
1	C	469	ASP	9.5
1	E	300	TYR	9.4
1	A	300	TYR	9.3
1	D	80	THR	9.1
1	A	295	THR	9.1
1	E	312	ARG	9.1
1	E	80	THR	9.1
1	D	301	GLY	9.1
1	C	302	SER	8.9
1	D	309	THR	8.9
1	E	297	TYR	8.8
1	C	33	HIS	8.6
1	C	304	SER	8.6
1	C	309	THR	8.6
1	E	309	THR	8.6
1	E	469	ASP	8.5
1	E	36	LEU	8.5
1	B	81	ASN	8.5
1	B	306	SER	8.4
1	B	467	LEU	8.3
1	A	80	THR	8.2
1	E	301	GLY	8.2
1	B	34	GLU	8.1
1	E	311	PHE	8.0
1	E	468	ASN	7.9
1	B	80	THR	7.9
1	D	467	LEU	7.9
1	D	34	GLU	7.8
1	A	81	ASN	7.8
1	E	81	ASN	7.7
1	D	305	GLN	7.7
1	C	310	LEU	7.7

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Mol	Chain	Res	Type	RSRZ
1	C	77	SER	7.6
1	B	304	SER	7.5
1	D	78	ILE	7.5
1	D	465	TYR	7.4
1	E	302	SER	7.4
1	D	303	GLY	7.4
1	C	312	ARG	7.2
1	A	34	GLU	7.2
1	E	465	TYR	7.2
1	B	35	ALA	7.1
1	D	295	THR	7.1
1	C	81	ASN	7.1
1	E	34	GLU	7.0
1	C	295	THR	7.0
1	D	306	SER	6.9
1	B	300	TYR	6.8
1	C	314	ILE	6.8
1	D	368	ALA	6.8
1	B	368	ALA	6.7
1	B	294	ASN	6.7
1	C	296	LYS	6.7
1	C	297	TYR	6.7
1	A	306	SER	6.6
1	E	390	THR	6.6
1	D	35	ALA	6.6
1	D	31	PRO	6.6
1	C	305	GLN	6.4
1	B	302	SER	6.4
1	C	80	THR	6.3
1	D	312	ARG	6.1
1	E	78	ILE	6.1
1	A	467	LEU	6.1
1	C	3	LYS	6.1
1	E	304	SER	6.0
1	A	301	GLY	6.0
1	D	36	LEU	5.9
1	B	297	TYR	5.8
1	D	308	LYS	5.8
1	A	4	ARG	5.8
1	A	312	ARG	5.7
1	D	310	LEU	5.7
1	E	307	ASP	5.7

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Mol	Chain	Res	Type	RSRZ
1	D	294	ASN	5.6
1	C	311	PHE	5.6
1	A	314	ILE	5.6
1	B	308	LYS	5.5
1	B	305	GLN	5.5
1	B	464	ARG	5.4
1	B	313	PRO	5.4
1	B	314	ILE	5.4
1	C	32	GLY	5.4
1	B	33	HIS	5.4
1	A	464	ARG	5.3
1	D	313	PRO	5.3
1	C	79	LEU	5.3
1	D	390	THR	5.2
1	E	310	LEU	5.2
1	A	297	TYR	5.2
1	B	312	ARG	5.2
1	D	314	ILE	5.1
1	B	3	LYS	5.0
1	E	308	LYS	5.0
1	D	297	TYR	5.0
1	D	311	PHE	5.0
1	C	299	VAL	5.0
1	C	303	GLY	5.0
1	C	393	ASP	4.9
1	A	294	ASN	4.9
1	A	309	THR	4.9
1	A	3	LYS	4.9
1	B	82	GLY	4.9
1	D	315	GLY	4.9
1	E	83	ILE	4.9
1	A	390	THR	4.9
1	A	302	SER	4.8
1	C	307	ASP	4.8
1	C	36	LEU	4.8
1	C	4	ARG	4.8
1	E	305	GLN	4.8
1	E	306	SER	4.8
1	A	32	GLY	4.7
1	B	390	THR	4.6
1	B	37	ASP	4.6
1	E	461	MET	4.6

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Mol	Chain	Res	Type	RSRZ
1	A	313	PRO	4.5
1	A	368	ALA	4.5
1	C	315	GLY	4.5
1	A	315	GLY	4.5
1	E	3	LYS	4.5
1	E	314	ILE	4.5
1	C	308	LYS	4.5
1	B	295	THR	4.5
1	B	465	TYR	4.4
1	E	316	ILE	4.4
1	B	4	ARG	4.4
1	B	5	ILE	4.4
1	E	464	ARG	4.4
1	C	390	THR	4.4
1	E	295	THR	4.4
1	C	316	ILE	4.3
1	B	36	LEU	4.3
1	D	3	LYS	4.3
1	D	77	SER	4.3
1	A	296	LYS	4.2
1	D	81	ASN	4.2
1	D	464	ARG	4.2
1	E	313	PRO	4.2
1	B	301	GLY	4.2
1	C	294	ASN	4.2
1	C	466	ASN	4.2
1	B	296	LYS	4.1
1	D	307	ASP	4.1
1	C	395	TYR	4.0
1	A	316	ILE	4.0
1	C	319	ASN	4.0
1	A	31	PRO	4.0
1	C	306	SER	4.0
1	D	461	MET	3.9
1	E	294	ASN	3.9
1	C	465	TYR	3.9
1	E	466	ASN	3.8
1	D	369	THR	3.8
1	C	313	PRO	3.8
1	A	35	ALA	3.8
1	E	77	SER	3.8
1	E	367	ASN	3.8

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Mol	Chain	Res	Type	RSRZ
1	B	79	LEU	3.8
1	C	464	ARG	3.7
1	A	292	PHE	3.7
1	B	293	GLU	3.7
1	D	4	ARG	3.7
1	E	292	PHE	3.6
1	D	466	ASN	3.6
1	D	5	ILE	3.6
1	B	31	PRO	3.6
1	B	461	MET	3.6
1	D	318	ARG	3.6
1	D	293	GLU	3.6
1	B	307	ASP	3.6
1	E	366	LYS	3.6
1	C	34	GLU	3.5
1	D	302	SER	3.5
1	B	319	ASN	3.5
1	B	299	VAL	3.5
1	A	307	ASP	3.5
1	B	76	ASN	3.4
1	C	392	TYR	3.4
1	B	311	PHE	3.4
1	B	77	SER	3.4
1	D	319	ASN	3.4
1	B	364	GLN	3.4
1	B	363	VAL	3.3
1	E	363	VAL	3.3
1	D	393	ASP	3.2
1	B	78	ILE	3.2
1	B	348	PHE	3.2
1	D	296	LYS	3.2
1	C	394	PHE	3.1
1	E	368	ALA	3.1
1	C	344	GLY	3.1
1	B	393	ASP	3.1
1	D	363	VAL	3.1
1	C	5	ILE	3.1
1	D	460	ASN	3.1
1	B	39	GLN	3.1
1	C	40	ARG	3.1
1	E	315	GLY	3.0
1	A	305	GLN	3.0

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Mol	Chain	Res	Type	RSRZ
1	E	392	TYR	3.0
1	E	463	LEU	3.0
1	A	299	VAL	3.0
1	A	320	HIS	3.0
1	E	42	VAL	3.0
1	E	31	PRO	2.9
1	D	47	GLU	2.9
1	A	304	SER	2.9
1	B	392	TYR	2.9
1	C	298	ASP	2.9
1	C	82	GLY	2.8
1	C	6	LYS	2.8
1	C	391	ASP	2.7
1	C	396	VAL	2.7
1	A	311	PHE	2.7
1	B	343	TYR	2.7
1	B	367	ASN	2.7
1	B	369	THR	2.7
1	E	395	TYR	2.7
1	A	308	LYS	2.7
1	B	391	ASP	2.7
1	B	315	GLY	2.6
1	C	78	ILE	2.6
1	D	463	LEU	2.6
1	B	38	PRO	2.6
1	A	82	GLY	2.6
1	E	298	ASP	2.6
1	C	50	PRO	2.6
1	D	427	ILE	2.5
1	E	296	LYS	2.5
1	C	83	ILE	2.5
1	A	298	ASP	2.5
1	D	40	ARG	2.5
1	A	293	GLU	2.5
1	B	330	ASN	2.5
1	B	463	LEU	2.5
1	A	461	MET	2.5
1	A	79	LEU	2.5
1	A	392	TYR	2.5
1	E	425	LYS	2.4
1	E	4	ARG	2.4
1	C	292	PHE	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	361	THR	2.4
1	E	317	ASN	2.4
1	A	369	THR	2.3
1	D	292	PHE	2.3
1	D	76	ASN	2.3
1	C	368	ALA	2.3
1	B	320	HIS	2.3
1	D	392	TYR	2.3
1	A	78	ILE	2.3
1	B	466	ASN	2.2
1	B	394	PHE	2.2
1	C	369	THR	2.2
1	E	396	VAL	2.2
1	E	393	ASP	2.2
1	A	77	SER	2.2
1	A	36	LEU	2.2
1	C	66	ASP	2.1
1	A	76	ASN	2.1
1	A	5	ILE	2.1
1	A	319	ASN	2.1
1	E	79	LEU	2.1
1	D	6	LYS	2.1
1	B	30	ASP	2.1
1	D	291	HIS	2.1
1	C	323	HIS	2.1
1	A	367	ASN	2.1
1	D	30	ASP	2.0
1	E	391	ASP	2.0

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	EDO	A	504	4/4	0.74	0.24	37,37,42,42	0
2	CO	C	501	1/1	0.77	0.10	90,90,90,90	0
3	EDO	A	505	4/4	0.78	0.25	30,34,38,43	0
2	CO	D	501	1/1	0.79	0.09	91,91,91,91	0
3	EDO	C	504	4/4	0.80	0.20	37,41,46,46	0
2	CO	B	501	1/1	0.84	0.07	81,81,81,81	0
2	CO	A	501	1/1	0.89	0.37	85,85,85,85	0
2	CO	C	502	1/1	0.93	0.05	70,70,70,70	0
4	ACT	B	502	4/4	0.94	0.15	33,46,47,47	0
3	EDO	C	503	4/4	0.95	0.12	36,39,39,44	0
3	EDO	A	503	4/4	0.98	0.13	29,32,35,35	0
2	CO	E	501	1/1	0.98	0.15	60,60,60,60	0
2	CO	A	502	1/1	0.99	0.09	50,50,50,50	0

6.5 Other polymers [i](#)

There are no such residues in this entry.