



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:31 AM UTC

PDB ID : 2SCU / pdb_00002scu
Title : A detailed description of the structure of Succinyl-CoA synthetase from Escherichia coli
Authors : Fraser, M.E.; Wolodko, W.T.; James, M.N.G.; Bridger, W.A.
Deposited on : 1998-09-24
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

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

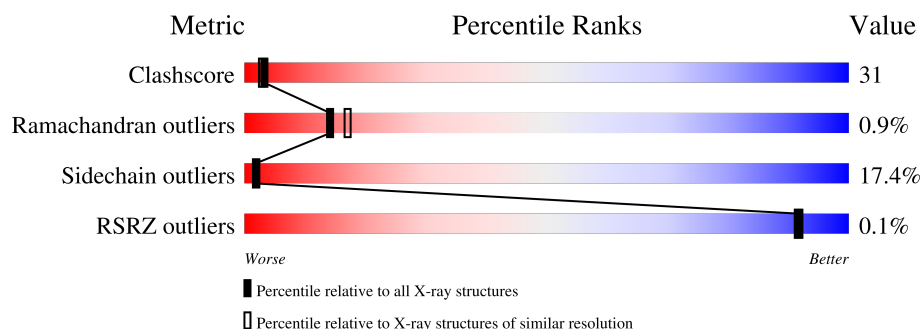
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	288	
1	D	288	
2	B	388	
2	E	388	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 10508 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 PROTEIN (SUCCINYL-COA LIGASE).

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	286	Total	C	N	O	P	S	0	0	0
			2065	1307	345	401	1	11			
1	D	286	Total	C	N	O	P	S	0	0	0
			2065	1307	345	401	1	11			

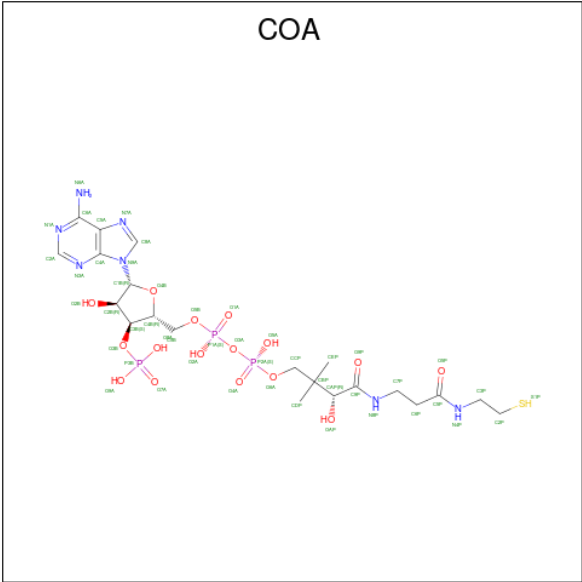
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	246	NEP	HIS	modified residue	UNP P07459
D	246	NEP	HIS	modified residue	UNP P07459

- Molecule 2 is a protein called PROTEIN (SUCCINYL-COA LIGASE).

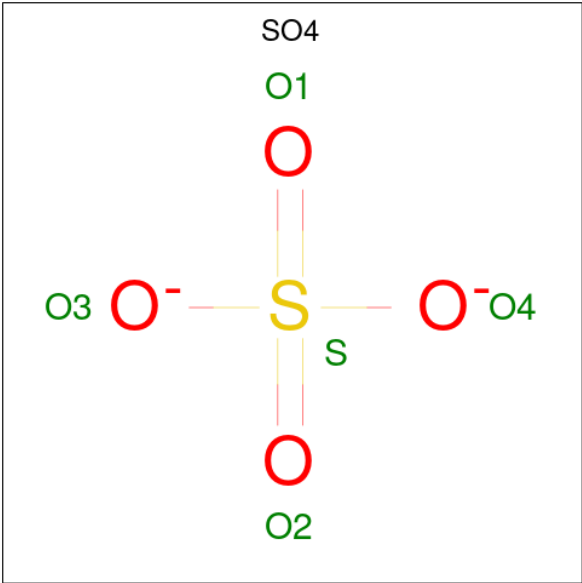
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	385	Total	C	N	O	S	0	0	0
			2885	1823	505	544	13			
2	E	385	Total	C	N	O	S	0	0	0
			2885	1823	505	544	13			

- Molecule 3 is COENZYME A (CCD ID: COA) (formula: $C_{21}H_{36}N_7O_{16}P_3S$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
3	D	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	O S	0	0
			5	4 1		
4	E	1	Total	O S	0	0
			5	4 1		

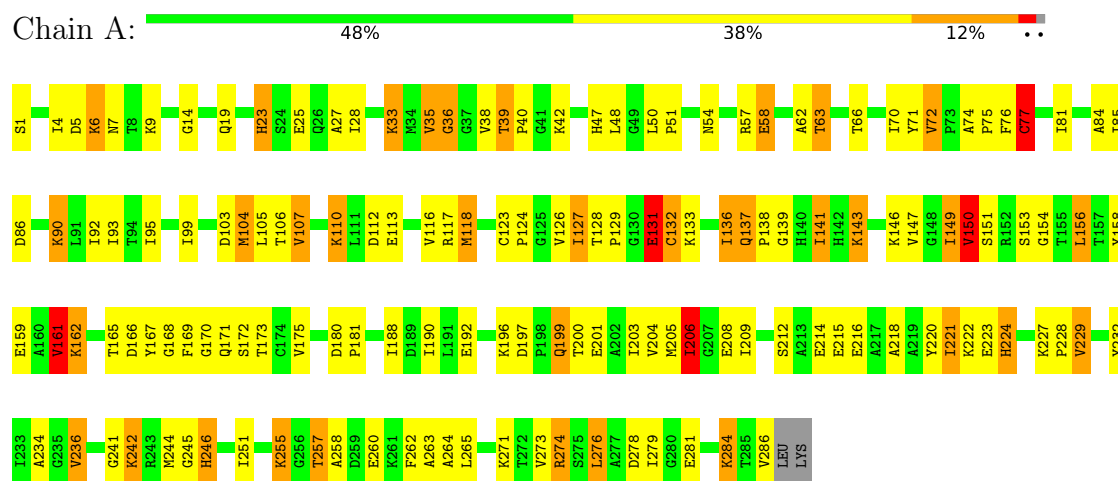
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	100	Total 100	O 100	0	0
5	B	169	Total 169	O 169	0	0
5	D	91	Total 91	O 91	0	0
5	E	142	Total 142	O 142	0	0

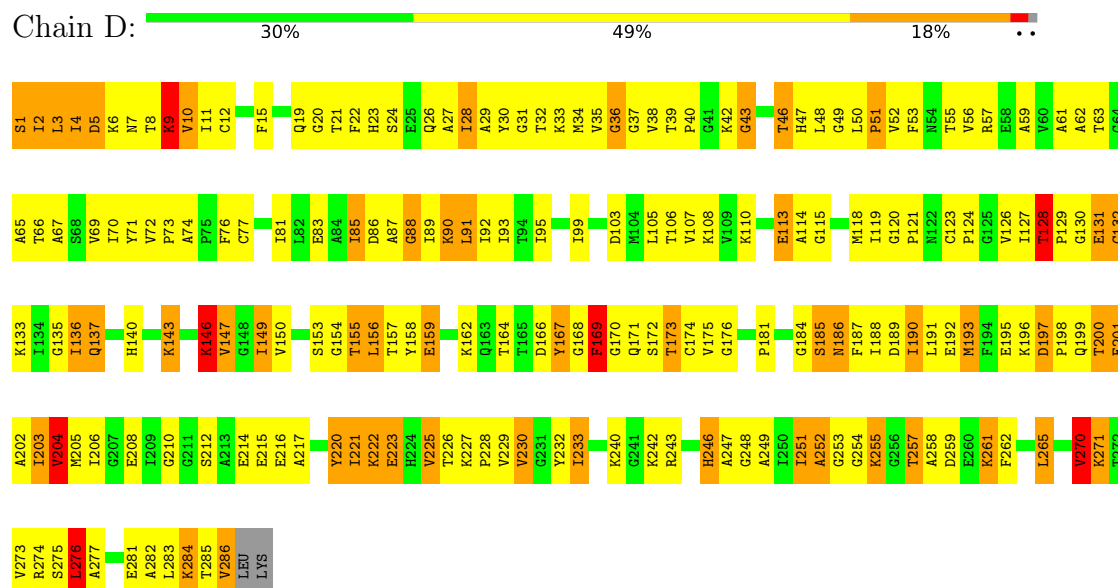
3 Residue-property plots

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

• Molecule 1: PROTEIN (SUCCINYL-COA LIGASE)

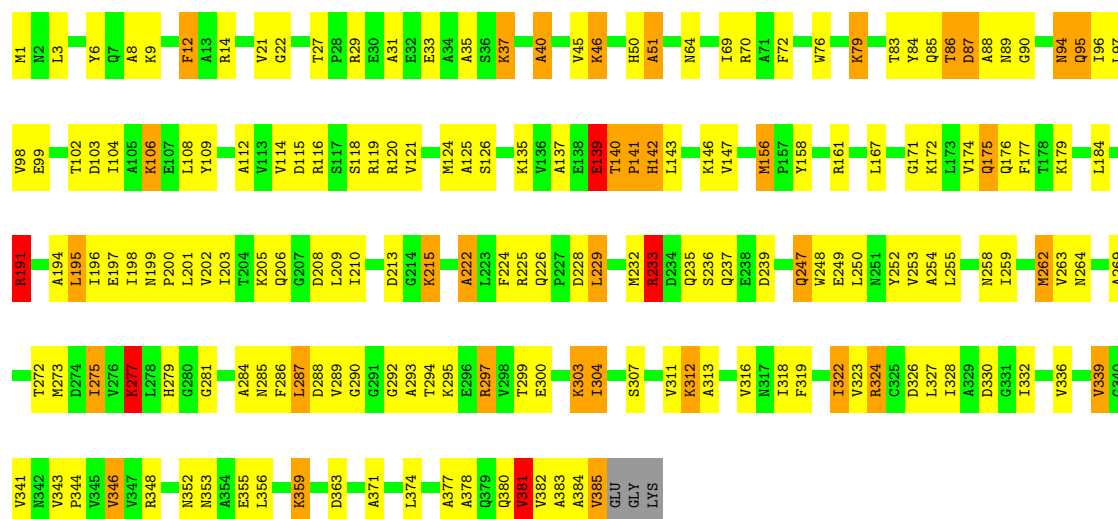


• Molecule 1: PROTEIN (SUCCINYL-COA LIGASE)

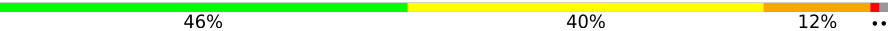


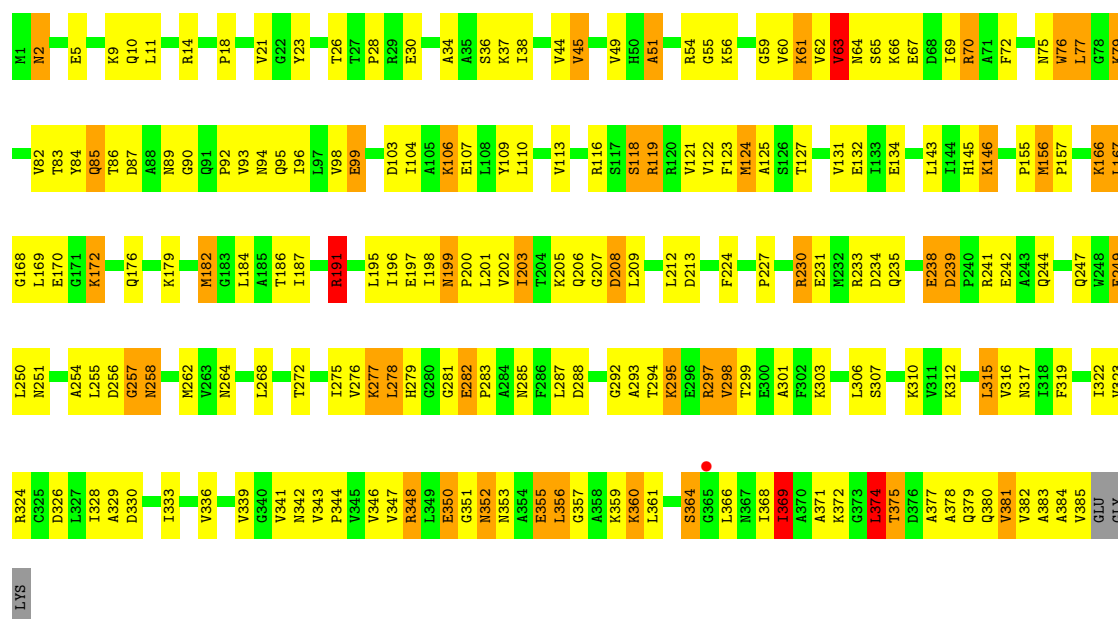
• Molecule 2: PROTEIN (SUCCINYL-COA LIGASE)

Chain B:  52% 37% 9% ..



• Molecule 2: PROTEIN (SUCCINYL-COA LIGASE)

Chain E:  46% 40% 12% ..



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 2 2	Depositor
Cell constants a, b, c, α , β , γ	98.68Å 98.68Å 403.76Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.30 8.00 – 2.30	Depositor EDS
% Data completeness (in resolution range)	93.0 (8.00-2.30) 90.2 (8.00-2.30)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.85 (at 2.29Å)	Xtriage
Refinement program	TNT 5EB	Depositor
R, R_{free}	0.195 , (Not available) 0.189 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	31.1	Xtriage
Anisotropy	0.158	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.18 , 70.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10508	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.16% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, NEP, COA

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	1.50	11/2083 (0.5%)	1.62	36/2820 (1.3%)
1	D	1.42	8/2083 (0.4%)	1.68	41/2820 (1.5%)
2	B	1.48	14/2927 (0.5%)	1.57	40/3961 (1.0%)
2	E	1.45	20/2927 (0.7%)	1.57	35/3961 (0.9%)
All	All	1.46	53/10020 (0.5%)	1.60	152/13562 (1.1%)

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	1

All (53) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	222	ALA	CA-CB	-8.99	1.38	1.53
2	E	69	ILE	CA-CB	-8.19	1.44	1.54
1	D	249	ALA	CA-CB	-8.05	1.42	1.52
2	B	146	LYS	CA-C	-8.02	1.42	1.52
2	B	232	MET	SD-CE	-7.94	1.59	1.79
2	E	121	VAL	CA-CB	7.72	1.63	1.54
1	A	84	ALA	CA-C	7.39	1.62	1.52
2	E	258	ASN	CA-C	-7.38	1.44	1.53
2	B	114	VAL	CA-CB	-7.23	1.45	1.54
2	B	156	MET	SD-CE	-7.17	1.61	1.79
2	B	228	ASP	CA-C	-7.12	1.43	1.52
1	A	104	MET	SD-CE	-6.96	1.62	1.79
1	D	270	VAL	CA-CB	6.52	1.62	1.54
2	E	182	MET	SD-CE	-6.42	1.63	1.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	116	VAL	CA-CB	-6.31	1.46	1.54
1	D	85	ILE	CA-CB	-6.29	1.47	1.54
2	E	26	THR	CA-CB	-6.27	1.44	1.53
2	B	289	VAL	CA-CB	-6.00	1.46	1.53
2	E	113	VAL	CA-CB	-5.99	1.46	1.54
2	E	77	LEU	CA-C	-5.96	1.45	1.52
2	E	156	MET	SD-CE	-5.88	1.64	1.79
1	D	258	ALA	CA-CB	-5.87	1.43	1.53
2	B	228	ASP	C-O	-5.86	1.17	1.24
2	E	23	TYR	CA-C	-5.73	1.45	1.52
1	A	150	VAL	C-O	-5.68	1.18	1.24
1	A	150	VAL	CA-C	-5.65	1.45	1.52
2	E	203	ILE	CA-CB	-5.62	1.47	1.54
2	B	76	TRP	CA-C	-5.56	1.45	1.52
2	B	316	VAL	CA-CB	-5.56	1.47	1.54
1	D	115	GLY	CA-C	5.54	1.57	1.51
2	E	30	GLU	CA-C	-5.52	1.45	1.52
2	E	92	PRO	CA-C	-5.49	1.46	1.52
2	E	23	TYR	N-CA	-5.48	1.39	1.46
2	E	336	VAL	CA-CB	-5.34	1.47	1.54
1	A	62	ALA	C-O	-5.29	1.18	1.24
2	E	118	SER	CA-C	-5.27	1.45	1.52
2	E	301	ALA	CA-CB	-5.24	1.45	1.53
1	A	263	ALA	CA-CB	-5.22	1.44	1.53
2	E	369	ILE	CA-CB	5.21	1.60	1.53
1	D	74	ALA	CA-CB	-5.21	1.47	1.53
2	B	198	ILE	CA-C	5.18	1.58	1.52
1	A	260	GLU	CA-C	-5.16	1.46	1.52
1	D	21	THR	CA-CB	-5.14	1.44	1.53
2	B	112	ALA	C-O	5.12	1.30	1.23
2	B	35	ALA	CA-CB	-5.10	1.45	1.53
2	B	381	VAL	CA-CB	-5.10	1.48	1.54
1	A	232	TYR	CA-C	5.09	1.58	1.52
2	E	208	ASP	CA-C	-5.08	1.46	1.52
1	D	113	GLU	C-O	-5.05	1.17	1.24
1	A	23	HIS	CA-CB	-5.03	1.44	1.53
2	E	34	ALA	CA-CB	-5.02	1.45	1.53
1	A	77	CYS	N-CA	-5.02	1.40	1.46
2	E	93	VAL	CA-CB	-5.02	1.48	1.54

All (152) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	374	LEU	N-CA-C	12.68	126.49	111.02
2	E	257	GLY	N-CA-C	-10.30	96.28	110.80
1	D	265	LEU	N-CA-C	-9.70	99.76	111.69
2	E	359	LYS	N-CA-C	-9.63	100.73	111.14
2	B	40	ALA	N-CA-C	-9.53	96.41	110.52
1	A	284	LYS	N-CA-C	-8.88	101.68	111.36
2	B	64	ASN	N-CA-C	8.56	123.95	113.17
2	E	380	GLN	N-CA-C	8.41	120.07	111.07
2	B	37	LYS	N-CA-C	-8.35	101.96	112.90
1	A	262	PHE	N-CA-C	-8.32	101.91	110.97
2	E	63	VAL	N-CA-C	8.12	120.66	108.80
1	A	126	VAL	N-CA-C	8.01	119.66	108.12
1	A	103	ASP	N-CA-C	-7.90	102.75	111.36
1	D	128	THR	N-CA-C	-7.81	94.18	109.10
2	B	381	VAL	CB-CA-C	-7.79	102.00	111.97
1	D	2	ILE	N-CA-C	7.62	121.52	110.09
1	A	206	ILE	CB-CA-C	-7.57	99.91	110.96
1	D	4	ILE	N-CA-C	7.55	118.04	108.82
2	B	259	ILE	N-CA-C	7.41	118.54	107.80
1	D	70	ILE	N-CA-C	7.38	118.50	107.80
1	D	217	ALA	N-CA-C	-7.36	102.95	112.23
2	B	21	VAL	N-CA-C	-7.32	99.23	108.89
1	D	203	ILE	N-CA-C	7.29	118.37	108.17
1	D	257	THR	N-CA-C	-7.28	101.14	110.53
1	D	175	VAL	N-CA-C	7.26	118.36	107.75
2	E	351	GLY	N-CA-C	7.19	122.37	112.52
2	B	226	GLN	CA-C-N	7.16	128.78	119.84
2	B	226	GLN	C-N-CA	7.16	128.78	119.84
1	A	14	GLY	CA-C-N	7.10	129.79	120.28
1	A	14	GLY	C-N-CA	7.10	129.79	120.28
1	D	103	ASP	N-CA-C	-7.05	103.02	111.69
2	B	176	GLN	N-CA-C	-7.04	103.54	111.14
2	E	76	TRP	N-CA-C	6.97	121.83	113.12
2	B	228	ASP	CB-CA-C	-6.96	99.24	110.79
2	E	113	VAL	CB-CA-C	-6.94	99.91	111.29
1	A	107	VAL	N-CA-C	-6.92	103.73	110.72
1	D	220	TYR	N-CA-C	-6.91	104.11	112.54
1	A	38	VAL	N-CA-C	6.83	117.96	108.12
2	E	201	LEU	N-CA-C	-6.82	97.43	108.41
1	A	150	VAL	CB-CA-C	-6.81	100.01	110.50
1	D	262	PHE	N-CA-C	-6.77	103.59	110.97
2	B	104	ILE	N-CA-C	6.75	118.18	107.98
2	E	85	GLN	OE1-CD-NE2	6.75	129.35	122.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	139	GLY	N-CA-C	6.74	121.88	114.40
2	E	285	ASN	N-CA-C	6.66	118.98	108.79
2	B	201	LEU	N-CA-C	-6.60	98.48	109.24
1	A	150	VAL	N-CA-C	-6.56	98.69	108.46
2	E	64	ASN	N-CA-C	6.53	122.15	112.94
1	A	149	ILE	N-CA-C	6.52	117.24	108.11
2	E	96	ILE	N-CA-C	-6.44	99.20	108.48
1	D	270	VAL	CB-CA-C	6.41	120.02	110.98
2	B	8	ALA	N-CA-C	-6.40	104.23	111.14
1	D	193	MET	N-CA-C	-6.39	104.53	112.90
2	B	191	ARG	CB-CA-C	-6.38	100.42	110.94
1	A	161	VAL	N-CA-C	-6.35	104.33	110.42
2	E	342	ASN	N-CA-C	6.29	120.16	112.23
2	E	93	VAL	CB-CA-C	-6.28	103.36	110.96
2	B	226	GLN	C-N-CD	-6.26	99.34	125.00
2	B	253	VAL	N-CA-C	-6.25	99.71	108.27
1	D	169	PHE	N-CA-C	6.23	124.07	110.80
2	B	86	THR	N-CA-C	-6.22	101.00	109.95
1	D	38	VAL	N-CA-C	6.20	116.95	107.77
2	B	147	VAL	N-CA-C	-6.17	99.70	108.65
1	D	159	GLU	N-CA-C	-6.16	104.19	111.03
1	A	188	ILE	N-CA-C	6.11	117.58	110.62
1	A	241	GLY	N-CA-C	6.11	123.75	115.32
2	E	230	ARG	N-CA-C	-6.10	104.63	111.28
1	D	36	GLY	N-CA-C	6.10	118.22	110.96
2	E	167	LEU	N-CA-C	-6.09	105.83	113.20
1	D	204	VAL	CB-CA-C	-6.08	102.64	110.98
2	B	239	ASP	N-CA-C	-6.08	100.56	109.50
2	B	297	ARG	NE-CZ-NH1	-6.01	115.49	121.50
1	D	273	VAL	CB-CA-C	-6.00	102.68	110.84
2	B	224	PHE	CA-C-N	-5.96	113.14	122.49
2	B	224	PHE	C-N-CA	-5.96	113.14	122.49
1	D	9	LYS	N-CA-C	-5.96	100.00	109.59
2	E	44	VAL	CA-C-N	-5.95	115.81	123.19
2	E	44	VAL	C-N-CA	-5.95	115.81	123.19
2	E	18	PRO	N-CA-C	5.92	120.20	110.55
2	B	27	THR	N-CA-C	-5.88	98.89	108.82
1	D	5	ASP	N-CA-C	5.88	115.60	107.73
2	E	191	ARG	NE-CZ-NH1	-5.88	115.62	121.50
1	D	88	GLY	N-CA-C	5.83	123.41	115.30
1	D	43	GLY	N-CA-C	-5.82	104.63	112.14
2	E	59	GLY	N-CA-C	-5.82	105.68	115.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	223	GLU	N-CA-C	5.80	120.35	113.16
1	A	199	GLN	CA-C-N	-5.79	114.95	123.05
1	A	199	GLN	C-N-CA	-5.79	114.95	123.05
1	A	149	ILE	CA-C-N	-5.78	114.90	122.94
1	A	149	ILE	C-N-CA	-5.78	114.90	122.94
2	E	208	ASP	N-CA-C	-5.77	100.29	109.23
2	B	139	GLU	N-CA-C	5.76	118.43	111.40
2	E	99	GLU	N-CA-C	5.73	118.58	109.81
1	A	127	ILE	N-CA-C	5.71	116.34	108.12
1	A	116	VAL	N-CA-C	-5.68	100.25	108.89
2	E	37	LYS	N-CA-C	-5.67	105.18	111.36
1	A	47	HIS	N-CA-C	-5.67	100.44	109.23
1	A	214	GLU	N-CA-C	-5.67	105.01	111.07
2	B	307	SER	N-CA-C	-5.67	105.25	111.82
2	B	46	LYS	N-CA-C	5.66	118.32	108.76
2	B	346	VAL	N-CA-C	-5.63	100.32	108.71
1	A	72	VAL	CB-CA-C	-5.63	104.35	110.37
1	D	253	GLY	N-CA-C	-5.61	108.12	115.47
1	A	220	TYR	N-CA-C	-5.61	105.55	112.90
2	E	186	THR	N-CA-C	5.59	117.05	111.07
1	D	83	GLU	N-CA-C	-5.55	105.23	111.28
2	E	239	ASP	N-CA-C	-5.54	101.22	109.42
2	B	51	ALA	N-CA-C	5.51	117.99	110.55
1	D	132	CYS	N-CA-C	5.49	118.14	108.75
2	E	198	ILE	CB-CA-C	-5.46	104.43	111.53
1	D	61	ALA	N-CA-C	-5.44	104.77	111.40
1	D	252	ALA	N-CA-C	5.42	117.57	108.73
1	D	131	GLU	N-CA-C	5.42	118.24	111.24
2	E	199	ASN	N-CA-CB	-5.40	103.58	111.20
1	A	112	ASP	N-CA-C	5.40	117.17	111.28
1	D	201	GLU	N-CA-C	5.38	119.01	112.23
1	A	85	ILE	CB-CA-C	-5.36	105.02	112.04
2	B	233	ARG	NE-CZ-NH1	-5.36	116.14	121.50
1	D	197	ASP	CA-C-N	5.35	126.53	119.84
1	D	197	ASP	C-N-CA	5.35	126.53	119.84
1	A	224	HIS	N-CA-C	5.34	120.97	113.02
2	B	124	MET	CB-CA-C	-5.34	99.94	109.71
2	B	194	ALA	N-CA-C	-5.33	107.43	114.31
2	E	66	LYS	N-CA-C	-5.30	105.51	111.28
1	A	27	ALA	N-CA-C	-5.28	105.19	111.69
2	B	72	PHE	N-CA-C	-5.26	104.98	111.40
1	A	131	GLU	N-CA-C	5.26	120.17	113.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	316	VAL	CB-CA-C	-5.25	104.02	111.21
1	A	162	LYS	N-CA-C	5.22	117.71	111.71
2	B	94	ASN	N-CA-C	-5.21	106.31	113.30
2	E	352	ASN	N-CA-C	5.21	116.66	109.15
1	A	58	GLU	N-CA-C	-5.16	105.55	111.07
1	A	36	GLY	N-CA-C	5.16	117.71	110.38
2	B	12	PHE	N-CA-C	-5.16	104.92	111.11
1	D	76	PHE	N-CA-C	-5.15	106.39	113.30
2	E	224	PHE	N-CA-C	-5.14	106.11	112.38
1	D	51	PRO	CA-C-N	-5.12	116.83	123.19
1	D	51	PRO	C-N-CA	-5.12	116.83	123.19
1	D	62	ALA	N-CA-C	5.11	119.09	113.21
1	D	258	ALA	N-CA-C	5.11	117.75	111.82
1	A	200	THR	CB-CA-C	5.11	118.57	110.19
1	A	63	THR	N-CA-C	5.10	120.50	113.97
2	B	174	VAL	CB-CA-C	-5.10	105.41	112.24
2	B	121	VAL	N-CA-C	-5.06	102.21	108.89
2	E	51	ALA	N-CA-C	5.06	117.21	110.53
1	D	146	LYS	CA-C-N	-5.05	116.58	123.10
1	D	146	LYS	C-N-CA	-5.05	116.58	123.10
2	B	142	HIS	N-CA-C	-5.04	107.13	113.28
2	B	171	GLY	N-CA-C	5.03	118.74	111.24
2	E	10	GLN	N-CA-CB	5.03	117.51	110.12
2	E	38	ILE	N-CA-C	-5.03	105.94	110.82
2	B	277	LYS	N-CA-C	-5.01	105.51	110.97

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	106	THR	Mainchain

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	2065	0	2116	105	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	2065	0	2116	213	0
2	B	2885	0	2941	156	0
2	E	2885	0	2941	158	0
3	A	48	0	32	5	0
3	D	48	0	32	2	0
4	B	5	0	0	0	0
4	E	5	0	0	1	0
5	A	100	0	0	8	0
5	B	169	0	0	11	0
5	D	91	0	0	2	0
5	E	142	0	0	9	0
All	All	10508	0	10178	616	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 31.

All (616) 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:D:66:THR:HB	1:D:90:LYS:HD3	1.27	1.14
1:D:203:ILE:HB	1:D:229:VAL:HG22	1.12	1.05
1:D:146:LYS:HB2	1:D:201:GLU:HG3	1.40	1.03
1:D:221:ILE:HA	1:D:225:VAL:HG23	1.38	1.03
1:A:4:ILE:HD12	1:A:132:CYS:HB3	1.40	1.01
2:E:306:LEU:HD11	2:E:341:VAL:HG22	1.44	0.98
2:E:103:ASP:HB3	2:E:205:LYS:HG3	1.47	0.95
2:B:312:LYS:HB3	2:B:385:VAL:HG22	1.51	0.93
1:D:93:ILE:HD13	1:D:119:ILE:HB	1.54	0.89
1:D:19:GLN:HG3	3:D:301:COA:H132	1.51	0.89
2:B:287:LEU:HD12	2:B:288:ASP:N	1.88	0.89
2:E:306:LEU:CD1	2:E:341:VAL:HG22	2.04	0.89
2:E:239:ASP:HB3	2:E:242:GLU:HG3	1.56	0.88
1:D:221:ILE:HA	1:D:225:VAL:CG2	2.04	0.87
1:D:7:ASN:HA	1:D:33:LYS:NZ	1.88	0.87
1:D:4:ILE:HD11	1:D:126:VAL:HG12	1.56	0.86
2:E:176:GLN:HE22	2:E:209:LEU:H	1.22	0.85
2:E:361:LEU:HD22	2:E:368:ILE:HG21	1.59	0.84
1:A:274:ARG:HG3	1:A:274:ARG:HH11	1.42	0.84
2:B:324:ARG:HH21	2:B:327:LEU:HD11	1.43	0.83
1:D:205:MET:HE1	1:D:265:LEU:HD21	1.61	0.82
1:D:203:ILE:HB	1:D:229:VAL:CG2	2.04	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:192:GLU:HB2	1:D:220:TYR:OH	1.81	0.81
1:D:66:THR:HB	1:D:90:LYS:CD	2.10	0.80
1:D:149:ILE:HG23	1:D:204:VAL:HB	1.63	0.80
1:A:6:LYS:HB3	1:A:131:GLU:HB3	1.63	0.80
1:D:265:LEU:O	1:D:270:VAL:HG23	1.82	0.79
2:E:235:GLN:HA	2:E:238:GLU:HG3	1.63	0.78
1:A:228:PRO:HB2	1:A:286:VAL:HG11	1.66	0.77
1:D:146:LYS:CB	1:D:201:GLU:HG3	2.12	0.77
2:E:103:ASP:HB3	2:E:205:LYS:CG	2.14	0.77
1:D:149:ILE:HD12	1:D:174:CYS:SG	2.24	0.77
2:E:254:ALA:O	2:E:255:LEU:HD23	1.84	0.77
1:D:3:LEU:HD21	1:D:193:MET:HE1	1.65	0.77
2:E:292:GLY:O	2:E:294:THR:HG23	1.85	0.77
1:D:271:LYS:NZ	1:D:285:THR:HG21	1.99	0.77
1:D:232:TYR:C	1:D:233:ILE:HD13	2.09	0.76
2:B:355:GLU:HG3	5:B:1246:HOH:O	1.83	0.76
1:D:93:ILE:CD1	1:D:119:ILE:HB	2.15	0.76
2:E:75:ASN:O	2:E:79:LYS:HD3	1.86	0.76
2:B:254:ALA:O	2:B:255:LEU:HD12	1.86	0.76
2:E:279:HIS:HE1	2:E:375:THR:HG23	1.50	0.76
1:D:5:ASP:HB2	1:D:131:GLU:OE2	1.86	0.76
2:B:205:LYS:HB2	2:B:206:GLN:NE2	2.01	0.75
1:D:8:THR:O	1:D:33:LYS:HB2	1.87	0.75
1:A:153:SER:HB3	1:A:246:NEP:HE1	1.67	0.75
2:E:124:MET:HE2	2:E:146:LYS:HD3	1.68	0.75
2:E:343:VAL:HB	2:E:344:PRO:HD2	1.69	0.75
2:B:324:ARG:HH21	2:B:327:LEU:CD1	1.99	0.74
2:E:124:MET:CE	2:E:146:LYS:HD3	2.16	0.74
1:A:19:GLN:HG3	3:A:300:COA:H132	1.69	0.74
1:D:7:ASN:HA	1:D:33:LYS:HZ2	1.50	0.74
2:E:381:VAL:O	2:E:385:VAL:HG23	1.86	0.74
1:D:147:VAL:HG23	1:D:170:GLY:O	1.88	0.73
2:B:51:ALA:CB	2:B:86:THR:HG22	2.18	0.73
1:D:2:ILE:HG12	1:D:173:THR:HG21	1.69	0.73
2:E:106:LYS:HG3	2:E:107:GLU:H	1.54	0.72
2:E:56:LYS:HG2	5:E:1365:HOH:O	1.89	0.72
1:A:223:GLU:HB3	1:A:224:HIS:CD2	2.24	0.72
1:D:127:ILE:HD12	1:D:133:LYS:HG3	1.70	0.72
2:B:249:GLU:OE1	2:E:70:ARG:NH2	2.23	0.71
1:D:66:THR:CB	1:D:90:LYS:HD3	2.15	0.71
2:E:233:ARG:HG2	2:E:234:ASP:N	2.04	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:176:GLN:NE2	2:E:209:LEU:H	1.88	0.71
2:B:269:ALA:O	2:B:273:MET:HG3	1.90	0.71
1:D:254:GLY:C	1:D:255:LYS:HD2	2.16	0.70
2:E:378:ALA:O	2:E:382:VAL:HG23	1.92	0.70
1:A:39:THR:HG21	1:A:42:LYS:HD2	1.74	0.69
2:B:248:TRP:HE3	2:B:297:ARG:HH12	1.39	0.69
1:D:50:LEU:HB3	1:D:51:PRO:HD2	1.74	0.69
1:D:203:ILE:CB	1:D:229:VAL:HG22	2.07	0.69
1:A:95:ILE:HG22	3:A:300:COA:HN4	1.58	0.69
1:D:4:ILE:CD1	1:D:126:VAL:HG12	2.21	0.69
2:B:248:TRP:HE3	2:B:297:ARG:NH1	1.89	0.68
1:D:202:ALA:HB2	1:D:228:PRO:HG2	1.74	0.68
2:E:124:MET:HE1	5:E:1401:HOH:O	1.94	0.68
2:E:369:ILE:HD12	2:E:369:ILE:N	2.08	0.68
2:B:135:LYS:O	2:B:139:GLU:HB2	1.93	0.68
1:D:2:ILE:CG1	1:D:173:THR:HG21	2.24	0.68
2:B:324:ARG:NH2	2:B:327:LEU:HD11	2.08	0.68
2:B:205:LYS:HB2	2:B:206:GLN:HE22	1.59	0.67
2:B:341:VAL:HG12	2:B:343:VAL:H	1.58	0.67
1:D:252:ALA:O	1:D:255:LYS:HD3	1.94	0.67
1:D:3:LEU:HD21	1:D:193:MET:SD	2.33	0.67
2:E:202:VAL:HG21	2:E:212:LEU:HD22	1.75	0.67
1:D:271:LYS:HZ2	1:D:285:THR:HG21	1.59	0.67
1:A:255:LYS:NZ	1:A:255:LYS:HB3	2.09	0.67
1:D:208:GLU:OE2	1:D:246:NEP:ND1	2.28	0.67
1:A:197:ASP:O	1:A:227:LYS:NZ	2.28	0.66
2:B:348:ARG:C	2:B:348:ARG:HD2	2.20	0.66
2:E:279:HIS:CE1	2:E:375:THR:HG23	2.29	0.66
2:E:323:VAL:HB	2:E:328:ILE:HD11	1.77	0.66
2:E:155:PRO:O	2:E:182:MET:HE1	1.95	0.66
1:A:159:GLU:OE2	2:B:348:ARG:NH2	2.29	0.66
1:D:240:LYS:HG2	1:D:251:ILE:HG21	1.78	0.66
1:A:124:PRO:HG3	1:A:154:GLY:HA2	1.77	0.66
1:D:187:PHE:HB2	5:D:1309:HOH:O	1.95	0.66
1:D:3:LEU:HD21	1:D:193:MET:CE	2.27	0.65
1:D:57:ARG:NH2	1:D:86:ASP:OD2	2.29	0.65
1:D:156:LEU:HD13	1:D:206:ILE:HG21	1.78	0.65
1:A:57:ARG:NH2	1:A:86:ASP:OD1	2.27	0.65
2:B:87:ASP:OD1	2:B:88:ALA:N	2.29	0.65
1:A:167:TYR:HB3	1:A:169:PHE:CE2	2.31	0.65
2:E:106:LYS:HG3	2:E:107:GLU:N	2.09	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:87:ASP:OD1	2:B:89:ASN:N	2.23	0.65
2:E:383:ALA:O	2:E:385:VAL:N	2.30	0.65
2:B:324:ARG:HH21	2:B:327:LEU:CG	2.09	0.65
1:D:108:LYS:NZ	1:D:184:GLY:O	2.27	0.65
1:A:9:LYS:HG2	1:A:35:VAL:HG11	1.79	0.65
1:D:28:ILE:HG22	1:D:29:ALA:N	2.10	0.65
1:A:223:GLU:HB3	1:A:224:HIS:HD2	1.61	0.65
1:D:92:ILE:O	1:D:118:MET:HA	1.97	0.65
1:D:7:ASN:OD1	1:D:33:LYS:NZ	2.30	0.64
2:E:329:ALA:O	2:E:333:ILE:HG13	1.97	0.64
2:B:37:LYS:NZ	5:B:1124:HOH:O	2.30	0.64
2:B:172:LYS:NZ	2:B:208:ASP:OD1	2.30	0.64
1:D:124:PRO:HG3	1:D:154:GLY:HA2	1.79	0.64
1:D:2:ILE:HG12	1:D:173:THR:CG2	2.26	0.64
1:D:77:CYS:SG	1:D:99:ILE:HD11	2.37	0.64
1:A:212:SER:O	1:A:216:GLU:HG3	1.97	0.64
1:D:215:GLU:N	1:D:215:GLU:OE1	2.26	0.64
2:B:106:LYS:HD2	2:B:108:LEU:HD21	1.80	0.64
1:D:71:TYR:CE1	1:D:95:ILE:HG13	2.33	0.64
1:D:212:SER:O	1:D:216:GLU:HG3	1.98	0.64
2:E:355:GLU:HA	2:E:355:GLU:OE1	1.98	0.64
2:B:258:ASN:HB2	2:B:312:LYS:HB2	1.79	0.64
1:D:81:ILE:O	1:D:85:ILE:HG13	1.98	0.64
1:D:248:GLY:O	2:E:116:ARG:NH2	2.27	0.64
2:B:273:MET:HE3	2:B:285:ASN:O	1.98	0.63
1:D:53:PHE:CD2	1:D:59:ALA:HA	2.34	0.63
2:B:70:ARG:NH2	2:E:249:GLU:OE2	2.31	0.63
1:D:229:VAL:HG12	1:D:270:VAL:CG1	2.29	0.63
1:D:259:ASP:OD1	1:D:274:ARG:NH1	2.28	0.63
2:E:75:ASN:ND2	5:E:1371:HOH:O	2.30	0.63
2:E:156:MET:HE3	2:E:157:PRO:HD2	1.80	0.63
2:E:83:THR:OG1	2:E:86:THR:HG23	1.98	0.63
1:D:49:GLY:O	1:D:50:LEU:HD23	1.98	0.63
1:D:53:PHE:CE2	1:D:59:ALA:HA	2.34	0.63
2:B:235:GLN:HB2	5:B:1217:HOH:O	1.97	0.63
2:E:347:VAL:HG12	2:E:348:ARG:H	1.63	0.63
1:D:1:SER:N	1:D:197:ASP:OD2	2.28	0.62
1:A:4:ILE:HD12	1:A:132:CYS:CB	2.23	0.62
1:D:164:THR:HG22	1:D:283:LEU:HD12	1.81	0.62
1:D:186:ASN:HD22	1:D:186:ASN:N	1.97	0.62
1:D:149:ILE:HG12	1:D:204:VAL:CG2	2.30	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:186:ASN:HD22	1:D:186:ASN:H	1.48	0.62
1:D:187:PHE:CE2	1:D:214:GLU:HG3	2.34	0.62
1:A:141:ILE:HG13	1:A:161:VAL:HG11	1.80	0.62
2:E:278:LEU:HD23	2:E:279:HIS:CD2	2.35	0.62
2:E:295:LYS:NZ	2:E:295:LYS:HB3	2.14	0.61
2:E:352:ASN:O	2:E:353:ASN:HB2	1.99	0.61
2:E:54:ARG:HB2	4:E:401:SO4:O3	2.01	0.61
2:B:29:ARG:O	2:B:33:GLU:HG3	2.01	0.61
1:D:221:ILE:HG22	1:D:222:LYS:N	2.15	0.61
2:B:287:LEU:HD12	2:B:288:ASP:H	1.66	0.61
1:D:143:LYS:O	1:D:171:GLN:N	2.28	0.61
2:E:51:ALA:CB	2:E:86:THR:HG22	2.31	0.61
2:B:247:GLN:HG2	2:E:77:LEU:HB3	1.81	0.60
1:D:186:ASN:H	1:D:186:ASN:ND2	1.99	0.60
1:D:233:ILE:HD13	1:D:233:ILE:N	2.14	0.60
1:A:129:PRO:HG2	1:A:171:GLN:HB2	1.83	0.60
1:D:149:ILE:HG12	1:D:204:VAL:HG21	1.83	0.60
1:A:6:LYS:HE2	5:A:1002:HOH:O	2.00	0.60
2:E:312:LYS:HB2	2:E:385:VAL:HG13	1.83	0.60
1:D:4:ILE:HD12	1:D:132:CYS:SG	2.42	0.59
1:D:181:PRO:CA	2:E:116:ARG:HD3	2.32	0.59
1:D:257:THR:O	1:D:261:LYS:HD2	2.02	0.59
1:D:30:TYR:OH	1:D:129:PRO:HA	2.01	0.59
2:B:371:ALA:CB	2:B:377:ALA:HB2	2.32	0.59
1:D:210:GLY:HA2	5:D:1311:HOH:O	2.03	0.59
1:D:222:LYS:HG2	1:D:223:GLU:N	2.18	0.59
1:A:6:LYS:O	1:A:33:LYS:NZ	2.35	0.59
2:E:348:ARG:CZ	2:E:350:GLU:HG2	2.33	0.59
1:D:67:ALA:HA	1:D:91:LEU:O	2.02	0.58
2:E:315:LEU:C	2:E:315:LEU:HD12	2.28	0.58
1:A:143:LYS:HG2	1:A:170:GLY:HA3	1.84	0.58
1:D:119:ILE:HD13	1:D:185:SER:OG	2.04	0.58
1:D:146:LYS:HB2	1:D:201:GLU:CG	2.26	0.58
2:E:312:LYS:CB	2:E:385:VAL:HG13	2.34	0.58
1:D:181:PRO:O	2:E:116:ARG:HD3	2.03	0.58
2:B:250:LEU:HB3	2:B:287:LEU:HD11	1.86	0.58
2:B:299:THR:HG23	2:B:339:VAL:HG23	1.85	0.58
1:A:70:ILE:HG23	1:A:72:VAL:HG23	1.84	0.58
1:A:127:ILE:HG13	1:A:132:CYS:O	2.03	0.58
1:D:56:VAL:HG12	1:D:87:ALA:HB3	1.85	0.58
1:D:167:TYR:CD2	1:D:284:LYS:HD2	2.39	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:45:VAL:HG12	2:B:98:VAL:HG22	1.86	0.58
2:E:294:THR:O	2:E:298:VAL:HG23	2.02	0.57
1:D:67:ALA:HB1	1:D:91:LEU:HD23	1.87	0.57
1:A:5:ASP:OD1	1:A:7:ASN:N	2.33	0.57
2:E:172:LYS:NZ	2:E:207:GLY:O	2.31	0.57
2:E:272:THR:O	2:E:275:ILE:HG22	2.04	0.57
1:D:12:CYS:HB3	1:D:15:PHE:HB2	1.86	0.57
1:D:105:LEU:C	1:D:105:LEU:HD23	2.29	0.57
1:D:67:ALA:CB	1:D:91:LEU:HD23	2.34	0.57
1:D:124:PRO:O	1:D:135:GLY:HA3	2.04	0.57
2:B:119:ARG:NH1	2:B:119:ARG:HG3	2.19	0.57
1:D:195:GLU:OE1	1:D:226:THR:N	2.37	0.57
1:A:9:LYS:HG2	1:A:35:VAL:CG1	2.34	0.56
2:B:287:LEU:HD12	2:B:287:LEU:C	2.29	0.56
2:B:371:ALA:HB3	2:B:377:ALA:HB2	1.86	0.56
1:D:143:LYS:HG3	1:D:170:GLY:HA2	1.85	0.56
1:D:187:PHE:HE2	1:D:214:GLU:HG3	1.69	0.56
2:E:287:LEU:C	2:E:287:LEU:HD23	2.30	0.56
1:A:150:VAL:HG13	1:A:190:ILE:HG21	1.87	0.56
2:B:197:GLU:HB3	2:B:215:LYS:HG2	1.86	0.56
1:A:71:TYR:CE1	1:A:95:ILE:HG13	2.39	0.56
2:E:61:LYS:HG3	2:E:72:PHE:CE2	2.40	0.56
2:B:254:ALA:C	2:B:255:LEU:HD12	2.31	0.56
1:D:149:ILE:HD12	1:D:174:CYS:HG	1.71	0.56
2:E:371:ALA:HB3	2:E:377:ALA:HB2	1.86	0.56
2:B:120:ARG:HG2	2:B:120:ARG:HH11	1.71	0.56
2:B:126:SER:HB2	2:B:143:LEU:O	2.06	0.56
1:D:20:GLY:HA2	1:D:71:TYR:CD2	2.41	0.56
2:E:251:ASN:HB2	2:E:288:ASP:HB3	1.87	0.56
2:E:103:ASP:CB	2:E:205:LYS:HG3	2.31	0.55
2:B:94:ASN:HD22	2:E:247:GLN:HE22	1.54	0.55
2:E:235:GLN:CA	2:E:238:GLU:HG3	2.35	0.55
2:E:315:LEU:HD12	2:E:316:VAL:N	2.20	0.55
2:B:84:TYR:CE1	2:B:85:GLN:HG2	2.41	0.55
1:D:46:THR:HA	1:D:50:LEU:O	2.06	0.55
1:D:275:SER:C	1:D:277:ALA:H	2.13	0.55
2:E:254:ALA:C	2:E:255:LEU:HD23	2.31	0.55
2:B:206:GLN:HG2	5:B:1196:HOH:O	2.06	0.55
1:A:33:LYS:HE2	5:A:1015:HOH:O	2.06	0.55
1:D:159:GLU:HG3	1:D:276:LEU:CD1	2.37	0.55
1:D:223:GLU:O	1:D:223:GLU:HG2	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:303:LYS:HG3	2:E:339:VAL:HG22	1.89	0.55
2:B:352:ASN:O	2:B:353:ASN:HB2	2.08	0.54
1:D:155:THR:HB	2:E:268:LEU:HB2	1.88	0.54
1:D:202:ALA:HA	1:D:228:PRO:HD2	1.89	0.54
1:D:12:CYS:HA	1:D:69:VAL:HG12	1.90	0.54
1:D:123:CYS:O	3:D:301:COA:H21	2.08	0.54
2:B:311:VAL:C	2:B:312:LYS:HD3	2.32	0.54
2:E:324:ARG:HB3	2:E:326:ASP:OD1	2.06	0.54
1:D:166:ASP:C	1:D:168:GLY:H	2.16	0.54
2:B:381:VAL:HG23	2:B:382:VAL:H	1.72	0.53
1:D:191:LEU:HD11	1:D:221:ILE:HD11	1.89	0.53
1:D:30:TYR:OH	1:D:130:GLY:N	2.34	0.53
2:E:106:LYS:HB3	2:E:203:ILE:HD12	1.89	0.53
1:D:47:HIS:O	1:D:48:LEU:HB2	2.08	0.53
2:B:137:ALA:O	2:B:141:PRO:HB3	2.09	0.53
2:B:249:GLU:CD	2:E:70:ARG:HH22	2.17	0.53
1:D:9:LYS:HG3	1:D:65:ALA:HA	1.91	0.53
2:E:250:LEU:HD21	2:E:297:ARG:HG3	1.91	0.53
1:D:230:VAL:CG2	1:D:283:LEU:HD23	2.39	0.53
1:D:275:SER:O	1:D:277:ALA:N	2.41	0.53
1:D:200:THR:O	1:D:227:LYS:HE2	2.08	0.53
2:E:347:VAL:HG12	2:E:348:ARG:N	2.23	0.52
2:B:106:LYS:HB3	2:B:203:ILE:HD12	1.91	0.52
1:A:276:LEU:HD11	2:B:374:LEU:CD2	2.39	0.52
1:A:221:ILE:HG22	1:A:222:LYS:N	2.24	0.52
2:B:1:MET:HE1	2:B:229:LEU:O	2.09	0.52
2:B:252:TYR:HE2	2:B:254:ALA:HB2	1.75	0.52
1:D:166:ASP:O	1:D:168:GLY:N	2.43	0.52
2:E:323:VAL:HG12	2:E:328:ILE:HG13	1.91	0.52
1:A:74:ALA:HB3	1:A:75:PRO:CD	2.40	0.52
1:D:251:ILE:HG22	1:D:251:ILE:O	2.09	0.52
2:E:235:GLN:HG3	5:E:1441:HOH:O	2.09	0.52
2:B:119:ARG:HG3	2:B:119:ARG:HH11	1.73	0.52
2:B:297:ARG:HG3	2:B:297:ARG:HH11	1.74	0.52
2:B:324:ARG:HH21	2:B:327:LEU:HG	1.75	0.52
2:E:49:VAL:HG22	2:E:54:ARG:HD3	1.91	0.52
2:E:348:ARG:HD3	2:E:348:ARG:C	2.35	0.52
1:D:29:ALA:C	1:D:31:GLY:H	2.17	0.52
1:D:158:TYR:N	1:D:158:TYR:CD1	2.75	0.51
1:A:36:GLY:HA2	1:A:50:LEU:HB3	1.92	0.51
2:E:65:SER:HB2	2:E:67:GLU:OE1	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:5:ASP:O	1:A:7:ASN:N	2.43	0.51
2:B:213:ASP:HB3	5:B:1192:HOH:O	2.09	0.51
2:B:272:THR:HA	2:B:275:ILE:HG22	1.92	0.51
1:A:251:ILE:HD13	1:A:257:THR:HG22	1.93	0.51
2:B:252:TYR:CE2	2:B:254:ALA:HB2	2.45	0.51
1:D:192:GLU:HB2	1:D:220:TYR:HH	1.76	0.51
1:D:15:PHE:CD2	1:D:37:GLY:HA3	2.46	0.51
1:D:92:ILE:CG2	1:D:118:MET:HG3	2.41	0.51
1:A:156:LEU:HD13	1:A:206:ILE:CG2	2.41	0.51
2:B:86:THR:OG1	2:B:90:GLY:HA2	2.11	0.51
2:B:184:LEU:HD22	2:B:196:ILE:HD13	1.92	0.51
1:A:147:VAL:CG1	1:A:204:VAL:HG23	2.40	0.51
2:B:297:ARG:HH11	2:B:297:ARG:CG	2.22	0.51
5:B:1233:HOH:O	2:E:28:PRO:HG2	2.10	0.50
1:D:7:ASN:HA	1:D:33:LYS:HZ3	1.75	0.50
2:B:312:LYS:CB	2:B:385:VAL:HG22	2.33	0.50
1:A:255:LYS:HB3	1:A:255:LYS:HZ3	1.76	0.50
2:B:9:LYS:O	2:B:12:PHE:HB2	2.12	0.50
2:E:250:LEU:HD21	2:E:297:ARG:CG	2.41	0.50
2:B:120:ARG:HG2	2:B:120:ARG:NH1	2.26	0.50
2:E:357:GLY:O	2:E:361:LEU:HG	2.11	0.50
1:D:1:SER:O	1:D:1:SER:OG	2.29	0.50
1:D:7:ASN:C	1:D:33:LYS:HD2	2.37	0.50
1:D:232:TYR:O	1:D:233:ILE:HD13	2.10	0.50
2:B:195:LEU:HG	2:B:196:ILE:N	2.27	0.50
1:D:203:ILE:O	1:D:229:VAL:HA	2.12	0.50
2:E:371:ALA:CB	2:E:377:ALA:HA	2.42	0.50
1:A:161:VAL:HG12	1:A:162:LYS:N	2.25	0.50
1:D:92:ILE:HB	1:D:118:MET:HG3	1.92	0.50
1:A:92:ILE:HB	1:A:118:MET:HG3	1.93	0.50
2:B:95:GLN:NE2	5:B:1143:HOH:O	2.44	0.50
1:D:146:LYS:HD3	1:D:201:GLU:CG	2.41	0.50
1:D:154:GLY:O	1:D:157:THR:HB	2.12	0.49
1:D:187:PHE:O	1:D:190:ILE:N	2.44	0.49
1:A:138:PRO:O	1:A:141:ILE:HG12	2.12	0.49
1:A:158:TYR:CD1	1:A:158:TYR:N	2.78	0.49
1:A:167:TYR:CB	1:A:169:PHE:CE2	2.95	0.49
1:D:119:ILE:HD13	1:D:185:SER:HG	1.77	0.49
1:A:74:ALA:HB3	1:A:75:PRO:HD3	1.93	0.49
2:B:327:LEU:O	2:B:330:ASP:HB2	2.12	0.49
2:E:233:ARG:HG2	2:E:234:ASP:H	1.74	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:303:LYS:HD3	2:B:339:VAL:HG22	1.94	0.49
2:B:380:GLN:O	2:B:383:ALA:HB3	2.12	0.49
1:D:240:LYS:HG2	1:D:251:ILE:CG2	2.43	0.49
1:D:271:LYS:HZ3	1:D:285:THR:HG21	1.76	0.49
2:B:273:MET:HE3	2:B:285:ASN:C	2.37	0.49
2:B:359:LYS:HD3	2:B:363:ASP:OD2	2.13	0.49
2:E:110:LEU:CD2	2:E:184:LEU:HD12	2.43	0.49
1:A:151:SER:OG	1:A:206:ILE:HB	2.13	0.49
2:B:50:HIS:CD2	2:B:237:GLN:HG3	2.47	0.49
1:D:255:LYS:HD2	1:D:255:LYS:N	2.28	0.49
2:E:383:ALA:C	2:E:385:VAL:H	2.21	0.49
1:A:218:ALA:HB1	1:A:264:ALA:O	2.12	0.49
2:B:300:GLU:O	2:B:304:ILE:HD12	2.12	0.49
2:B:322:ILE:HD13	2:B:322:ILE:H	1.76	0.49
1:D:186:ASN:HD22	1:D:186:ASN:C	2.21	0.49
2:B:161:ARG:NH1	5:B:1174:HOH:O	2.31	0.49
1:D:124:PRO:HA	1:D:136:ILE:HG12	1.95	0.48
2:B:258:ASN:ND2	2:B:385:VAL:HG11	2.28	0.48
2:B:378:ALA:O	2:B:381:VAL:HG23	2.14	0.48
2:E:82:VAL:HG22	2:E:90:GLY:CA	2.43	0.48
2:B:119:ARG:HB2	5:B:1154:HOH:O	2.13	0.48
1:D:143:LYS:HG3	1:D:170:GLY:CA	2.44	0.48
1:A:110:LYS:HD2	1:A:110:LYS:O	2.14	0.48
1:A:251:ILE:HG23	1:A:255:LYS:O	2.13	0.48
1:D:181:PRO:C	2:E:116:ARG:HD3	2.39	0.48
1:A:159:GLU:CD	2:B:348:ARG:HH22	2.21	0.48
5:A:1355:HOH:O	2:E:36:SER:HB2	2.13	0.48
1:A:23:HIS:CE1	1:A:136:ILE:HG22	2.48	0.48
1:A:66:THR:HG22	5:A:1042:HOH:O	2.13	0.48
1:D:12:CYS:HB3	1:D:15:PHE:CD1	2.49	0.48
1:D:197:ASP:HA	1:D:198:PRO:HD2	1.37	0.48
2:E:205:LYS:C	2:E:207:GLY:H	2.22	0.48
2:E:299:THR:HG23	2:E:339:VAL:HG23	1.94	0.48
2:B:175:GLN:H	2:B:175:GLN:HG2	1.15	0.48
2:E:176:GLN:NE2	5:E:1417:HOH:O	2.47	0.48
2:E:292:GLY:O	2:E:294:THR:N	2.45	0.48
2:E:87:ASP:CG	2:E:89:ASN:H	2.22	0.48
2:B:272:THR:O	2:B:275:ILE:HG22	2.12	0.48
2:E:45:VAL:HG12	2:E:98:VAL:HG22	1.96	0.47
2:E:196:ILE:HG22	2:E:197:GLU:N	2.28	0.47
1:A:77:CYS:HB3	1:A:99:ILE:HD13	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:79:LYS:HD3	2:B:79:LYS:N	2.28	0.47
1:D:34:MET:HE3	1:D:34:MET:HB3	1.76	0.47
1:D:128:THR:HG23	1:D:131:GLU:HB2	1.96	0.47
1:D:172:SER:HB3	1:D:199:GLN:HG2	1.97	0.47
1:D:11:ILE:HG22	1:D:36:GLY:O	2.14	0.47
2:E:76:TRP:O	2:E:79:LYS:HB2	2.14	0.47
1:D:7:ASN:HA	1:D:33:LYS:HD2	1.94	0.47
1:A:127:ILE:CD1	1:A:133:LYS:HB2	2.45	0.47
1:A:228:PRO:CB	1:A:286:VAL:HG11	2.39	0.47
2:B:249:GLU:O	2:B:290:GLY:HA3	2.14	0.47
1:D:159:GLU:HG3	1:D:276:LEU:HD11	1.96	0.47
2:B:83:THR:OG1	2:B:86:THR:HG23	2.14	0.47
1:A:199:GLN:O	1:A:199:GLN:HG2	2.15	0.47
2:B:125:ALA:HB1	2:B:167:LEU:HD11	1.96	0.47
2:B:273:MET:HE3	2:B:286:PHE:HA	1.97	0.47
2:B:319:PHE:CD1	2:B:319:PHE:C	2.92	0.47
1:D:127:ILE:HG13	1:D:133:LYS:HA	1.96	0.47
1:D:200:THR:O	1:D:200:THR:HG22	2.14	0.47
1:D:252:ALA:C	1:D:254:GLY:H	2.21	0.47
1:D:282:ALA:O	1:D:286:VAL:HG23	2.15	0.47
2:E:277:LYS:HA	2:E:281:GLY:O	2.15	0.47
1:A:205:MET:HE1	1:A:265:LEU:HD21	1.96	0.47
1:A:228:PRO:CB	1:A:286:VAL:CG1	2.93	0.47
2:B:324:ARG:HE	2:B:324:ARG:HB2	1.36	0.47
2:B:356:LEU:O	2:B:356:LEU:HD12	2.15	0.47
2:E:131:VAL:HG12	2:E:132:GLU:O	2.15	0.47
2:E:343:VAL:HB	2:E:344:PRO:CD	2.41	0.47
1:D:167:TYR:HD2	1:D:284:LYS:HD2	1.80	0.47
1:D:221:ILE:HG13	1:D:225:VAL:HG21	1.97	0.47
1:A:242:LYS:HD2	5:A:1081:HOH:O	2.15	0.46
2:B:140:THR:O	2:B:142:HIS:N	2.48	0.46
1:D:191:LEU:HD23	1:D:191:LEU:HA	1.60	0.46
1:A:192:GLU:O	1:A:192:GLU:HG2	2.14	0.46
1:D:22:PHE:CD1	1:D:22:PHE:C	2.94	0.46
2:E:166:LYS:C	2:E:168:GLY:H	2.22	0.46
1:A:274:ARG:HG3	1:A:274:ARG:NH1	2.18	0.46
2:B:279:HIS:O	2:B:382:VAL:HG21	2.15	0.46
1:D:92:ILE:CB	1:D:118:MET:HG3	2.45	0.46
2:E:323:VAL:HG12	2:E:324:ARG:N	2.30	0.46
1:A:167:TYR:OH	1:A:281:GLU:HG2	2.16	0.46
1:A:224:HIS:CD2	1:A:224:HIS:N	2.84	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:235:GLN:HA	2:E:238:GLU:CG	2.41	0.46
1:D:127:ILE:HG13	1:D:132:CYS:O	2.15	0.46
1:A:137:GLN:O	1:A:137:GLN:HG2	2.16	0.46
2:B:102:THR:CG2	2:B:103:ASP:N	2.77	0.46
2:B:140:THR:O	2:B:140:THR:OG1	2.32	0.46
2:B:248:TRP:CE3	2:B:297:ARG:NH1	2.75	0.46
1:D:53:PHE:CD2	1:D:59:ALA:CB	2.99	0.46
1:D:56:VAL:CG1	1:D:87:ALA:HB3	2.45	0.46
2:E:282:GLU:HA	2:E:283:PRO:HD3	1.77	0.46
2:B:106:LYS:CD	2:B:108:LEU:HD21	2.46	0.45
1:D:230:VAL:HG21	1:D:283:LEU:HD23	1.96	0.45
2:E:303:LYS:HG3	2:E:339:VAL:CG2	2.46	0.45
1:A:54:ASN:HB2	1:A:58:GLU:OE1	2.16	0.45
2:B:31:ALA:O	2:B:69:ILE:HG21	2.16	0.45
2:E:84:TYR:CE1	2:E:85:GLN:HG2	2.51	0.45
1:A:255:LYS:NZ	1:A:255:LYS:CB	2.79	0.45
1:D:39:THR:HG21	1:D:42:LYS:HD2	1.98	0.45
2:E:5:GLU:OE2	2:E:9:LYS:NZ	2.50	0.45
2:E:104:ILE:HG23	2:E:202:VAL:HG13	1.99	0.45
2:E:241:ARG:HH11	2:E:307:SER:HG	1.64	0.45
1:A:118:MET:HE2	1:A:118:MET:HB3	1.77	0.45
3:A:300:COA:H8A	5:A:1356:HOH:O	2.15	0.45
1:A:54:ASN:HB2	5:A:1022:HOH:O	2.17	0.45
2:B:51:ALA:HB3	2:B:86:THR:HG22	1.95	0.45
1:D:8:THR:HG22	1:D:10:VAL:HG23	1.97	0.45
1:D:156:LEU:HD13	1:D:206:ILE:CG2	2.46	0.45
2:E:124:MET:HA	2:E:145:HIS:O	2.16	0.45
2:E:369:ILE:N	2:E:369:ILE:CD1	2.79	0.45
2:B:292:GLY:O	2:B:294:THR:N	2.46	0.45
1:D:6:LYS:HB2	1:D:131:GLU:HG2	1.99	0.45
1:D:53:PHE:CD2	1:D:59:ALA:CA	2.99	0.45
1:D:186:ASN:ND2	1:D:189:ASP:CG	2.74	0.45
2:E:317:ASN:ND2	2:E:374:LEU:CD1	2.79	0.45
1:A:35:VAL:HG21	1:A:63:THR:HB	1.99	0.45
1:D:9:LYS:HB3	1:D:9:LYS:HE2	1.20	0.45
1:D:124:PRO:HD2	1:D:176:GLY:HA3	1.99	0.45
2:B:108:LEU:HD11	2:B:203:ILE:HD11	1.99	0.45
1:D:229:VAL:O	1:D:270:VAL:HG12	2.17	0.45
2:E:119:ARG:NH1	2:E:119:ARG:HG3	2.32	0.45
2:B:299:THR:HG23	2:B:339:VAL:CG2	2.47	0.45
1:D:46:THR:HG22	1:D:50:LEU:O	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:132:GLU:HB3	2:E:134:GLU:OE1	2.16	0.45
2:E:208:ASP:HB2	5:E:1425:HOH:O	2.17	0.45
2:E:277:LYS:O	2:E:277:LYS:HD3	2.17	0.45
1:D:143:LYS:CG	1:D:170:GLY:HA2	2.47	0.45
1:D:255:LYS:N	1:D:255:LYS:CD	2.79	0.45
1:A:201:GLU:O	1:A:228:PRO:HD2	2.17	0.44
2:B:22:GLY:HA3	2:B:99:GLU:HB3	1.99	0.44
2:B:258:ASN:ND2	2:B:385:VAL:CG1	2.80	0.44
1:D:92:ILE:HG22	1:D:118:MET:HG3	1.98	0.44
2:E:292:GLY:C	2:E:294:THR:HG23	2.42	0.44
2:B:3:LEU:HD23	2:B:3:LEU:HA	1.72	0.44
2:B:199:ASN:HA	2:B:200:PRO:HA	1.75	0.44
1:D:29:ALA:C	1:D:31:GLY:N	2.75	0.44
1:D:53:PHE:CD2	1:D:59:ALA:HB2	2.53	0.44
1:D:164:THR:HG22	1:D:283:LEU:CD1	2.44	0.44
2:E:323:VAL:CG1	2:E:328:ILE:HG13	2.47	0.44
1:D:221:ILE:CA	1:D:225:VAL:HG23	2.27	0.44
2:E:110:LEU:HD23	2:E:184:LEU:HD12	1.98	0.44
1:A:40:PRO:HD3	3:A:300:COA:C2A	2.47	0.44
1:A:137:GLN:H	1:A:137:GLN:CD	2.25	0.44
2:B:70:ARG:HH22	2:E:249:GLU:CD	2.25	0.44
2:B:248:TRP:CD1	2:B:300:GLU:HG3	2.53	0.44
2:E:179:LYS:HB3	5:E:1493:HOH:O	2.17	0.44
1:A:156:LEU:HD13	1:A:206:ILE:HG21	1.99	0.44
2:B:120:ARG:HA	2:B:120:ARG:HD3	1.72	0.44
2:B:94:ASN:HB2	5:B:1140:HOH:O	2.17	0.44
2:B:297:ARG:CZ	2:B:297:ARG:HB2	2.46	0.44
1:A:147:VAL:HG11	1:A:204:VAL:HG23	1.98	0.44
1:A:236:VAL:HA	1:A:258:ALA:HB3	2.00	0.44
2:B:277:LYS:HA	2:B:281:GLY:O	2.18	0.44
2:E:227:PRO:HA	2:E:230:ARG:CZ	2.48	0.44
2:B:297:ARG:NH1	2:B:297:ARG:CG	2.79	0.44
2:B:380:GLN:O	2:B:384:ALA:N	2.39	0.44
1:A:205:MET:CE	1:A:265:LEU:HD21	2.48	0.44
2:B:83:THR:H	2:B:86:THR:CG2	2.30	0.44
2:E:51:ALA:HB3	2:E:86:THR:HG22	1.99	0.44
1:A:5:ASP:OD1	1:A:7:ASN:HB2	2.18	0.43
2:B:262:MET:HE2	2:B:262:MET:HB2	1.81	0.43
2:B:328:ILE:O	2:B:332:ILE:HG13	2.18	0.43
2:E:123:PHE:O	2:E:146:LYS:HA	2.18	0.43
2:E:119:ARG:HG3	2:E:119:ARG:HH11	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:243:ARG:NH1	1:D:243:ARG:HG2	2.33	0.43
2:E:330:ASP:OD1	2:E:360:LYS:NZ	2.51	0.43
2:E:383:ALA:C	2:E:385:VAL:N	2.76	0.43
1:A:203:ILE:HB	1:A:229:VAL:HG13	1.99	0.43
2:B:156:MET:HE3	2:B:156:MET:HB3	1.70	0.43
2:B:284:ALA:O	2:B:285:ASN:HB3	2.18	0.43
1:D:9:LYS:H	1:D:9:LYS:HG2	1.54	0.43
2:E:166:LYS:C	2:E:168:GLY:N	2.77	0.43
1:A:6:LYS:CB	1:A:131:GLU:HB3	2.43	0.43
1:D:39:THR:CG2	1:D:42:LYS:HD2	2.48	0.43
1:D:110:LYS:O	1:D:114:ALA:N	2.44	0.43
1:D:120:GLY:HA3	1:D:121:PRO:HA	1.75	0.43
1:D:188:ILE:O	1:D:188:ILE:HG22	2.17	0.43
2:E:258:ASN:OD1	2:E:258:ASN:N	2.50	0.43
2:E:366:LEU:N	2:E:366:LEU:HD23	2.31	0.43
1:A:5:ASP:C	1:A:7:ASN:N	2.77	0.43
1:A:208:GLU:HA	1:A:234:ALA:O	2.19	0.43
2:B:84:TYR:CD1	2:B:84:TYR:C	2.96	0.43
2:B:158:TYR:CD1	2:B:158:TYR:C	2.97	0.43
1:D:186:ASN:ND2	1:D:186:ASN:C	2.76	0.43
2:E:109:TYR:HE2	2:E:197:GLU:OE2	2.02	0.43
2:E:118:SER:C	2:E:119:ARG:HG3	2.44	0.43
2:E:202:VAL:CG1	2:E:203:ILE:N	2.80	0.43
1:A:123:CYS:O	3:A:300:COA:H22	2.19	0.43
1:D:186:ASN:ND2	1:D:189:ASP:OD2	2.52	0.43
2:E:312:LYS:HB2	2:E:385:VAL:CG1	2.46	0.43
1:A:208:GLU:OE2	1:A:246:NEP:ND1	2.51	0.43
2:B:381:VAL:HG23	2:B:382:VAL:N	2.33	0.43
1:D:43:GLY:HA2	1:D:52:VAL:O	2.18	0.43
1:D:233:ILE:HD12	1:D:233:ILE:HA	1.82	0.43
2:E:67:GLU:CD	2:E:67:GLU:H	2.27	0.43
2:E:82:VAL:HG22	2:E:90:GLY:N	2.34	0.43
2:B:248:TRP:CG	2:B:300:GLU:HG3	2.54	0.42
2:B:277:LYS:HA	2:B:277:LYS:HD2	1.78	0.42
2:B:324:ARG:HB3	2:B:326:ASP:OD1	2.19	0.42
1:D:2:ILE:O	1:D:4:ILE:N	2.51	0.42
2:E:125:ALA:HB1	2:E:167:LEU:HD11	2.01	0.42
2:B:83:THR:C	2:B:85:GLN:H	2.27	0.42
2:B:275:ILE:HG21	2:B:374:LEU:HD11	2.01	0.42
1:D:110:LYS:HD2	1:D:110:LYS:HA	1.77	0.42
2:E:199:ASN:HA	2:E:200:PRO:HA	1.71	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:143:LYS:HG2	1:A:143:LYS:O	2.16	0.42
1:A:180:ASP:HB3	1:A:181:PRO:CD	2.48	0.42
2:E:346:VAL:CG2	2:E:381:VAL:HG13	2.49	0.42
2:E:356:LEU:HD13	2:E:356:LEU:HA	1.75	0.42
2:E:356:LEU:O	2:E:360:LYS:HB3	2.19	0.42
2:B:40:ALA:O	5:B:1128:HOH:O	2.21	0.42
2:B:233:ARG:O	2:B:233:ARG:HG2	2.18	0.42
2:E:212:LEU:HD12	2:E:212:LEU:HA	1.63	0.42
2:B:115:ASP:OD2	2:B:118:SER:N	2.50	0.42
2:B:279:HIS:O	2:B:382:VAL:HG11	2.19	0.42
2:B:327:LEU:HA	2:B:327:LEU:HD23	1.52	0.42
2:E:191:ARG:HD2	2:E:191:ARG:HA	1.36	0.42
1:D:143:LYS:HE3	1:D:143:LYS:HB2	1.82	0.42
1:D:166:ASP:C	1:D:168:GLY:N	2.78	0.42
1:D:2:ILE:HG13	1:D:173:THR:HG21	2.01	0.42
2:E:187:ILE:HG23	2:E:191:ARG:HG2	2.01	0.42
2:E:381:VAL:HG23	2:E:382:VAL:N	2.34	0.42
1:A:39:THR:CG2	1:A:42:LYS:HD2	2.47	0.42
1:D:2:ILE:HD11	1:D:190:ILE:CG2	2.49	0.42
1:D:146:LYS:HD3	1:D:201:GLU:HG3	2.02	0.42
1:D:169:PHE:N	1:D:169:PHE:CD1	2.84	0.42
1:D:243:ARG:HD2	1:D:247:ALA:HA	2.02	0.42
2:E:2:ASN:HB3	5:E:1334:HOH:O	2.19	0.42
2:E:196:ILE:CG2	2:E:197:GLU:N	2.82	0.42
2:B:313:ALA:HB2	2:B:385:VAL:HG23	2.01	0.42
1:D:24:SER:O	1:D:27:ALA:N	2.52	0.42
2:E:361:LEU:O	2:E:364:SER:HB3	2.19	0.42
1:A:5:ASP:C	1:A:7:ASN:H	2.27	0.41
1:A:149:ILE:HG12	1:A:204:VAL:HB	2.02	0.41
1:A:212:SER:HA	1:A:215:GLU:OE1	2.20	0.41
1:A:244:MET:O	1:A:246:NEP:N	2.53	0.41
2:B:50:HIS:CG	2:B:237:GLN:HG3	2.55	0.41
2:E:62:VAL:O	2:E:63:VAL:HG12	2.20	0.41
1:A:223:GLU:CB	1:A:224:HIS:CD2	3.00	0.41
2:B:95:GLN:HE21	2:B:95:GLN:HB2	1.22	0.41
2:B:140:THR:N	2:B:141:PRO:CD	2.79	0.41
2:B:140:THR:N	2:B:141:PRO:HD3	2.36	0.41
2:B:222:ALA:O	2:B:225:ARG:N	2.32	0.41
2:B:300:GLU:HA	2:B:303:LYS:HG3	2.02	0.41
2:B:343:VAL:HB	2:B:344:PRO:HD2	2.01	0.41
1:D:1:SER:N	1:D:197:ASP:CG	2.78	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:155:THR:HG21	2:E:264:ASN:O	2.19	0.41
1:D:252:ALA:C	1:D:254:GLY:N	2.77	0.41
1:A:274:ARG:NH1	1:A:274:ARG:CG	2.79	0.41
2:B:6:TYR:CD1	2:B:6:TYR:C	2.98	0.41
2:B:247:GLN:HE22	2:E:94:ASN:HD22	1.68	0.41
1:A:35:VAL:CG2	1:A:63:THR:HB	2.51	0.41
2:B:46:LYS:N	2:B:97:LEU:O	2.45	0.41
2:B:140:THR:C	2:B:142:HIS:H	2.29	0.41
1:D:3:LEU:CD2	1:D:193:MET:HE1	2.40	0.41
2:B:140:THR:OG1	2:B:143:LEU:HB2	2.21	0.41
2:B:209:LEU:HD23	2:B:209:LEU:HA	1.57	0.41
1:D:9:LYS:HE2	1:D:35:VAL:HG11	2.02	0.41
1:D:9:LYS:HB2	1:D:35:VAL:HG21	2.02	0.41
1:D:57:ARG:HA	1:D:87:ALA:HB1	2.03	0.41
1:D:128:THR:CG2	1:D:131:GLU:HB2	2.50	0.41
1:D:202:ALA:CB	1:D:228:PRO:HD2	2.49	0.41
2:E:191:ARG:N	2:E:191:ARG:CD	2.80	0.41
2:E:213:ASP:HB3	5:E:1424:HOH:O	2.20	0.41
2:E:347:VAL:CG1	2:E:348:ARG:H	2.33	0.41
1:D:155:THR:C	1:D:157:THR:N	2.78	0.41
1:D:275:SER:C	1:D:277:ALA:N	2.77	0.41
1:A:33:LYS:HB2	5:A:1003:HOH:O	2.20	0.41
2:B:324:ARG:O	2:B:327:LEU:N	2.50	0.41
2:E:315:LEU:HB2	2:E:381:VAL:HG11	2.03	0.41
2:E:319:PHE:CD1	2:E:319:PHE:C	2.99	0.41
2:B:177:PHE:CD1	2:B:177:PHE:C	2.98	0.41
2:B:191:ARG:HA	2:B:191:ARG:HD2	1.54	0.41
1:D:23:HIS:CD2	1:D:136:ILE:HG22	2.56	0.41
1:D:227:LYS:HB3	1:D:228:PRO:CD	2.49	0.41
1:A:1:SER:N	1:A:197:ASP:OD2	2.43	0.41
1:A:273:VAL:HG13	1:A:278:ASP:HB2	2.03	0.41
2:B:292:GLY:O	2:B:294:THR:HG23	2.21	0.41
2:B:336:VAL:HG13	2:B:341:VAL:HB	2.02	0.41
2:E:206:GLN:N	2:E:206:GLN:CD	2.79	0.41
2:E:323:VAL:HG12	2:E:324:ARG:O	2.20	0.41
2:E:346:VAL:HG21	2:E:381:VAL:HG13	2.03	0.41
1:A:90:LYS:HZ2	1:A:90:LYS:HG2	1.62	0.41
1:A:166:ASP:C	1:A:168:GLY:H	2.29	0.41
1:A:223:GLU:C	1:A:224:HIS:CD2	2.99	0.41
2:B:109:TYR:CD1	2:B:109:TYR:C	2.99	0.41
2:B:263:VAL:HG12	2:B:264:ASN:N	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:72:VAL:HG13	1:D:73:PRO:HD2	2.03	0.41
1:A:6:LYS:HE3	1:A:6:LYS:HB2	1.63	0.40
2:B:295:LYS:HE3	2:B:295:LYS:HB3	1.89	0.40
1:D:12:CYS:O	1:D:15:PHE:HB2	2.21	0.40
1:D:32:THR:HG23	1:D:132:CYS:SG	2.61	0.40
1:D:147:VAL:O	1:D:171:GLN:HA	2.21	0.40
2:E:55:GLY:HA2	2:E:60:VAL:HB	2.03	0.40
2:E:257:GLY:HA3	2:E:282:GLU:O	2.20	0.40
1:A:151:SER:HA	1:A:206:ILE:O	2.21	0.40
1:D:86:ASP:C	1:D:88:GLY:H	2.30	0.40
2:E:84:TYR:CD1	2:E:85:GLN:HG2	2.56	0.40
2:B:346:VAL:CG2	2:B:381:VAL:HG13	2.52	0.40
1:D:89:ILE:HD13	1:D:89:ILE:HA	1.94	0.40
1:D:140:HIS:C	1:D:140:HIS:HD1	2.29	0.40
1:A:50:LEU:HB3	1:A:51:PRO:HD2	2.04	0.40
1:D:137:GLN:CD	1:D:137:GLN:H	2.29	0.40
1:A:159:GLU:OE2	2:B:319:PHE:HD2	2.04	0.40
1:A:173:THR:HG22	1:A:175:VAL:HG23	2.03	0.40
1:D:214:GLU:OE1	1:D:261:LYS:NZ	2.53	0.40
2:E:124:MET:HE3	2:E:124:MET:HB3	1.64	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	283/288 (98%)	262 (93%)	18 (6%)	3 (1%)	11	13
1	D	283/288 (98%)	244 (86%)	34 (12%)	5 (2%)	6	6
2	B	383/388 (99%)	368 (96%)	13 (3%)	2 (0%)	24	31
2	E	383/388 (99%)	361 (94%)	20 (5%)	2 (0%)	24	31
All	All	1332/1352 (98%)	1235 (93%)	85 (6%)	12 (1%)	14	17

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	293	ALA
2	E	384	ALA
1	D	3	LEU
1	D	169	PHE
1	D	276	LEU
1	A	48	LEU
1	D	167	TYR
2	E	293	ALA
2	B	141	PRO
1	D	40	PRO
1	A	236	VAL
1	A	245	GLY

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	215/217 (99%)	171 (80%)	44 (20%)	1	1
1	D	215/217 (99%)	168 (78%)	47 (22%)	1	1
2	B	296/298 (99%)	261 (88%)	35 (12%)	5	6
2	E	296/298 (99%)	244 (82%)	52 (18%)	2	2
All	All	1022/1030 (99%)	844 (83%)	178 (17%)	2	2

All (178) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	LYS
1	A	25	GLU
1	A	28	ILE
1	A	33	LYS
1	A	35	VAL
1	A	39	THR
1	A	76	PHE
1	A	77	CYS

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Mol	Chain	Res	Type
1	A	81	ILE
1	A	90	LYS
1	A	93	ILE
1	A	104	MET
1	A	105	LEU
1	A	107	VAL
1	A	110	LYS
1	A	113	GLU
1	A	117	ARG
1	A	118	MET
1	A	128	THR
1	A	131	GLU
1	A	132	CYS
1	A	136	ILE
1	A	137	GLN
1	A	141	ILE
1	A	143	LYS
1	A	146	LYS
1	A	150	VAL
1	A	156	LEU
1	A	161	VAL
1	A	165	THR
1	A	172	SER
1	A	196	LYS
1	A	206	ILE
1	A	209	ILE
1	A	221	ILE
1	A	229	VAL
1	A	242	LYS
1	A	255	LYS
1	A	257	THR
1	A	271	LYS
1	A	274	ARG
1	A	276	LEU
1	A	279	ILE
1	A	284	LYS
2	B	14	ARG
2	B	79	LYS
2	B	87	ASP
2	B	95	GLN
2	B	96	ILE
2	B	106	LYS

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Mol	Chain	Res	Type
2	B	116	ARG
2	B	139	GLU
2	B	140	THR
2	B	175	GLN
2	B	179	LYS
2	B	191	ARG
2	B	195	LEU
2	B	202	VAL
2	B	210	ILE
2	B	215	LYS
2	B	229	LEU
2	B	233	ARG
2	B	236	SER
2	B	247	GLN
2	B	262	MET
2	B	275	ILE
2	B	277	LYS
2	B	287	LEU
2	B	303	LYS
2	B	304	ILE
2	B	312	LYS
2	B	318	ILE
2	B	322	ILE
2	B	323	VAL
2	B	324	ARG
2	B	339	VAL
2	B	359	LYS
2	B	381	VAL
2	B	385	VAL
1	D	1	SER
1	D	9	LYS
1	D	10	VAL
1	D	26	GLN
1	D	28	ILE
1	D	46	THR
1	D	55	THR
1	D	63	THR
1	D	90	LYS
1	D	91	LEU
1	D	106	THR
1	D	107	VAL
1	D	113	GLU

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Mol	Chain	Res	Type
1	D	128	THR
1	D	136	ILE
1	D	137	GLN
1	D	143	LYS
1	D	146	LYS
1	D	147	VAL
1	D	149	ILE
1	D	150	VAL
1	D	153	SER
1	D	155	THR
1	D	156	LEU
1	D	162	LYS
1	D	173	THR
1	D	185	SER
1	D	186	ASN
1	D	190	ILE
1	D	196	LYS
1	D	200	THR
1	D	204	VAL
1	D	221	ILE
1	D	222	LYS
1	D	225	VAL
1	D	230	VAL
1	D	233	ILE
1	D	242	LYS
1	D	251	ILE
1	D	255	LYS
1	D	261	LYS
1	D	270	VAL
1	D	271	LYS
1	D	276	LEU
1	D	281	GLU
1	D	284	LYS
1	D	286	VAL
2	E	2	ASN
2	E	11	LEU
2	E	14	ARG
2	E	21	VAL
2	E	45	VAL
2	E	61	LYS
2	E	63	VAL
2	E	70	ARG

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Mol	Chain	Res	Type
2	E	79	LYS
2	E	95	GLN
2	E	99	GLU
2	E	106	LYS
2	E	119	ARG
2	E	122	VAL
2	E	124	MET
2	E	127	THR
2	E	143	LEU
2	E	146	LYS
2	E	166	LYS
2	E	169	LEU
2	E	170	GLU
2	E	172	LYS
2	E	191	ARG
2	E	195	LEU
2	E	231	GLU
2	E	238	GLU
2	E	244	GLN
2	E	249	GLU
2	E	256	ASP
2	E	262	MET
2	E	276	VAL
2	E	277	LYS
2	E	278	LEU
2	E	282	GLU
2	E	295	LYS
2	E	297	ARG
2	E	298	VAL
2	E	310	LYS
2	E	315	LEU
2	E	322	ILE
2	E	348	ARG
2	E	350	GLU
2	E	355	GLU
2	E	356	LEU
2	E	360	LYS
2	E	364	SER
2	E	369	ILE
2	E	372	LYS
2	E	374	LEU
2	E	375	THR

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Mol	Chain	Res	Type
2	E	379	GLN
2	E	381	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	7	ASN
1	A	137	GLN
1	A	140	HIS
1	A	224	HIS
2	B	2	ASN
2	B	50	HIS
2	B	64	ASN
2	B	94	ASN
2	B	95	GLN
2	B	206	GLN
2	B	279	HIS
1	D	19	GLN
1	D	186	ASN
2	E	89	ASN
2	E	94	ASN
2	E	95	GLN
2	E	176	GLN
2	E	279	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 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
1	NEP	A	246	1	11,14,15	1.57	2 (18%)	8,20,22	1.46	2 (25%)
1	NEP	D	246	1	11,14,15	1.48	2 (18%)	8,20,22	1.74	2 (25%)

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
1	NEP	A	246	1	-	3/5/12/14	0/1/1/1
1	NEP	D	246	1	-	2/5/12/14	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	246	NEP	P-O2P	-3.83	1.46	1.56
1	D	246	NEP	P-O2P	-3.64	1.47	1.56
1	A	246	NEP	P-O1P	-3.08	1.48	1.56
1	D	246	NEP	P-O1P	-2.25	1.50	1.56

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	246	NEP	O2P-P-O3P	-3.76	103.69	112.95
1	A	246	NEP	O2P-P-O3P	-2.58	106.60	112.95
1	A	246	NEP	CE1-ND1-CG	2.09	109.14	105.80
1	D	246	NEP	CE1-ND1-CG	2.01	109.02	105.80

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	246	NEP	O-C-CA-CB
1	D	246	NEP	CA-CB-CG-CD2
1	D	246	NEP	CA-CB-CG-ND1
1	A	246	NEP	CA-CB-CG-ND1
1	A	246	NEP	CA-CB-CG-CD2

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	246	NEP	3	0
1	D	246	NEP	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 ligands 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	COA	D	301	-	47,50,50	1.48	5 (10%)	69,75,75	1.62	14 (20%)
3	COA	A	300	-	47,50,50	1.11	3 (6%)	69,75,75	1.48	10 (14%)
4	SO4	E	401	-	4,4,4	0.86	0	6,6,6	0.85	0
4	SO4	B	400	-	4,4,4	0.51	0	6,6,6	0.39	0

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	COA	D	301	-	-	8/48/64/64	0/3/3/3
3	COA	A	300	-	-	6/48/64/64	0/3/3/3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	301	COA	P2A-O3A	4.66	1.64	1.59
3	A	300	COA	P2A-O3A	-3.41	1.55	1.59
3	D	301	COA	CEP-CBP	-3.12	1.47	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	301	COA	P1A-O3A	2.88	1.62	1.59
3	A	300	COA	C2A-N1A	-2.65	1.29	1.33
3	A	300	COA	P3B-O3B	2.49	1.63	1.59
3	D	301	COA	OAP-CAP	2.33	1.46	1.42
3	D	301	COA	C4A-N9A	2.16	1.42	1.37

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	300	COA	O3A-P1A-O1A	-5.75	93.39	110.70
3	D	301	COA	O2A-P1A-O3A	5.14	121.17	107.27
3	D	301	COA	CDP-CBP-CAP	4.11	115.77	108.77
3	D	301	COA	O9A-P3B-O3B	3.68	120.18	105.85
3	A	300	COA	O4B-C1B-C2B	-3.18	99.81	106.62
3	D	301	COA	CEP-CBP-CAP	-3.17	103.36	108.77
3	D	301	COA	C5A-N7A-C8A	3.02	108.20	103.45
3	D	301	COA	C4A-C5A-N7A	-2.99	107.17	110.58
3	A	300	COA	O2B-C2B-C3B	2.92	119.36	111.19
3	A	300	COA	O5A-P2A-O3A	2.71	114.61	107.27
3	A	300	COA	O5A-P2A-O4A	2.71	125.03	112.44
3	A	300	COA	OAP-CAP-C9P	-2.69	98.13	109.38
3	D	301	COA	O3A-P1A-O1A	-2.68	102.65	110.70
3	A	300	COA	C6A-C5A-C4A	-2.41	113.89	117.18
3	A	300	COA	O5A-P2A-O6A	-2.41	96.67	107.57
3	D	301	COA	O5A-P2A-O3A	2.33	113.56	107.27
3	D	301	COA	C3P-N4P-C5P	-2.32	118.50	122.82
3	D	301	COA	P3B-O3B-C3B	-2.31	117.27	123.43
3	D	301	COA	C5A-C4A-N3A	-2.25	123.61	126.72
3	D	301	COA	N9A-C8A-N7A	-2.24	110.75	113.94
3	A	300	COA	C6P-C7P-N8P	-2.17	107.39	112.00
3	A	300	COA	C7P-C6P-C5P	-2.07	108.94	112.39
3	D	301	COA	O2B-C2B-C1B	-2.05	103.06	110.10
3	D	301	COA	N3A-C2A-N1A	2.04	131.67	128.58

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	301	COA	C5P-C6P-C7P-N8P
3	A	300	COA	C2B-C3B-O3B-P3B
3	D	301	COA	C2B-C1B-N9A-C8A
3	A	300	COA	C4B-C3B-O3B-P3B

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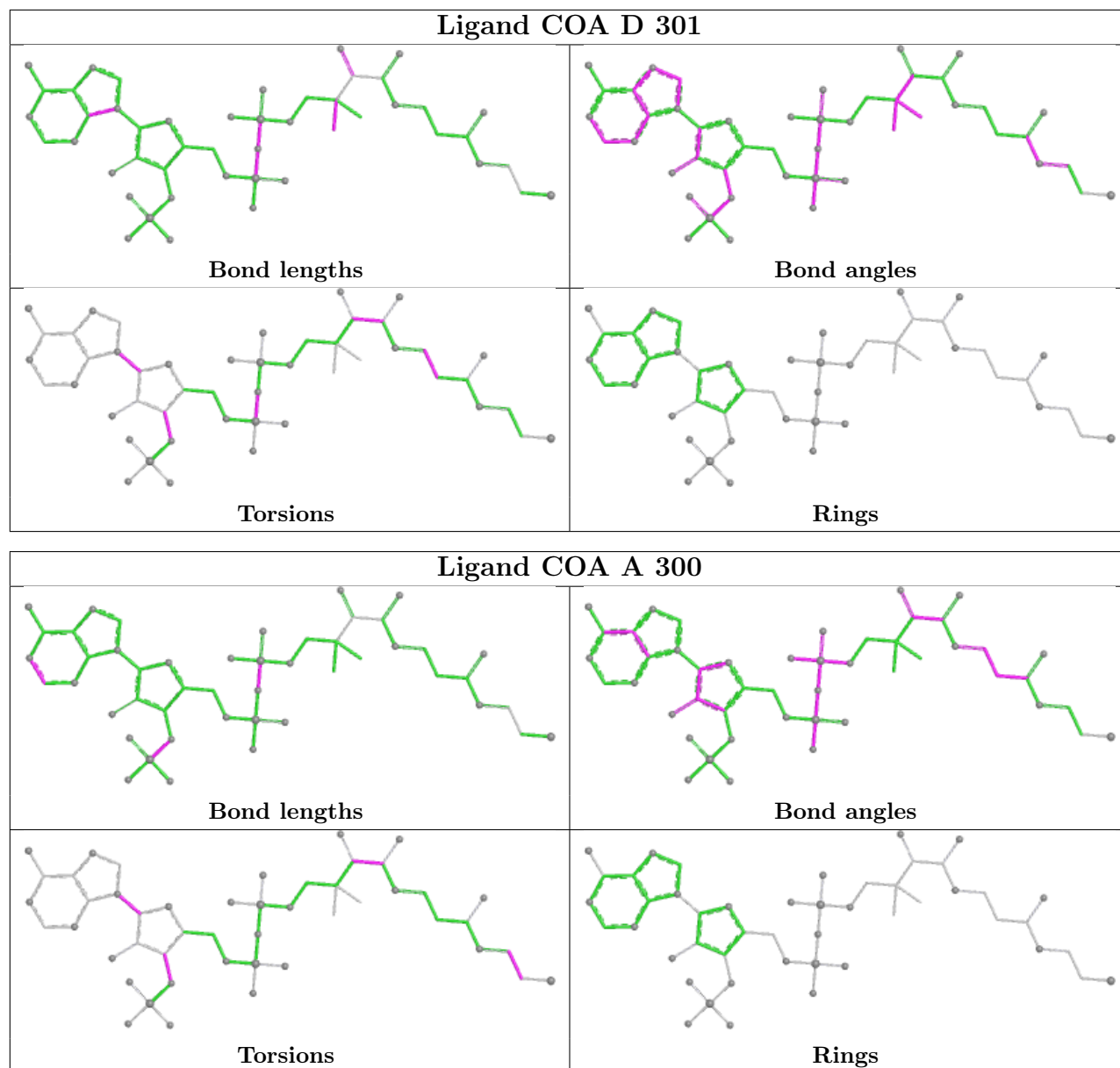
Mol	Chain	Res	Type	Atoms
3	A	300	COA	S1P-C2P-C3P-N4P
3	A	300	COA	C2B-C1B-N9A-C4A
3	D	301	COA	C2B-C1B-N9A-C4A
3	A	300	COA	C2B-C1B-N9A-C8A
3	D	301	COA	C2B-C3B-O3B-P3B
3	D	301	COA	O4B-C1B-N9A-C8A
3	D	301	COA	P2A-O3A-P1A-O1A
3	D	301	COA	P2A-O3A-P1A-O2A
3	A	300	COA	N8P-C9P-CAP-OAP
3	D	301	COA	N8P-C9P-CAP-OAP

There are no ring outliers.

3 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	301	COA	2	0
3	A	300	COA	5	0
4	E	401	SO4	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	285/288 (98%)	-0.89	0	100 100	10, 29, 54, 73	0
1	D	285/288 (98%)	-0.48	0	100 100	13, 40, 65, 85	0
2	B	385/388 (99%)	-0.82	0	100 100	10, 31, 58, 81	0
2	E	385/388 (99%)	-0.75	1 (0%)	90 90	10, 32, 66, 87	0
All	All	1340/1352 (99%)	-0.74	1 (0%)	92 91	10, 32, 62, 87	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	365	GLY	2.2

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	NEP	D	246	14/15	0.96	0.05	19,25,39,43	0
1	NEP	A	246	14/15	0.98	0.04	11,27,41,43	0

6.3 Carbohydrates [i](#)

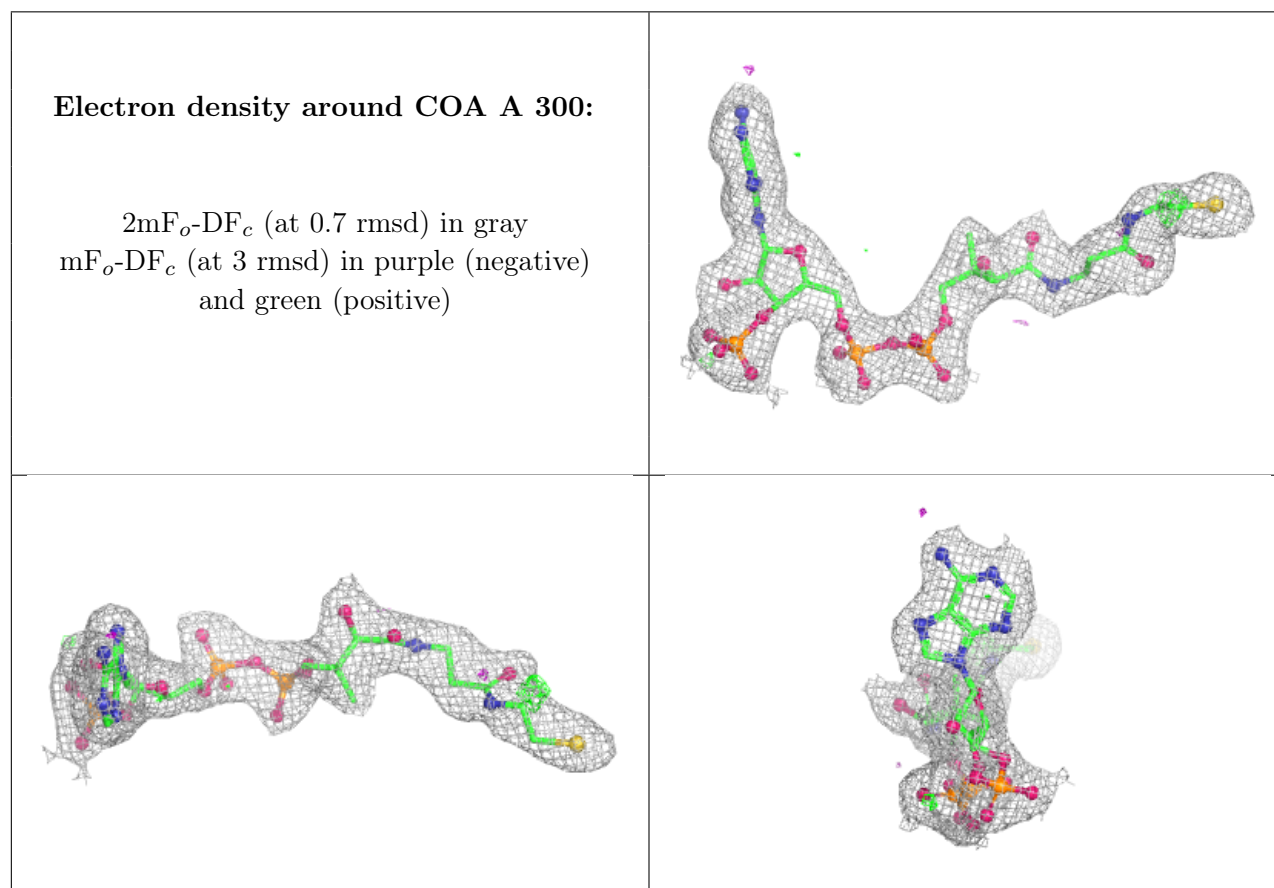
There are no oligosaccharides in this entry.

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.

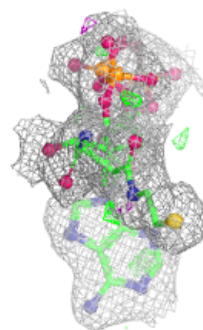
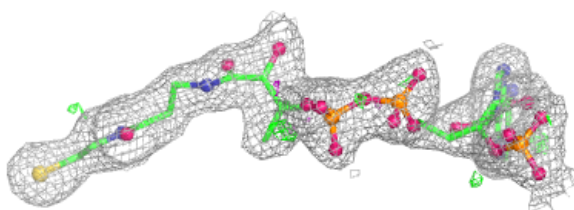
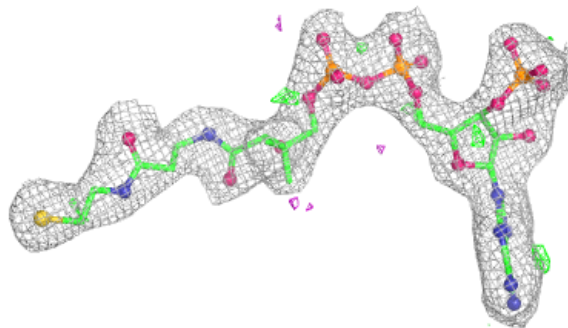
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	COA	A	300	48/48	0.98	0.04	16,24,36,42	0
4	SO4	B	400	5/5	0.98	0.05	70,71,71,72	0
3	COA	D	301	48/48	0.99	0.04	13,22,30,39	0
4	SO4	E	401	5/5	0.99	0.04	47,48,48,48	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



Electron density around COA D 301:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.