



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:06 PM UTC

PDB ID : 1TU0 / pdb_00001tu0
Title : Aspartate Transcarbamoylase Catalytic Chain Mutant E50A Complex with Phosphonoacetamide
Authors : Stieglitz, K.; Stec, B.; Baker, D.P.; Kantrowitz, E.R.
Deposited on : 2004-06-23
Resolution : 2.55 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
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

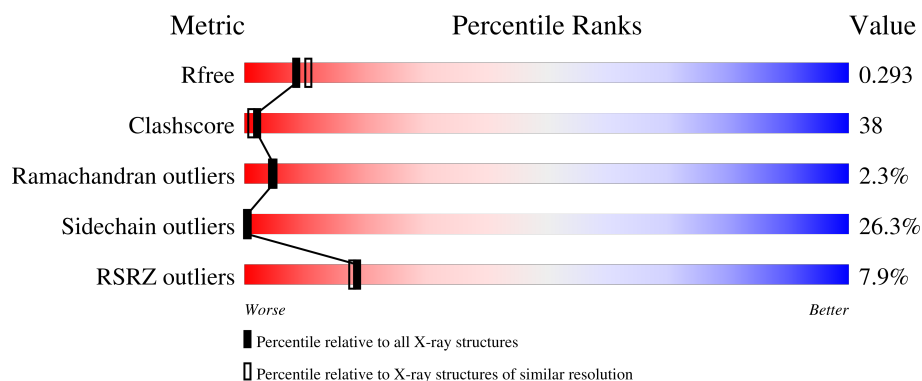
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.55 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}	180053	1091 (2.54-2.54)
Clashscore	190562	1120 (2.54-2.54)
Ramachandran outliers	187476	1106 (2.54-2.54)
Sidechain outliers	187428	1106 (2.54-2.54)
RSRZ outliers	180081	1091 (2.54-2.54)

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	310	5% 35% 46% 17% .
1	C	310	5% 47% 36% 15% .
2	B	153	14% 20% 51% 23% 6%
2	D	153	14% 31% 45% 21% .

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	PCT	C	1312	-	X	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7596 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 Aspartate carbamoyltransferase catalytic chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	310	Total	C	N	O	S	0	0	0
			2411	1525	423	454	9			
1	C	310	Total	C	N	O	S	0	0	0
			2411	1525	423	454	9			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	50	ALA	GLU	engineered mutation	UNP P0A786
C	50	ALA	GLU	engineered mutation	UNP P0A786

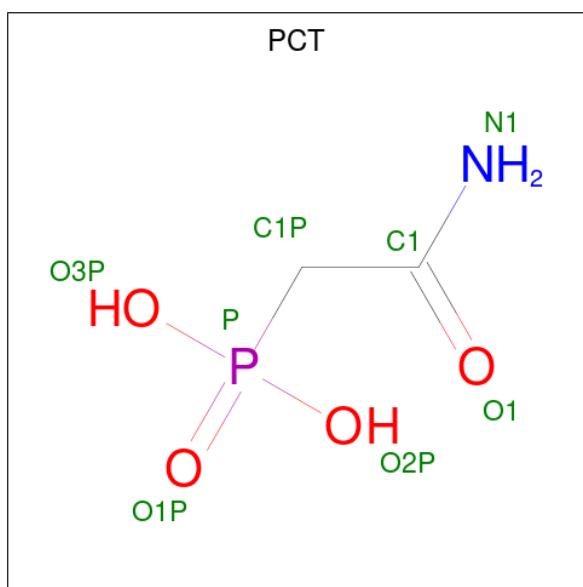
- Molecule 2 is a protein called Aspartate carbamoyltransferase regulatory chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	153	Total	C	N	O	S	0	0	0
			1201	752	213	230	6			
2	D	153	Total	C	N	O	S	0	0	0
			1201	752	213	230	6			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1	MET	-	initiating methionine	UNP P0A7F3
D	1	MET	-	initiating methionine	UNP P0A7F3

- Molecule 3 is PHOSPHONOACETAMIDE (CCD ID: PCT) (formula: C₂H₆NO₄P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			8	2	1	4	1		
3	C	1	Total	C	N	O	P	0	0
			8	2	1	4	1		

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Zn	0	0
			1	1		
4	D	1	Total	Zn	0	0
			1	1		

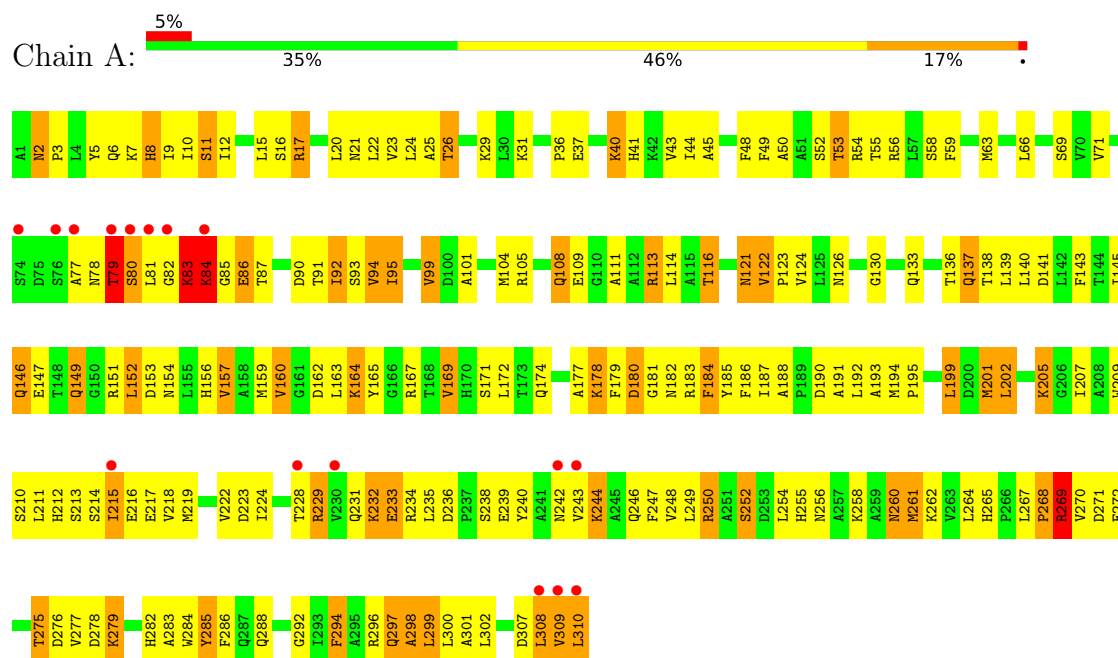
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	119	Total	O	0	0
			119	119		
5	B	53	Total	O	0	0
			53	53		
5	C	131	Total	O	0	0
			131	131		
5	D	51	Total	O	0	0
			51	51		

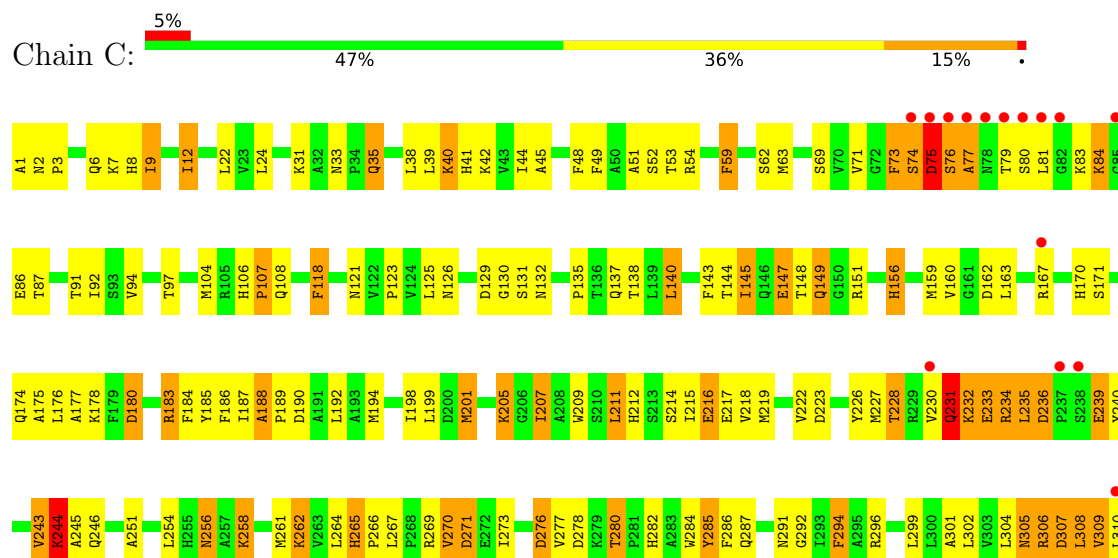
3 Residue-property plots

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.

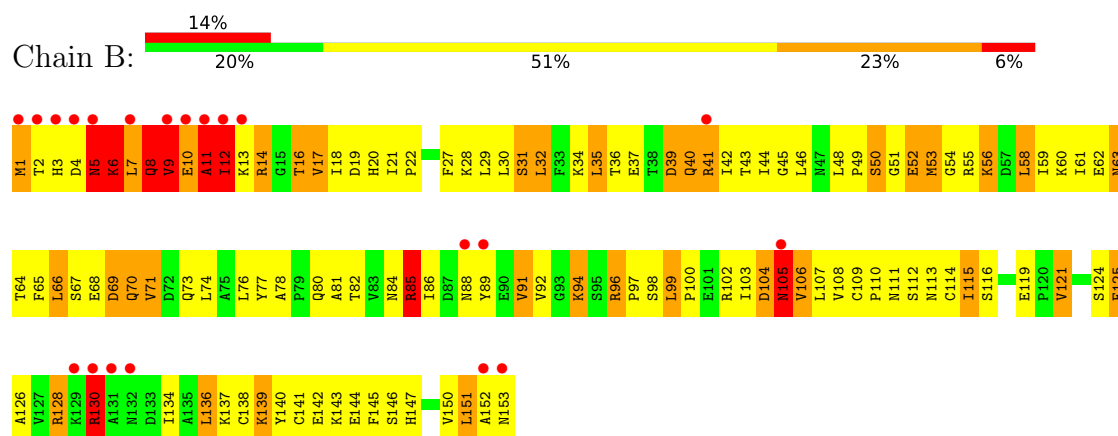
- Molecule 1: Aspartate carbamoyltransferase catalytic chain



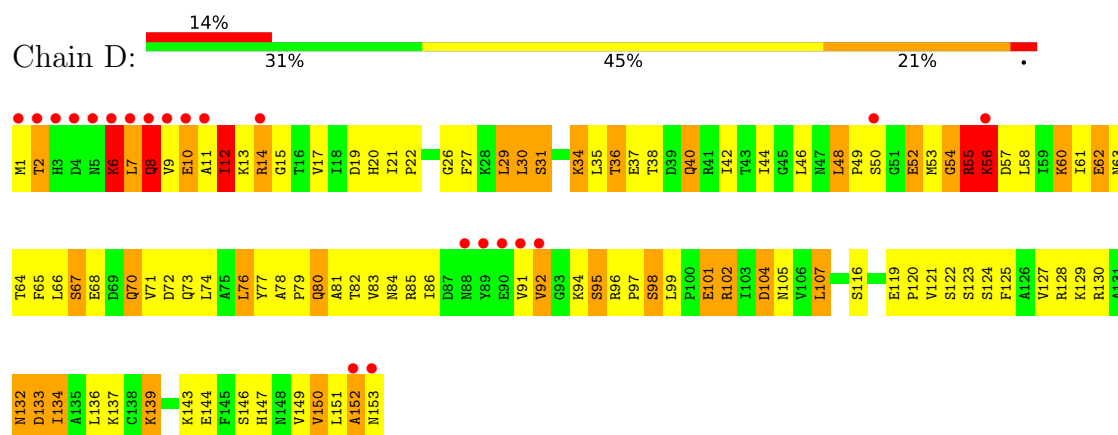
- Molecule 1: Aspartate carbamoyltransferase catalytic chain



● Molecule 2: Aspartate carbamoyltransferase regulatory chain



● Molecule 2: Aspartate carbamoyltransferase regulatory chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 3 2 1	Depositor
Cell constants a, b, c, α , β , γ	122.20Å 122.20Å 142.70Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 2.55 30.00 – 2.55	Depositor EDS
% Data completeness (in resolution range)	94.0 (30.00-2.55) 97.7 (30.00-2.55)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.27 (at 2.55Å)	Xtriage
Refinement program	SHELXL-97	Depositor
R, R_{free}	0.211 , 0.279 0.213 , 0.293	Depositor DCC
R_{free} test set	1994 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	22.5	Xtriage
Anisotropy	0.409	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 324.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.043 for -h,-k,l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	7596	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.98% 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: ZN, PCT

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	0.74	4/2457 (0.2%)	1.55	29/3334 (0.9%)
1	C	0.62	4/2457 (0.2%)	1.55	30/3334 (0.9%)
2	B	2.28	9/1219 (0.7%)	1.74	37/1647 (2.2%)
2	D	1.23	9/1219 (0.7%)	1.62	26/1647 (1.6%)
All	All	1.19	26/7352 (0.4%)	1.60	122/9962 (1.2%)

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	C	0	1
2	B	0	3
2	D	0	2
All	All	0	9

All (26) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	105	ASN	C-N	43.74	1.74	1.33
2	B	105	ASN	N-CA	32.39	1.88	1.46
2	B	8	GLN	C-N	-29.55	0.93	1.33
2	B	9	VAL	C-N	27.66	1.73	1.33
2	D	152	ALA	C-N	26.25	1.70	1.33
1	A	309	VAL	C-N	25.87	1.69	1.33
2	B	5	ASN	C-N	24.05	1.67	1.33
2	B	11	ALA	C-N	-23.92	1.01	1.33
2	D	56	LYS	C-N	17.86	1.57	1.33
2	D	8	GLN	C-N	16.20	1.54	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	153	ASN	C-OXT	14.55	1.52	1.23
2	D	7	LEU	C-N	-13.63	1.14	1.33
1	C	75	ASP	C-N	-12.63	1.11	1.33
1	C	51	ALA	C-N	-12.28	1.16	1.33
1	C	309	VAL	C-N	11.86	1.50	1.33
1	A	77	ALA	C-N	9.39	1.46	1.33
2	B	12	ILE	C-N	8.92	1.46	1.33
2	D	55	ARG	C-N	-8.31	1.22	1.33
2	D	11	ALA	C-N	-7.82	1.23	1.33
2	D	12	ILE	C-N	-7.47	1.23	1.33
1	C	74	SER	C-N	-6.21	1.25	1.33
1	A	80	SER	N-CA	-6.13	1.38	1.46
2	D	104	ASP	C-N	-5.62	1.25	1.33
2	B	6	LYS	C-N	5.37	1.41	1.33
2	D	133	ASP	C-N	5.12	1.46	1.33
1	A	79	THR	C-N	-5.03	1.27	1.34

All (122) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	8	GLN	O-C-N	23.91	150.73	122.75
1	C	309	VAL	O-C-N	-23.10	93.69	122.57
1	A	79	THR	CA-C-N	16.57	144.14	120.28
1	A	79	THR	C-N-CA	16.57	144.14	120.28
2	D	8	GLN	O-C-N	15.77	143.56	122.59
2	B	105	ASN	CA-C-N	-14.11	105.70	122.35
2	B	105	ASN	C-N-CA	-14.11	105.70	122.35
1	C	74	SER	CA-C-N	13.37	147.07	121.54
1	C	74	SER	C-N-CA	13.37	147.07	121.54
1	A	309	VAL	O-C-N	-12.38	109.42	122.05
2	D	104	ASP	CA-C-N	12.09	144.64	121.54
2	D	104	ASP	C-N-CA	12.09	144.64	121.54
1	A	85	GLY	N-CA-C	11.98	127.69	114.40
1	C	51	ALA	O-C-N	-11.12	109.20	122.87
1	C	51	ALA	CA-C-N	10.62	141.83	121.54
1	C	51	ALA	C-N-CA	10.62	141.83	121.54
2	B	12	ILE	O-C-N	10.49	135.68	122.57
1	C	309	VAL	CA-C-N	10.12	139.93	121.70
1	C	309	VAL	C-N-CA	10.12	139.93	121.70
2	D	152	ALA	O-C-N	10.11	135.19	123.06
2	B	8	GLN	CA-C-N	-9.92	104.11	121.97
2	B	8	GLN	C-N-CA	-9.92	104.11	121.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	269	ARG	CD-NE-CZ	9.78	138.09	124.40
1	A	84	LYS	O-C-N	-9.08	112.43	122.79
2	D	133	ASP	O-C-N	-9.00	112.99	123.25
2	D	104	ASP	O-C-N	-8.96	112.91	122.94
2	D	11	ALA	CA-C-N	8.88	137.95	121.97
2	D	11	ALA	C-N-CA	8.88	137.95	121.97
2	D	56	LYS	CA-C-N	-8.65	110.79	122.99
2	D	56	LYS	C-N-CA	-8.65	110.79	122.99
2	D	105	ASN	CA-C-N	-8.35	106.95	121.97
2	D	105	ASN	C-N-CA	-8.35	106.95	121.97
2	D	56	LYS	O-C-N	8.24	134.72	122.94
1	C	74	SER	CA-C-O	-7.96	112.08	120.99
2	D	152	ALA	CA-C-N	-7.86	107.56	121.70
2	D	152	ALA	C-N-CA	-7.86	107.56	121.70
2	D	12	ILE	O-C-N	7.82	132.35	122.57
1	C	294	PHE	CA-CB-CG	-7.58	106.22	113.80
2	B	31	SER	CA-C-N	7.48	130.80	120.63
2	B	31	SER	C-N-CA	7.48	130.80	120.63
1	A	77	ALA	O-C-N	7.39	132.42	122.59
1	A	84	LYS	CB-CA-C	7.34	124.73	109.68
2	D	105	ASN	O-C-N	7.21	132.17	122.59
2	D	8	GLN	CA-C-N	-7.19	112.56	122.92
2	D	8	GLN	C-N-CA	-7.19	112.56	122.92
1	C	77	ALA	CA-C-N	7.16	135.54	122.79
1	C	77	ALA	C-N-CA	7.16	135.54	122.79
2	B	6	LYS	O-C-N	7.04	131.96	122.59
2	B	5	ASN	CA-C-N	6.91	134.74	121.54
2	B	5	ASN	C-N-CA	6.91	134.74	121.54
2	B	105	ASN	O-C-N	6.89	131.75	122.59
1	A	84	LYS	N-CA-CB	6.82	120.11	110.36
2	B	104	ASP	CA-C-N	6.76	134.45	121.54
2	B	104	ASP	C-N-CA	6.76	134.45	121.54
1	C	75	ASP	N-CA-C	6.68	125.03	110.80
1	A	84	LYS	CA-C-O	-6.60	114.21	121.87
2	B	130	ARG	CA-C-N	6.55	134.04	121.54
2	B	130	ARG	C-N-CA	6.55	134.04	121.54
1	C	75	ASP	O-C-N	-6.38	114.11	122.59
2	B	12	ILE	CA-C-N	-6.33	109.45	121.54
2	B	12	ILE	C-N-CA	-6.33	109.45	121.54
1	A	260	ASN	CA-CB-CG	6.33	118.93	112.60
1	A	294	PHE	CA-CB-CG	-6.27	107.53	113.80
2	D	11	ALA	O-C-N	-6.24	116.02	122.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	286	PHE	CA-CB-CG	-6.16	107.64	113.80
2	D	6	LYS	CA-C-N	6.06	131.60	122.87
2	D	6	LYS	C-N-CA	6.06	131.60	122.87
1	C	188	ALA	O-C-N	6.05	126.18	121.88
1	A	8	HIS	CA-CB-CG	6.04	119.84	113.80
2	B	9	VAL	CA-C-N	-6.03	112.39	122.64
2	B	9	VAL	C-N-CA	-6.03	112.39	122.64
1	C	73	PHE	CA-CB-CG	5.92	119.72	113.80
2	B	6	LYS	CA-C-N	-5.91	112.21	122.37
2	B	6	LYS	C-N-CA	-5.91	112.21	122.37
1	A	309	VAL	CA-C-N	5.89	132.30	121.70
1	A	309	VAL	C-N-CA	5.89	132.30	121.70
1	A	298	ALA	CA-C-N	5.81	128.38	120.54
1	A	298	ALA	C-N-CA	5.81	128.38	120.54
1	A	111	ALA	CA-C-N	5.80	128.53	120.29
1	A	111	ALA	C-N-CA	5.80	128.53	120.29
1	A	286	PHE	CA-C-N	5.80	127.98	120.44
1	A	286	PHE	C-N-CA	5.80	127.98	120.44
1	A	184	PHE	CA-CB-CG	-5.78	108.02	113.80
1	A	80	SER	N-CA-C	5.75	118.33	111.71
1	A	268	PRO	CA-C-N	-5.70	114.15	122.65
1	A	268	PRO	C-N-CA	-5.70	114.15	122.65
1	C	307	ASP	CA-C-N	-5.69	114.85	122.42
1	C	307	ASP	C-N-CA	-5.69	114.85	122.42
1	C	107	PRO	CA-C-N	-5.66	114.22	122.65
1	C	107	PRO	C-N-CA	-5.66	114.22	122.65
1	C	33	ASN	CA-C-N	5.63	125.81	119.90
1	C	33	ASN	C-N-CA	5.63	125.81	119.90
2	B	115	ILE	CA-C-N	5.63	128.60	120.38
2	B	115	ILE	C-N-CA	5.63	128.60	120.38
1	A	26	THR	O-C-N	5.56	127.87	122.09
2	B	85	ARG	CA-C-N	-5.55	115.28	122.99
2	B	85	ARG	C-N-CA	-5.55	115.28	122.99
2	B	115	ILE	O-C-N	5.54	127.46	121.87
2	D	12	ILE	CA-C-N	-5.50	112.48	120.29
2	D	12	ILE	C-N-CA	-5.50	112.48	120.29
1	A	122	VAL	CA-C-O	5.48	124.81	119.71
1	C	118	PHE	CA-CB-CG	-5.47	108.33	113.80
2	B	152	ALA	N-CA-C	-5.24	107.02	113.41
1	C	9	ILE	CA-C-N	-5.20	117.87	122.97
1	C	9	ILE	C-N-CA	-5.20	117.87	122.97
2	B	104	ASP	O-C-N	5.20	129.08	123.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	106	VAL	N-CA-C	-5.19	107.35	111.81
1	A	269	ARG	NE-CZ-NH2	5.17	123.86	119.20
1	C	48	PHE	CA-CB-CG	-5.17	108.64	113.80
1	C	156	HIS	CA-CB-CG	-5.14	108.66	113.80
1	C	236	ASP	CA-CB-CG	5.09	117.69	112.60
2	B	4	ASP	CA-CB-CG	5.08	117.68	112.60
1	A	269	ARG	NE-CZ-NH1	-5.08	116.42	121.50
2	D	54	GLY	CA-C-N	5.05	130.61	123.14
2	D	54	GLY	C-N-CA	5.05	130.61	123.14
2	B	152	ALA	CA-C-N	5.04	130.76	121.70
2	B	152	ALA	C-N-CA	5.04	130.76	121.70
2	B	99	LEU	CA-C-O	5.03	124.83	119.80
2	B	130	ARG	CA-C-O	-5.01	113.35	120.51
2	B	125	PHE	CA-C-N	-5.00	116.34	122.84
2	B	125	PHE	C-N-CA	-5.00	116.34	122.84
1	C	265	HIS	O-C-N	5.00	127.07	121.32

There are no chirality outliers.

All (9) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	83	LYS	Mainchain
1	A	84	LYS	Peptide,Mainchain
2	B	11	ALA	Mainchain
2	B	128	ARG	Mainchain
2	B	8	GLN	Mainchain
1	C	73	PHE	Mainchain
2	D	132	ASN	Mainchain
2	D	133	ASP	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	2411	0	2421	185	0
1	C	2411	0	2418	119	0
2	B	1201	0	1215	136	5

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	1201	0	1216	116	0
3	A	8	0	4	1	0
3	C	8	0	4	6	0
4	B	1	0	0	0	0
4	D	1	0	0	0	0
5	A	119	0	0	9	0
5	B	53	0	0	11	0
5	C	131	0	0	6	5
5	D	51	0	0	9	0
All	All	7596	0	7278	544	5

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 38.

All (544) 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:A:309:VAL:C	1:A:310:LEU:N	1.69	1.50
2:D:152:ALA:C	2:D:153:ASN:N	1.70	1.47
2:B:9:VAL:C	2:B:10:GLU:N	1.73	1.46
2:B:105:ASN:C	2:B:106:VAL:N	1.74	1.45
2:B:105:ASN:N	2:B:105:ASN:CA	1.88	1.36
2:B:9:VAL:HG12	2:B:10:GLU:N	1.59	1.15
2:B:17:VAL:HG22	2:B:60:LYS:HG2	1.43	1.00
2:B:9:VAL:CG1	2:B:10:GLU:N	2.29	0.95
1:A:29:LYS:NZ	1:A:310:LEU:HB2	1.84	0.93
2:B:30:LEU:HA	2:B:35:LEU:HD12	1.52	0.90
1:C:236:ASP:HB3	1:C:239:GLU:HB3	1.52	0.89
1:C:219:MET:HE3	1:C:254:LEU:HA	1.54	0.88
2:B:12:ILE:HG22	2:B:62:GLU:OE2	1.76	0.86
2:D:146:SER:HB3	2:D:149:VAL:HG23	1.59	0.85
1:A:29:LYS:NZ	1:A:310:LEU:CB	2.40	0.85
2:B:49:PRO:HB2	5:B:206:HOH:O	1.77	0.85
2:D:130:ARG:HD2	5:D:204:HOH:O	1.77	0.84
2:D:136:LEU:HD12	2:D:150:VAL:HG21	1.59	0.83
1:A:187:ILE:HG12	1:A:212:HIS:HB2	1.60	0.83
1:A:159:MET:HE3	1:A:172:LEU:HD23	1.61	0.83
1:C:194:MET:HE3	1:C:198:ILE:HG21	1.58	0.83
1:C:54:ARG:HB3	3:C:1312:PCT:O1P	1.79	0.82
2:B:107:LEU:HD22	2:B:150:VAL:HG12	1.58	0.82
1:C:205:LYS:HB3	1:C:207:ILE:HD12	1.63	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:29:LYS:HZ1	1:A:310:LEU:HB2	1.45	0.81
1:A:183:ARG:HH22	1:A:210:SER:H	1.30	0.80
1:A:183:ARG:HH12	1:A:210:SER:HB3	1.47	0.79
2:B:66:LEU:HD12	2:B:71:VAL:HG23	1.64	0.79
2:D:152:ALA:C	2:D:153:ASN:CA	2.55	0.79
2:B:30:LEU:HD11	2:B:44:ILE:HG12	1.63	0.79
2:B:105:ASN:C	2:B:106:VAL:CA	2.56	0.79
1:C:292:GLY:O	1:C:296:ARG:HG3	1.83	0.79
1:A:265:HIS:H	1:A:288:GLN:HE22	1.29	0.78
2:B:42:ILE:HB	2:D:46:LEU:HB2	1.63	0.78
1:A:163:LEU:HB3	1:A:194:MET:HE2	1.63	0.78
2:B:107:LEU:HD13	2:B:136:LEU:HD13	1.66	0.78
2:B:85:ARG:O	2:B:86:ILE:HD13	1.84	0.77
1:C:12:ILE:HD13	1:C:135:PRO:HA	1.66	0.77
1:A:113:ARG:O	1:A:116:THR:HB	1.83	0.77
2:B:46:LEU:HB2	2:D:42:ILE:HB	1.67	0.77
1:A:234:ARG:O	1:A:235:LEU:HD23	1.85	0.77
1:A:201:MET:HG2	1:A:202:LEU:HD23	1.68	0.76
2:B:80:GLN:HB2	5:B:184:HOH:O	1.86	0.75
2:D:66:LEU:H	2:D:85:ARG:HH12	1.34	0.74
1:A:154:ASN:HA	1:A:181:GLY:O	1.87	0.74
1:C:24:LEU:HD22	1:C:143:PHE:HB2	1.68	0.74
1:A:183:ARG:HH22	1:A:210:SER:N	1.85	0.74
2:B:99:LEU:HD12	2:B:100:PRO:HD2	1.68	0.74
2:B:50:SER:H	2:B:55:ARG:HA	1.51	0.73
1:A:90:ASP:O	1:A:94:VAL:HG13	1.88	0.73
1:C:52:SER:HB2	3:C:1312:PCT:P	2.28	0.73
1:A:229:ARG:HH11	1:A:229:ARG:HB3	1.53	0.73
1:A:160:VAL:HG13	1:A:187:ILE:HB	1.69	0.73
2:D:22:PRO:HD3	2:D:80:GLN:OE1	1.89	0.73
1:A:292:GLY:O	1:A:296:ARG:HG3	1.89	0.72
1:C:174:GLN:HG2	1:C:201:MET:HE1	1.70	0.72
1:A:79:THR:HG22	1:A:80:SER:H	1.53	0.72
1:A:50:ALA:HB3	1:A:105:ARG:HG2	1.70	0.72
1:A:153:ASP:OD2	1:A:179:PHE:HB3	1.89	0.72
1:A:29:LYS:HZ3	1:A:310:LEU:CB	2.00	0.72
1:A:153:ASP:HB3	1:A:154:ASN:ND2	2.04	0.72
2:D:76:LEU:HD12	2:D:151:LEU:HD21	1.72	0.71
1:C:301:ALA:O	1:C:305:ASN:HB2	1.90	0.71
1:A:307:ASP:OD1	1:A:308:LEU:HD22	1.89	0.71
1:A:223:ASP:O	1:A:261:MET:HA	1.91	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:163:LEU:HG	1:A:188:ALA:HB2	1.72	0.71
2:B:12:ILE:HG21	2:B:62:GLU:HB2	1.72	0.71
2:D:152:ALA:CA	2:D:153:ASN:N	2.54	0.71
1:C:184:PHE:HB2	1:C:209:TRP:HB3	1.72	0.71
2:B:28:LYS:O	2:B:32:LEU:HB2	1.90	0.71
1:C:231:GLN:O	1:C:234:ARG:HB2	1.91	0.70
1:A:285:TYR:HA	1:A:288:GLN:HE21	1.56	0.70
2:D:36:THR:HG23	5:D:160:HOH:O	1.92	0.70
2:D:52:GLU:OE1	2:D:53:MET:HG3	1.92	0.70
2:B:50:SER:OG	2:B:56:LYS:HD2	1.91	0.69
1:A:298:ALA:O	1:A:301:ALA:HB3	1.92	0.69
1:A:66:LEU:HD11	1:A:297:GLN:HG2	1.74	0.69
2:B:3:HIS:O	2:B:9:VAL:HB	1.93	0.69
2:B:22:PRO:HG3	5:B:184:HOH:O	1.91	0.69
2:B:14:ARG:HD2	2:B:63:ASN:HA	1.75	0.69
2:D:124:SER:HB3	2:D:139:LYS:HB2	1.75	0.68
2:D:104:ASP:HA	2:D:123:SER:O	1.93	0.68
2:D:50:SER:HB2	2:D:56:LYS:HG2	1.75	0.68
2:B:16:THR:HG22	2:B:64:THR:O	1.94	0.68
2:B:9:VAL:C	2:B:10:GLU:CA	2.65	0.68
1:C:243:VAL:HA	1:C:246:GLN:NE2	2.08	0.68
1:A:159:MET:HE2	1:A:169:VAL:HG22	1.75	0.68
1:C:59:PHE:O	1:C:63:MET:HG3	1.93	0.67
2:D:10:GLU:HG3	5:D:198:HOH:O	1.94	0.67
2:D:102:ARG:HD2	2:D:124:SER:OG	1.95	0.67
1:C:163:LEU:HG	1:C:188:ALA:HB2	1.75	0.67
2:D:147:HIS:HA	2:D:150:VAL:HG23	1.75	0.67
1:C:3:PRO:HG2	1:C:22:LEU:HD22	1.77	0.66
2:B:71:VAL:O	2:B:97:PRO:HB3	1.95	0.66
2:B:147:HIS:O	2:B:151:LEU:HB2	1.95	0.66
2:D:22:PRO:HA	2:D:53:MET:SD	2.35	0.66
2:D:34:LYS:HE3	2:D:34:LYS:H	1.59	0.66
1:C:1:ALA:HB2	1:C:306:ARG:NH2	2.11	0.66
2:D:34:LYS:HA	5:D:160:HOH:O	1.94	0.66
2:B:52:GLU:OE2	2:B:53:MET:HE2	1.97	0.65
2:B:104:ASP:OD1	2:B:124:SER:HB2	1.96	0.65
2:B:134:ILE:H	2:B:147:HIS:CD2	2.15	0.65
2:D:14:ARG:HA	2:D:86:ILE:O	1.96	0.65
1:A:108:GLN:HG2	2:B:115:ILE:HA	1.79	0.65
1:A:45:ALA:HB2	1:A:99:VAL:HG11	1.79	0.65
2:B:21:ILE:O	2:B:56:LYS:HB2	1.96	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:20:HIS:HB3	5:B:194:HOH:O	1.97	0.64
2:D:49:PRO:HA	2:D:54:GLY:O	1.97	0.64
1:C:52:SER:HB2	3:C:1312:PCT:O2P	1.98	0.64
2:D:56:LYS:HE3	2:D:58:LEU:HD12	1.80	0.64
1:A:201:MET:O	1:A:205:LYS:HB2	1.97	0.64
1:A:229:ARG:HB3	1:A:229:ARG:NH1	2.12	0.64
1:A:29:LYS:HZ3	1:A:310:LEU:HB3	1.62	0.63
2:B:20:HIS:NE2	2:B:53:MET:HE3	2.13	0.63
1:A:29:LYS:HZ1	1:A:310:LEU:CB	2.05	0.63
1:A:78:ASN:HA	1:A:83:LYS:HB3	1.81	0.63
1:A:186:PHE:O	1:A:211:LEU:HD23	1.98	0.63
2:B:111:ASN:HD22	2:B:114:CYS:HB2	1.62	0.62
2:D:1:MET:HE1	2:D:94:LYS:NZ	2.14	0.62
1:A:11:SER:HB2	1:A:133:GLN:HG3	1.82	0.62
1:C:81:LEU:HD22	1:C:86:GLU:OE1	2.00	0.62
1:C:160:VAL:O	1:C:228:THR:HG23	2.00	0.62
1:C:199:LEU:HD22	1:C:209:TRP:CH2	2.34	0.62
1:A:275:THR:O	1:A:278:ASP:HB2	2.00	0.62
1:C:175:ALA:O	1:C:178:LYS:HB2	1.99	0.62
1:C:231:GLN:HB3	1:C:233:GLU:OE1	1.99	0.62
2:D:17:VAL:HG22	2:D:60:LYS:HG2	1.82	0.62
2:D:27:PHE:O	2:D:30:LEU:HD12	1.99	0.62
2:D:67:SER:HB3	2:D:70:GLN:NE2	2.15	0.62
1:A:275:THR:HG23	5:A:1419:HOH:O	1.99	0.61
2:B:18:ILE:HG22	2:B:21:ILE:HD11	1.82	0.61
2:B:65:PHE:CD2	2:B:85:ARG:HG2	2.34	0.61
1:C:125:LEU:HD23	1:C:299:LEU:HD23	1.81	0.61
2:D:147:HIS:O	2:D:151:LEU:HD12	2.00	0.61
2:B:65:PHE:HD2	2:B:85:ARG:HG2	1.65	0.61
2:B:11:ALA:O	2:B:12:ILE:O	2.18	0.61
1:C:219:MET:HE1	1:C:254:LEU:HD23	1.83	0.61
1:A:164:LYS:HG3	1:A:193:ALA:O	2.01	0.60
1:A:187:ILE:HD13	1:A:214:SER:O	2.01	0.60
2:B:114:CYS:SG	2:B:116:SER:HB3	2.41	0.60
1:C:145:ILE:O	1:C:149:GLN:HB2	2.00	0.60
1:C:187:ILE:HG12	1:C:212:HIS:HB2	1.83	0.60
2:D:10:GLU:O	2:D:10:GLU:HG2	2.01	0.60
1:A:164:LYS:HE2	1:A:165:TYR:CZ	2.37	0.60
1:C:76:SER:HA	1:C:79:THR:OG1	2.01	0.60
2:B:9:VAL:CA	2:B:10:GLU:N	2.63	0.60
1:A:52:SER:HB2	1:A:105:ARG:NH1	2.16	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:85:ARG:HH11	2:B:85:ARG:HB3	1.66	0.60
2:D:70:GLN:O	2:D:73:GLN:HB2	2.00	0.60
1:C:244:LYS:HG3	1:C:245:ALA:N	2.16	0.59
1:A:108:GLN:HG3	2:B:113:ASN:O	2.02	0.59
1:C:131:SER:HB2	5:C:1333:HOH:O	2.01	0.59
1:C:86:GLU:HG2	1:C:91:THR:OG1	2.03	0.59
2:D:102:ARG:HA	2:D:125:PHE:O	2.02	0.59
1:A:31:LYS:HE2	1:A:147:GLU:OE1	2.03	0.59
1:C:81:LEU:HD13	1:C:91:THR:OG1	2.02	0.59
1:A:31:LYS:HE3	5:A:1367:HOH:O	2.02	0.59
1:A:59:PHE:HZ	1:A:136:THR:HG21	1.67	0.59
2:D:7:LEU:O	2:D:8:GLN:O	2.20	0.59
1:C:144:THR:O	1:C:148:THR:HG23	2.03	0.58
2:D:34:LYS:HB3	2:D:37:GLU:HG3	1.85	0.58
1:C:31:LYS:NZ	1:C:291:ASN:HD21	2.00	0.58
1:C:170:HIS:O	1:C:174:GLN:HG3	2.03	0.58
2:D:73:GLN:CG	5:D:203:HOH:O	2.52	0.58
1:A:240:TYR:O	1:A:244:LYS:HB2	2.04	0.58
1:C:81:LEU:HB2	1:C:86:GLU:CB	2.34	0.58
2:B:41:ARG:HA	2:D:46:LEU:O	2.04	0.58
1:A:249:LEU:HD12	1:A:250:ARG:H	1.68	0.57
2:B:54:GLY:O	2:B:55:ARG:HG3	2.05	0.57
2:D:72:ASP:HB3	2:D:98:SER:O	2.04	0.57
1:A:232:LYS:HG3	1:A:233:GLU:N	2.19	0.57
1:A:80:SER:C	1:A:81:LEU:HD12	2.30	0.57
2:B:143:LYS:HE2	5:B:168:HOH:O	2.03	0.57
1:C:287:GLN:HG3	5:C:1421:HOH:O	2.03	0.57
2:D:85:ARG:HG2	2:D:85:ARG:HH11	1.68	0.57
1:A:261:MET:HE2	1:A:282:HIS:HB3	1.85	0.57
2:D:53:MET:HE2	2:D:80:GLN:HE22	1.70	0.57
2:D:34:LYS:HE3	2:D:34:LYS:N	2.20	0.57
2:B:27:PHE:HE1	2:D:30:LEU:HD13	1.70	0.56
2:B:43:THR:HB	2:B:60:LYS:HB2	1.86	0.56
2:B:55:ARG:HH21	2:B:55:ARG:HB2	1.70	0.56
2:B:105:ASN:CA	2:B:106:VAL:N	2.66	0.56
1:C:189:PRO:HG2	1:C:192:LEU:HB2	1.88	0.56
2:B:66:LEU:HD11	2:B:70:GLN:HB2	1.86	0.56
2:B:102:ARG:HB2	2:B:102:ARG:HH11	1.70	0.56
1:A:66:LEU:CD1	1:A:297:GLN:HG2	2.34	0.56
2:B:66:LEU:HD13	2:B:70:GLN:HG3	1.87	0.56
2:B:107:LEU:CD1	2:B:136:LEU:HD13	2.34	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:58:SER:OG	1:A:296:ARG:HD2	2.06	0.56
1:C:261:MET:HG3	5:C:1321:HOH:O	2.05	0.56
1:A:83:LYS:HE2	1:A:83:LYS:C	2.31	0.56
2:B:50:SER:CB	2:B:56:LYS:HD2	2.36	0.56
2:B:52:GLU:HG2	2:B:53:MET:HG2	1.88	0.56
1:C:201:MET:O	1:C:201:MET:HG2	2.06	0.56
2:D:26:GLY:HA3	2:D:57:ASP:OD1	2.05	0.55
1:C:81:LEU:HB2	1:C:86:GLU:HB3	1.86	0.55
1:A:8:HIS:CE1	1:A:123:PRO:HA	2.41	0.55
1:A:82:GLY:N	5:A:1423:HOH:O	2.36	0.55
2:B:14:ARG:HA	2:B:86:ILE:O	2.06	0.55
2:D:78:ALA:HB1	2:D:81:ALA:HB2	1.88	0.55
2:B:86:ILE:HD11	2:B:91:VAL:HG13	1.88	0.55
1:C:226:TYR:OH	1:C:266:PRO:HG3	2.07	0.55
2:B:138:CYS:HB3	2:B:141:CYS:SG	2.46	0.55
1:C:156:HIS:HD2	1:C:183:ARG:HB2	1.72	0.54
2:D:71:VAL:HG13	2:D:83:VAL:HG21	1.89	0.54
2:D:146:SER:HB3	2:D:149:VAL:CG2	2.35	0.54
1:A:23:VAL:HG11	1:A:139:LEU:HD13	1.89	0.54
2:B:14:ARG:HG3	2:B:63:ASN:ND2	2.23	0.54
1:C:143:PHE:O	1:C:147:GLU:HB3	2.08	0.54
1:C:258:LYS:O	1:C:282:HIS:HE1	1.90	0.54
2:D:12:ILE:N	5:D:198:HOH:O	2.39	0.54
1:A:121:ASN:HA	5:A:1329:HOH:O	2.07	0.54
1:A:159:MET:HE1	1:A:169:VAL:O	2.08	0.54
2:B:8:GLN:C	2:B:9:VAL:HG23	2.33	0.54
2:B:78:ALA:HB1	2:B:81:ALA:HB2	1.89	0.54
1:A:16:SER:O	1:A:20:LEU:HG	2.08	0.54
1:A:29:LYS:NZ	1:A:310:LEU:HB3	2.17	0.54
1:A:261:MET:CE	1:A:282:HIS:HB3	2.38	0.54
1:A:184:PHE:HE1	1:A:207:ILE:HG21	1.72	0.54
1:A:199:LEU:HG	1:A:209:TRP:CH2	2.42	0.53
1:C:126:ASN:HD21	1:C:129:ASP:CG	2.16	0.53
2:D:50:SER:O	2:D:54:GLY:HA2	2.08	0.53
1:A:48:PHE:CD1	1:A:56:ARG:HG3	2.43	0.53
1:A:160:VAL:HG12	1:A:187:ILE:O	2.08	0.53
2:B:9:VAL:CG1	2:B:10:GLU:HG2	2.38	0.53
2:D:14:ARG:HD3	2:D:63:ASN:HA	1.91	0.53
1:A:8:HIS:O	1:A:9:ILE:HD13	2.09	0.53
1:A:114:LEU:HD12	2:B:121:VAL:HG21	1.89	0.53
2:B:12:ILE:CG2	2:B:62:GLU:OE2	2.53	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:14:ARG:HG2	2:D:15:GLY:N	2.23	0.53
1:A:15:LEU:O	1:A:178:LYS:HE2	2.08	0.53
1:A:52:SER:HB2	1:A:105:ARG:HH11	1.74	0.53
2:D:73:GLN:HG3	5:D:203:HOH:O	2.07	0.53
2:D:116:SER:HA	2:D:121:VAL:HG21	1.89	0.53
1:A:81:LEU:HG	1:A:86:GLU:HB3	1.91	0.53
2:D:67:SER:O	2:D:70:GLN:HB2	2.08	0.53
2:B:76:LEU:HD21	2:B:134:ILE:HD12	1.90	0.53
2:D:27:PHE:HA	2:D:30:LEU:HD11	1.89	0.53
2:D:79:PRO:HD2	5:D:195:HOH:O	2.08	0.53
1:A:16:SER:HB3	5:A:1328:HOH:O	2.09	0.53
1:A:269:ARG:HA	1:A:272:GLU:OE1	2.09	0.53
1:C:269:ARG:HH21	1:C:273:ILE:HG22	1.73	0.53
1:C:277:VAL:O	1:C:280:THR:HG23	2.08	0.53
1:A:54:ARG:HD2	3:A:1311:PCT:H1P2	1.90	0.52
1:A:141:ASP:O	1:A:145:ILE:HG13	2.09	0.52
1:A:262:LYS:HD2	1:A:284:TRP:CG	2.43	0.52
1:C:49:PHE:CE1	1:C:104:MET:HE3	2.44	0.52
1:C:184:PHE:O	1:C:209:TRP:HA	2.09	0.52
1:C:216:GLU:HG2	1:C:217:GLU:N	2.23	0.52
2:D:137:LYS:HB2	2:D:144:GLU:OE2	2.09	0.52
1:C:209:TRP:HZ3	1:C:211:LEU:HD21	1.74	0.52
1:A:12:ILE:HA	1:A:15:LEU:HD12	1.90	0.52
1:A:81:LEU:HA	1:A:86:GLU:HB3	1.92	0.52
1:C:156:HIS:CD2	1:C:183:ARG:HB2	2.45	0.52
2:B:17:VAL:O	2:B:17:VAL:HG12	2.09	0.52
1:C:59:PHE:O	1:C:62:SER:HB2	2.10	0.52
1:C:52:SER:CB	3:C:1312:PCT:O2P	2.57	0.52
2:D:96:ARG:CD	2:D:97:PRO:HD2	2.39	0.52
1:A:45:ALA:HA	1:A:71:VAL:O	2.08	0.52
2:B:130:ARG:HD2	5:B:179:HOH:O	2.08	0.52
1:A:5:TYR:O	1:A:6:GLN:HB2	2.10	0.52
1:A:91:THR:O	1:A:95:ILE:HG12	2.09	0.52
1:A:232:LYS:HB2	1:A:240:TYR:CD1	2.45	0.52
2:B:52:GLU:CG	2:B:53:MET:HG2	2.40	0.52
1:A:2:ASN:ND2	1:A:5:TYR:HB2	2.25	0.51
1:C:194:MET:CE	1:C:198:ILE:HG21	2.37	0.51
1:C:219:MET:CE	1:C:254:LEU:HD23	2.40	0.51
2:D:107:LEU:HD12	2:D:125:PHE:CD1	2.45	0.51
1:A:43:VAL:O	1:A:99:VAL:HB	2.10	0.51
1:A:162:ASP:OD2	1:A:165:TYR:HB2	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:7:LEU:HD12	2:D:10:GLU:HB2	1.93	0.51
2:B:8:GLN:C	2:B:9:VAL:CG2	2.81	0.51
1:C:118:PHE:HA	5:C:1434:HOH:O	2.10	0.51
2:D:40:GLN:HG2	2:D:62:GLU:O	2.10	0.51
1:C:1:ALA:HB2	1:C:306:ARG:CZ	2.40	0.51
2:D:48:LEU:O	2:D:54:GLY:O	2.29	0.51
1:C:230:VAL:O	1:C:240:TYR:HE2	1.92	0.51
1:C:186:PHE:CE1	1:C:194:MET:HE2	2.46	0.51
1:A:239:GLU:O	1:A:242:ASN:HB2	2.10	0.51
1:C:174:GLN:O	1:C:177:ALA:HB3	2.11	0.50
1:C:205:LYS:HB3	1:C:207:ILE:CD1	2.39	0.50
2:D:21:ILE:C	2:D:53:MET:HE1	2.36	0.50
1:A:262:LYS:HD2	1:A:284:TRP:CD2	2.46	0.50
1:C:239:GLU:O	1:C:243:VAL:HG22	2.10	0.50
1:A:83:LYS:HE2	1:A:83:LYS:O	2.10	0.50
2:B:110:PRO:HD2	2:B:145:PHE:CE1	2.46	0.50
2:B:1:MET:HE1	2:B:17:VAL:HG11	1.92	0.50
1:C:31:LYS:HD2	1:C:294:PHE:CE2	2.47	0.50
1:A:308:LEU:HD13	1:A:308:LEU:H	1.77	0.50
1:C:269:ARG:NH2	1:C:273:ILE:HG22	2.27	0.50
2:D:99:LEU:HD21	2:D:134:ILE:HG21	1.91	0.50
1:A:159:MET:HE1	1:A:172:LEU:HB3	1.94	0.50
1:A:191:ALA:O	1:A:192:LEU:HD23	2.11	0.50
2:B:20:HIS:HA	2:B:56:LYS:HG3	1.93	0.50
1:C:218:VAL:O	1:C:222:VAL:HG13	2.12	0.50
2:D:27:PHE:O	2:D:31:SER:OG	2.30	0.50
1:A:81:LEU:HD21	1:A:86:GLU:OE2	2.11	0.50
2:D:20:HIS:O	2:D:80:GLN:OE1	2.30	0.50
1:A:149:GLN:HE22	1:A:224:ILE:CD1	2.25	0.49
1:A:149:GLN:NE2	1:A:224:ILE:HG12	2.27	0.49
1:A:159:MET:CE	1:A:172:LEU:HB3	2.42	0.49
2:B:11:ALA:O	2:B:12:ILE:C	2.51	0.49
2:B:12:ILE:CG2	2:B:62:GLU:HB2	2.42	0.49
2:B:111:ASN:ND2	2:B:114:CYS:HB2	2.26	0.49
2:D:76:LEU:CD1	2:D:151:LEU:HD11	2.43	0.49
2:B:9:VAL:HG13	2:B:10:GLU:HG2	1.94	0.49
2:B:88:ASN:O	2:B:89:TYR:HB2	2.11	0.49
1:A:183:ARG:HH12	1:A:210:SER:CB	2.23	0.49
1:A:187:ILE:HD13	1:A:215:ILE:HA	1.94	0.49
2:B:19:ASP:O	2:B:20:HIS:HB2	2.12	0.49
1:C:239:GLU:O	1:C:239:GLU:HG2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:99:LEU:HD11	2:D:134:ILE:HD12	1.95	0.49
1:A:29:LYS:HZ3	1:A:310:LEU:HB2	1.62	0.49
1:A:249:LEU:HD12	1:A:250:ARG:N	2.28	0.49
2:B:86:ILE:CD1	2:B:91:VAL:HA	2.43	0.49
1:A:232:LYS:HB2	1:A:240:TYR:CG	2.48	0.48
1:C:24:LEU:CD2	1:C:143:PHE:HB2	2.41	0.48
1:C:270:VAL:HG13	1:C:271:ASP:H	1.78	0.48
2:D:12:ILE:HG21	2:D:62:GLU:HG3	1.95	0.48
1:C:40:LYS:O	1:C:41:HIS:HB2	2.13	0.48
1:C:160:VAL:HG22	1:C:187:ILE:HB	1.95	0.48
1:C:262:LYS:HE3	1:C:284:TRP:CE3	2.48	0.48
1:A:81:LEU:HG	1:A:86:GLU:CB	2.44	0.48
1:A:215:ILE:HD12	5:A:1369:HOH:O	2.13	0.48
1:C:278:ASP:OD2	1:C:285:TYR:OH	2.29	0.48
1:A:186:PHE:HB2	1:A:211:LEU:CD2	2.43	0.48
1:A:309:VAL:HG12	1:A:309:VAL:O	2.12	0.48
1:C:75:ASP:O	1:C:77:ALA:N	2.45	0.48
1:C:232:LYS:HA	1:C:240:TYR:CD2	2.49	0.48
1:A:81:LEU:HD23	1:A:86:GLU:HG2	1.95	0.48
1:A:212:HIS:CD2	1:A:218:VAL:HB	2.48	0.48
2:B:107:LEU:HD22	2:B:150:VAL:CG1	2.38	0.48
1:C:8:HIS:CE1	1:C:123:PRO:HA	2.48	0.48
1:C:269:ARG:HH12	1:C:278:ASP:CG	2.21	0.48
2:D:67:SER:HB3	2:D:70:GLN:HE22	1.78	0.48
2:B:94:LYS:O	2:B:94:LYS:HG2	2.13	0.48
1:A:24:LEU:HD23	1:A:143:PHE:HA	1.96	0.47
1:A:80:SER:O	1:A:81:LEU:HD12	2.14	0.47
1:A:236:ASP:HB3	1:A:239:GLU:H	1.79	0.47
2:B:50:SER:HB2	2:B:56:LYS:H	1.79	0.47
1:C:235:LEU:HB2	1:C:239:GLU:OE2	2.14	0.47
1:A:10:ILE:HA	1:A:126:ASN:HB2	1.95	0.47
1:A:187:ILE:O	1:A:187:ILE:HG22	2.13	0.47
1:A:201:MET:HG2	1:A:202:LEU:N	2.29	0.47
2:B:7:LEU:CD1	2:D:10:GLU:HB2	2.43	0.47
1:C:265:HIS:HA	1:C:266:PRO:HD3	1.73	0.47
2:D:17:VAL:HG22	2:D:60:LYS:CG	2.43	0.47
2:D:19:ASP:HB3	2:D:82:THR:HB	1.96	0.47
2:D:107:LEU:HD11	2:D:136:LEU:HD13	1.96	0.47
2:B:108:VAL:O	2:B:110:PRO:HD3	2.14	0.47
2:D:107:LEU:HB3	2:D:125:PHE:CE1	2.49	0.47
1:A:59:PHE:CZ	1:A:136:THR:HG21	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:98:SER:HA	5:B:181:HOH:O	2.13	0.47
1:A:31:LYS:HD2	1:A:294:PHE:CE2	2.50	0.47
1:A:157:VAL:HG13	1:A:224:ILE:HB	1.95	0.47
1:A:177:ALA:CB	1:A:201:MET:HE2	2.45	0.47
1:A:285:TYR:HA	1:A:288:GLN:NE2	2.26	0.47
2:B:29:LEU:HD21	2:B:77:TYR:HB2	1.96	0.47
2:B:70:GLN:HA	2:B:73:GLN:HG2	1.96	0.47
2:B:109:CYS:SG	2:B:111:ASN:HB3	2.55	0.47
2:D:48:LEU:O	2:D:55:ARG:HA	2.15	0.47
2:D:53:MET:CE	2:D:80:GLN:HE22	2.27	0.47
1:A:214:SER:O	1:A:217:GLU:HB3	2.15	0.47
1:A:146:GLN:HG3	1:A:147:GLU:N	2.30	0.47
2:B:30:LEU:HD23	2:B:35:LEU:CD1	2.45	0.46
2:B:46:LEU:HD12	2:D:44:ILE:HD11	1.96	0.46
2:B:80:GLN:OE1	2:B:80:GLN:HA	2.15	0.46
2:B:105:ASN:C	2:B:106:VAL:HA	2.40	0.46
1:A:137:GLN:O	1:A:140:LEU:HG	2.16	0.46
1:C:106:HIS:CG	1:C:107:PRO:HD2	2.50	0.46
1:C:234:ARG:HH21	1:C:234:ARG:HG3	1.79	0.46
2:D:1:MET:HE1	2:D:94:LYS:HZ1	1.79	0.46
2:D:1:MET:HE1	2:D:94:LYS:HZ2	1.78	0.46
2:D:35:LEU:O	2:D:38:THR:HG22	2.15	0.46
1:A:270:VAL:HG12	1:A:271:ASP:CG	2.40	0.46
2:D:22:PRO:HD3	2:D:80:GLN:CD	2.40	0.46
1:C:305:ASN:HB3	1:C:308:LEU:HD22	1.97	0.46
1:A:49:PHE:HE2	1:A:104:MET:HE3	1.81	0.46
2:B:138:CYS:O	2:B:142:GLU:HA	2.14	0.46
2:D:129:LYS:HE2	2:D:134:ILE:HD13	1.96	0.46
1:A:186:PHE:HB2	1:A:211:LEU:HD23	1.98	0.46
1:A:215:ILE:HD11	1:A:247:PHE:HA	1.97	0.46
2:B:49:PRO:HA	2:B:55:ARG:HG2	1.98	0.46
2:B:139:LYS:HD3	2:B:140:TYR:CZ	2.51	0.46
1:A:184:PHE:CE1	1:A:207:ILE:HG21	2.51	0.46
1:C:162:ASP:CG	1:C:192:LEU:HD13	2.40	0.46
2:D:99:LEU:CD1	2:D:134:ILE:HD12	2.46	0.46
2:B:102:ARG:HB2	2:B:102:ARG:NH1	2.29	0.46
1:C:81:LEU:HD11	1:C:91:THR:HG21	1.98	0.46
1:A:49:PHE:CE2	1:A:104:MET:HE3	2.51	0.45
1:A:185:TYR:CG	1:A:218:VAL:HG21	2.50	0.45
2:D:52:GLU:HG3	2:D:53:MET:N	2.30	0.45
1:C:31:LYS:HZ3	1:C:291:ASN:HD21	1.62	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:183:ARG:HG2	1:A:183:ARG:HH21	1.81	0.45
1:A:269:ARG:NH1	1:A:278:ASP:OD2	2.49	0.45
2:B:68:GLU:HA	2:B:68:GLU:OE2	2.16	0.45
2:B:125:PHE:HB3	2:B:136:LEU:HB3	1.98	0.45
1:A:267:LEU:HB3	1:A:268:PRO:HA	1.97	0.45
2:D:79:PRO:HG3	5:D:181:HOH:O	2.15	0.45
1:A:44:ILE:HD12	1:A:63:MET:HG2	1.98	0.45
1:A:212:HIS:CD2	1:A:217:GLU:HG2	2.52	0.45
1:A:307:ASP:OD1	1:A:308:LEU:N	2.50	0.45
2:B:19:ASP:OD1	2:B:56:LYS:NZ	2.50	0.45
2:B:82:THR:OG1	2:B:96:ARG:NH1	2.50	0.45
1:A:187:ILE:HD13	1:A:214:SER:C	2.41	0.45
2:B:39:ASP:N	2:B:39:ASP:OD1	2.50	0.45
1:C:130:GLY:O	1:C:167:ARG:NH2	2.50	0.45
1:C:45:ALA:HA	1:C:71:VAL:O	2.17	0.45
1:A:190:ASP:OD1	1:A:191:ALA:N	2.50	0.44
1:A:252:SER:O	1:A:255:HIS:ND1	2.50	0.44
1:A:308:LEU:HD13	1:A:308:LEU:N	2.32	0.44
1:A:92:ILE:HG22	1:A:93:SER:N	2.32	0.44
1:C:54:ARG:HD2	3:C:1312:PCT:H1P2	2.00	0.44
2:D:71:VAL:HG13	2:D:83:VAL:CG2	2.47	0.44
2:D:83:VAL:HB	2:D:95:SER:HB3	1.98	0.44
2:D:101:GLU:CD	2:D:101:GLU:H	2.25	0.44
1:A:40:LYS:O	1:A:41:HIS:HB2	2.18	0.44
2:B:39:ASP:O	2:D:55:ARG:HD3	2.18	0.44
1:C:180:ASP:N	1:C:180:ASP:OD1	2.50	0.44
1:C:31:LYS:HD2	1:C:294:PHE:CD2	2.53	0.44
1:C:94:VAL:O	1:C:97:THR:HG23	2.18	0.44
2:D:29:LEU:HD23	2:D:29:LEU:N	2.32	0.44
2:D:76:LEU:HD13	2:D:151:LEU:HD11	1.98	0.44
1:A:153:ASP:OD2	1:A:180:ASP:N	2.50	0.44
2:B:19:ASP:OD1	2:B:20:HIS:N	2.49	0.44
2:B:86:ILE:CD1	2:B:91:VAL:HG13	2.47	0.44
1:C:256:ASN:OD1	1:C:256:ASN:N	2.50	0.44
1:A:182:ASN:O	1:A:207:ILE:HG23	2.18	0.44
2:D:48:LEU:HB2	2:D:56:LYS:HG3	1.99	0.44
1:A:25:ALA:HA	5:A:1396:HOH:O	2.18	0.44
1:A:130:GLY:O	1:A:167:ARG:NH2	2.50	0.44
2:B:40:GLN:HE21	2:B:40:GLN:HB3	1.61	0.44
1:A:202:LEU:HD23	1:A:202:LEU:N	2.32	0.44
1:A:232:LYS:O	1:A:235:LEU:O	2.36	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:136:THR:HG22	1:A:299:LEU:HD12	2.00	0.43
1:A:48:PHE:CE1	1:A:56:ARG:HG3	2.54	0.43
2:B:58:LEU:HG	2:B:59:ILE:N	2.29	0.43
1:C:137:GLN:NE2	1:C:140:LEU:HD22	2.33	0.43
1:C:234:ARG:HG3	1:C:234:ARG:NH2	2.32	0.43
1:C:261:MET:HE3	1:C:282:HIS:ND1	2.33	0.43
1:C:302:LEU:HD23	1:C:308:LEU:HD23	2.00	0.43
2:D:17:VAL:CG2	2:D:86:ILE:HD12	2.48	0.43
2:D:92:VAL:O	2:D:92:VAL:HG13	2.17	0.43
1:A:159:MET:HE2	1:A:169:VAL:HA	2.00	0.43
1:C:3:PRO:HD2	1:C:22:LEU:HD22	2.00	0.43
2:D:58:LEU:HD21	2:D:60:LYS:HZ3	1.83	0.43
1:A:222:VAL:HG23	1:A:261:MET:HG3	2.00	0.43
2:B:5:ASN:HB2	5:B:202:HOH:O	2.18	0.43
2:B:80:GLN:O	2:B:96:ARG:NH1	2.50	0.43
2:B:99:LEU:CD1	2:B:100:PRO:HD2	2.41	0.43
2:B:147:HIS:O	2:B:151:LEU:HD23	2.18	0.43
1:A:36:PRO:HA	1:A:66:LEU:HA	2.00	0.43
1:A:154:ASN:HA	1:A:181:GLY:C	2.42	0.43
1:A:265:HIS:N	1:A:288:GLN:HE22	2.07	0.43
2:B:55:ARG:HB2	2:B:55:ARG:NH2	2.33	0.43
2:B:67:SER:OG	2:B:70:GLN:HG2	2.19	0.43
1:A:26:THR:HB	1:A:298:ALA:HB1	2.00	0.43
1:A:277:VAL:O	1:A:283:ALA:HB2	2.18	0.43
2:B:70:GLN:O	2:B:73:GLN:HB2	2.19	0.43
2:D:99:LEU:HD21	2:D:134:ILE:CG2	2.48	0.43
1:A:2:ASN:ND2	1:A:302:LEU:O	2.50	0.43
1:C:41:HIS:HD2	5:C:1427:HOH:O	2.00	0.43
1:A:52:SER:OG	1:A:55:THR:HB	2.18	0.43
2:D:20:HIS:HD2	2:D:82:THR:OG1	2.01	0.43
2:D:96:ARG:HA	2:D:96:ARG:HD3	1.83	0.43
1:A:3:PRO:HG2	1:A:22:LEU:HD22	2.00	0.42
1:A:229:ARG:HG3	1:A:272:GLU:OE1	2.19	0.42
1:C:262:LYS:HE3	1:C:284:TRP:CZ3	2.55	0.42
2:D:119:GLU:HB3	2:D:120:PRO:HD2	2.01	0.42
2:D:136:LEU:HD12	2:D:150:VAL:CG2	2.40	0.42
2:B:18:ILE:CG2	2:B:21:ILE:HD11	2.48	0.42
1:C:8:HIS:ND1	1:C:123:PRO:HA	2.33	0.42
2:D:58:LEU:HD21	2:D:60:LYS:NZ	2.33	0.42
1:C:35:GLN:HB3	1:C:38:LEU:HB2	2.02	0.42
2:D:65:PHE:CD2	2:D:85:ARG:HD3	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:199:LEU:HD12	1:A:199:LEU:HA	1.83	0.42
2:B:108:VAL:N	5:B:159:HOH:O	2.50	0.42
1:C:2:ASN:OD1	1:C:302:LEU:HB3	2.20	0.42
1:A:187:ILE:CD1	1:A:215:ILE:HA	2.50	0.42
1:A:235:LEU:HD22	1:A:239:GLU:OE2	2.20	0.42
2:B:50:SER:O	2:B:52:GLU:N	2.49	0.42
1:C:270:VAL:HG13	1:C:271:ASP:N	2.34	0.42
1:A:2:ASN:HD22	1:A:5:TYR:HB2	1.85	0.42
1:A:202:LEU:HA	1:A:207:ILE:HD12	2.02	0.42
1:A:223:ASP:HA	1:A:260:ASN:ND2	2.34	0.42
2:B:49:PRO:HA	2:B:55:ARG:CG	2.49	0.42
2:B:126:ALA:HB2	5:B:156:HOH:O	2.19	0.42
1:C:185:TYR:CD2	1:C:218:VAL:HG21	2.55	0.42
1:A:187:ILE:HD11	1:A:218:VAL:CG1	2.50	0.42
1:A:276:ASP:HA	1:A:279:LYS:HE3	2.02	0.42
2:B:1:MET:SD	2:B:17:VAL:HG11	2.60	0.42
2:B:76:LEU:HA	2:B:76:LEU:HD23	1.61	0.42
1:A:195:PRO:HA	5:A:1354:HOH:O	2.20	0.41
2:D:99:LEU:HG	2:D:127:VAL:HG11	2.01	0.41
2:B:110:PRO:CD	2:B:150:VAL:HG22	2.50	0.41
1:C:306:ARG:NH2	1:C:306:ARG:HG2	2.35	0.41
2:D:146:SER:O	2:D:150:VAL:HG23	2.20	0.41
1:A:270:VAL:HG12	1:A:271:ASP:N	2.35	0.41
2:B:22:PRO:HA	5:B:193:HOH:O	2.19	0.41
2:B:48:LEU:HB3	2:B:49:PRO:HD2	2.01	0.41
1:C:52:SER:OG	3:C:1312:PCT:O2P	2.37	0.41
1:C:227:MET:HB3	1:C:227:MET:HE3	1.61	0.41
1:A:101:ALA:HA	1:A:122:VAL:HG13	2.02	0.41
1:A:138:THR:HA	1:A:141:ASP:OD2	2.21	0.41
2:B:5:ASN:O	2:B:6:LYS:HB2	2.20	0.41
2:D:66:LEU:O	2:D:85:ARG:NH2	2.50	0.41
2:D:85:ARG:O	2:D:86:ILE:HG13	2.20	0.41
1:C:35:GLN:HA	5:C:1337:HOH:O	2.20	0.41
2:D:2:THR:O	2:D:2:THR:HG22	2.19	0.41
2:B:50:SER:HB3	2:B:54:GLY:N	2.35	0.41
2:D:116:SER:HA	2:D:121:VAL:CG2	2.50	0.41
2:D:147:HIS:CA	2:D:150:VAL:HG23	2.47	0.41
1:A:87:THR:HB	2:B:119:GLU:OE2	2.21	0.41
1:A:156:HIS:HB3	1:A:222:VAL:HA	2.03	0.41
2:D:38:THR:HG23	2:D:42:ILE:HD11	2.03	0.41
1:A:53:THR:HG22	1:A:54:ARG:N	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:152:LEU:HD12	1:A:152:LEU:HA	1.80	0.41
2:B:14:ARG:HG3	2:B:63:ASN:HD22	1.86	0.41
2:B:30:LEU:HD23	2:B:35:LEU:HD12	2.03	0.41
2:B:86:ILE:HD12	2:B:91:VAL:HA	2.02	0.41
1:C:104:MET:O	1:C:104:MET:HG3	2.20	0.41
2:D:76:LEU:HD22	2:D:76:LEU:HA	1.84	0.41
1:A:44:ILE:HD13	1:A:300:LEU:HD22	2.02	0.41
1:A:160:VAL:HG11	1:A:215:ILE:HG12	2.03	0.41
2:D:76:LEU:CD1	2:D:151:LEU:HD21	2.46	0.41
2:D:77:TYR:O	2:D:79:PRO:HD3	2.20	0.41
2:D:143:LYS:HA	2:D:143:LYS:HD3	1.72	0.41
1:A:17:ARG:O	1:A:21:ASN:OD1	2.39	0.40
2:B:45:GLY:HA3	2:B:48:LEU:HD11	2.02	0.40
1:C:199:LEU:HD22	1:C:209:TRP:CZ3	2.57	0.40
1:C:223:ASP:O	1:C:261:MET:HA	2.20	0.40
1:C:236:ASP:HB3	1:C:239:GLU:CB	2.37	0.40
2:D:6:LYS:HD2	2:D:6:LYS:HA	1.30	0.40
2:D:84:ASN:OD1	2:D:94:LYS:HG3	2.21	0.40
1:A:41:HIS:HB3	5:A:1320:HOH:O	2.20	0.40
1:A:122:VAL:HA	1:A:123:PRO:HD3	1.84	0.40
1:A:187:ILE:HA	1:A:212:HIS:O	2.21	0.40
1:C:39:LEU:HD13	1:C:304:LEU:HD12	2.02	0.40
1:C:42:LYS:HA	1:C:42:LYS:HD3	1.90	0.40
1:C:76:SER:O	1:C:76:SER:OG	2.29	0.40
1:C:176:LEU:HA	1:C:176:LEU:HD23	1.76	0.40
1:C:251:ALA:HB2	1:C:276:ASP:OD2	2.22	0.40
1:A:10:ILE:N	1:A:10:ILE:HD13	2.36	0.40
2:B:69:ASP:OD1	2:B:69:ASP:N	2.54	0.40

All (5) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:112:SER:OG	5:C:1441:HOH:O[2_655]	1.16	1.04
2:B:144:GLU:O	5:C:1425:HOH:O[2_655]	1.47	0.73
2:B:112:SER:N	5:C:1441:HOH:O[2_655]	1.92	0.28
2:B:112:SER:CB	5:C:1441:HOH:O[2_655]	1.95	0.25
2:B:112:SER:CA	5:C:1441:HOH:O[2_655]	2.18	0.02

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	308/310 (99%)	274 (89%)	31 (10%)	3 (1%)	12	17
1	C	308/310 (99%)	276 (90%)	24 (8%)	8 (3%)	4	3
2	B	151/153 (99%)	130 (86%)	15 (10%)	6 (4%)	2	1
2	D	151/153 (99%)	128 (85%)	19 (13%)	4 (3%)	4	3
All	All	918/926 (99%)	808 (88%)	89 (10%)	21 (2%)	5	4

All (21) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	79	THR
2	B	6	LYS
2	B	13	LYS
1	C	75	ASP
1	C	270	VAL
2	D	8	GLN
2	D	12	ILE
2	B	105	ASN
1	C	231	GLN
1	C	258	LYS
1	A	219	MET
2	B	12	ILE
1	C	132	ASN
2	D	132	ASN
1	A	244	LYS
1	C	244	LYS
2	B	51	GLY
1	C	84	LYS
1	C	309	VAL
2	D	29	LEU
2	B	9	VAL

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	260/260 (100%)	195 (75%)	65 (25%)	0	0
1	C	260/260 (100%)	200 (77%)	60 (23%)	1	1
2	B	137/137 (100%)	91 (66%)	46 (34%)	0	0
2	D	137/137 (100%)	99 (72%)	38 (28%)	0	0
All	All	794/794 (100%)	585 (74%)	209 (26%)	0	0

All (209) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	ASN
1	A	7	LYS
1	A	11	SER
1	A	17	ARG
1	A	37	GLU
1	A	40	LYS
1	A	53	THR
1	A	69	SER
1	A	83	LYS
1	A	84	LYS
1	A	86	GLU
1	A	92	ILE
1	A	94	VAL
1	A	95	ILE
1	A	99	VAL
1	A	108	GLN
1	A	109	GLU
1	A	113	ARG
1	A	116	THR
1	A	121	ASN
1	A	124	VAL
1	A	137	GLN
1	A	146	GLN
1	A	149	GLN

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Mol	Chain	Res	Type
1	A	151	ARG
1	A	152	LEU
1	A	157	VAL
1	A	160	VAL
1	A	164	LYS
1	A	169	VAL
1	A	171	SER
1	A	174	GLN
1	A	178	LYS
1	A	180	ASP
1	A	199	LEU
1	A	201	MET
1	A	202	LEU
1	A	205	LYS
1	A	213	SER
1	A	215	ILE
1	A	216	GLU
1	A	228	THR
1	A	229	ARG
1	A	231	GLN
1	A	232	LYS
1	A	233	GLU
1	A	238	SER
1	A	243	VAL
1	A	246	GLN
1	A	248	VAL
1	A	250	ARG
1	A	252	SER
1	A	254	LEU
1	A	256	ASN
1	A	258	LYS
1	A	261	MET
1	A	264	LEU
1	A	269	ARG
1	A	275	THR
1	A	279	LYS
1	A	285	TYR
1	A	297	GLN
1	A	299	LEU
1	A	308	LEU
1	A	310	LEU
2	B	1	MET

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Mol	Chain	Res	Type
2	B	2	THR
2	B	5	ASN
2	B	6	LYS
2	B	7	LEU
2	B	10	GLU
2	B	12	ILE
2	B	14	ARG
2	B	16	THR
2	B	17	VAL
2	B	31	SER
2	B	32	LEU
2	B	34	LYS
2	B	35	LEU
2	B	36	THR
2	B	37	GLU
2	B	39	ASP
2	B	40	GLN
2	B	41	ARG
2	B	50	SER
2	B	52	GLU
2	B	53	MET
2	B	56	LYS
2	B	58	LEU
2	B	61	ILE
2	B	63	ASN
2	B	66	LEU
2	B	69	ASP
2	B	70	GLN
2	B	71	VAL
2	B	74	LEU
2	B	84	ASN
2	B	85	ARG
2	B	91	VAL
2	B	92	VAL
2	B	94	LYS
2	B	96	ARG
2	B	103	ILE
2	B	121	VAL
2	B	128	ARG
2	B	130	ARG
2	B	136	LEU
2	B	137	LYS

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Mol	Chain	Res	Type
2	B	139	LYS
2	B	146	SER
2	B	151	LEU
1	C	6	GLN
1	C	7	LYS
1	C	9	ILE
1	C	12	ILE
1	C	35	GLN
1	C	40	LYS
1	C	44	ILE
1	C	53	THR
1	C	59	PHE
1	C	69	SER
1	C	74	SER
1	C	75	ASP
1	C	76	SER
1	C	80	SER
1	C	83	LYS
1	C	84	LYS
1	C	87	THR
1	C	92	ILE
1	C	108	GLN
1	C	121	ASN
1	C	138	THR
1	C	140	LEU
1	C	145	ILE
1	C	147	GLU
1	C	149	GLN
1	C	151	ARG
1	C	159	MET
1	C	171	SER
1	C	180	ASP
1	C	183	ARG
1	C	190	ASP
1	C	201	MET
1	C	205	LYS
1	C	207	ILE
1	C	211	LEU
1	C	214	SER
1	C	215	ILE
1	C	216	GLU
1	C	228	THR

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Mol	Chain	Res	Type
1	C	231	GLN
1	C	232	LYS
1	C	233	GLU
1	C	234	ARG
1	C	235	LEU
1	C	239	GLU
1	C	243	VAL
1	C	244	LYS
1	C	256	ASN
1	C	262	LYS
1	C	264	LEU
1	C	267	LEU
1	C	271	ASP
1	C	276	ASP
1	C	280	THR
1	C	285	TYR
1	C	305	ASN
1	C	306	ARG
1	C	307	ASP
1	C	308	LEU
1	C	310	LEU
2	D	2	THR
2	D	6	LYS
2	D	9	VAL
2	D	10	GLU
2	D	12	ILE
2	D	13	LYS
2	D	14	ARG
2	D	30	LEU
2	D	31	SER
2	D	34	LYS
2	D	36	THR
2	D	40	GLN
2	D	48	LEU
2	D	52	GLU
2	D	55	ARG
2	D	56	LYS
2	D	60	LYS
2	D	61	ILE
2	D	62	GLU
2	D	64	THR
2	D	67	SER

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Mol	Chain	Res	Type
2	D	68	GLU
2	D	70	GLN
2	D	74	LEU
2	D	76	LEU
2	D	80	GLN
2	D	91	VAL
2	D	92	VAL
2	D	95	SER
2	D	98	SER
2	D	101	GLU
2	D	102	ARG
2	D	107	LEU
2	D	122	SER
2	D	128	ARG
2	D	134	ILE
2	D	139	LYS
2	D	150	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	35	GLN
1	A	64	HIS
1	A	108	GLN
1	A	126	ASN
1	A	132	ASN
1	A	134	HIS
1	A	149	GLN
1	A	154	ASN
1	A	212	HIS
1	A	288	GLN
1	A	305	ASN
2	B	40	GLN
2	B	63	ASN
2	B	70	GLN
2	B	84	ASN
2	B	111	ASN
2	B	132	ASN
2	B	147	HIS
1	C	21	ASN
1	C	64	HIS
1	C	126	ASN

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Mol	Chain	Res	Type
1	C	137	GLN
1	C	154	ASN
1	C	156	HIS
1	C	246	GLN
1	C	291	ASN
1	C	305	ASN
2	D	20	HIS
2	D	40	GLN
2	D	80	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	PCT	A	1311	-	7,7,7	3.10	4 (57%)	9,10,10	1.58	1 (11%)
3	PCT	C	1312	-	7,7,7	3.12	4 (57%)	9,10,10	1.56	3 (33%)

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	PCT	A	1311	-	-	0/4/5/5	-
3	PCT	C	1312	-	-	2/4/5/5	-

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1312	PCT	P-O1P	5.32	1.61	1.50
3	A	1311	PCT	P-O1P	5.28	1.60	1.50
3	C	1312	PCT	P-C1P	4.45	1.86	1.79
3	A	1311	PCT	P-C1P	4.42	1.86	1.79
3	C	1312	PCT	P-O3P	3.47	1.62	1.55
3	A	1311	PCT	P-O3P	3.45	1.62	1.55
3	A	1311	PCT	P-O2P	2.57	1.60	1.55
3	C	1312	PCT	P-O2P	2.56	1.60	1.55

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1312	PCT	O1-C1-C1P	2.91	122.92	119.86
3	C	1312	PCT	O1P-P-C1P	-2.11	106.22	111.10
3	C	1312	PCT	O3P-P-O2P	2.02	113.71	107.96
3	A	1311	PCT	O1-C1-C1P	2.01	121.98	119.86

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	1312	PCT	O1-C1-C1P-P
3	C	1312	PCT	C1-C1P-P-O3P

There are no ring outliers.

2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1311	PCT	1	0
3	C	1312	PCT	6	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	B	5
2	D	2
1	C	2
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	105:ASN	C	106:VAL	N	1.74
1	B	9:VAL	C	10:GLU	N	1.73
1	D	152:ALA	C	153:ASN	N	1.70
1	A	309:VAL	C	310:LEU	N	1.69
1	B	5:ASN	C	6:LYS	N	1.67
1	C	51:ALA	C	52:SER	N	1.16
1	D	7:LEU	C	8:GLN	N	1.14
1	C	75:ASP	C	76:SER	N	1.11
1	B	11:ALA	C	12:ILE	N	1.01
1	B	8:GLN	C	9:VAL	N	0.93

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	310/310 (100%)	0.08	16 (5%) 33 32	3, 27, 104, 158	0
1	C	310/310 (100%)	-0.10	15 (4%) 35 35	2, 20, 95, 158	0
2	B	153/153 (100%)	0.79	21 (13%) 6 5	11, 49, 158, 158	1 (0%)
2	D	153/153 (100%)	0.83	21 (13%) 6 5	10, 55, 158, 158	3 (1%)
All	All	926/926 (100%)	0.26	73 (7%) 18 18	2, 35, 141, 158	4 (0%)

All (73) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	1	MET	6.2
1	A	79	THR	5.5
2	B	11	ALA	5.3
2	D	9	VAL	4.8
2	D	2	THR	4.4
2	B	12	ILE	4.4
1	C	76	SER	4.4
2	D	7	LEU	4.4
1	A	82	GLY	4.3
1	A	81	LEU	4.3
2	B	131	ALA	4.2
1	A	310	LEU	4.1
2	B	3	HIS	4.1
1	C	82	GLY	4.0
2	B	89	TYR	4.0
2	B	9	VAL	3.9
2	D	89	TYR	3.9
2	B	129	LYS	3.6
1	C	81	LEU	3.6
2	B	7	LEU	3.6
2	B	10	GLU	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	243	VAL	3.5
1	A	80	SER	3.5
1	C	80	SER	3.4
2	B	130	ARG	3.4
1	C	75	ASP	3.3
2	D	5	ASN	3.3
1	C	310	LEU	3.2
1	C	79	THR	3.1
1	A	309	VAL	3.1
1	C	77	ALA	3.1
2	D	6	LYS	3.1
1	C	78	ASN	3.0
1	C	85	GLY	3.0
2	D	3	HIS	3.0
2	B	41	ARG	3.0
2	D	11	ALA	2.9
2	B	105	ASN	2.9
2	B	2	THR	2.9
2	D	88	ASN	2.9
1	A	74	SER	2.9
1	A	215	ILE	2.8
2	D	1	MET	2.8
2	D	4	ASP	2.8
1	C	238	SER	2.8
2	D	153	ASN	2.7
2	D	92	VAL	2.7
1	A	308	LEU	2.7
2	B	153	ASN	2.7
1	A	230	VAL	2.7
2	D	8	GLN	2.7
1	A	76	SER	2.7
2	B	4	ASP	2.6
2	D	91	VAL	2.6
1	A	242	ASN	2.6
2	D	50	SER	2.6
1	C	167	ARG	2.4
2	B	132	ASN	2.4
2	B	152	ALA	2.4
1	C	230	VAL	2.4
2	D	56	LYS	2.3
2	B	5	ASN	2.3
1	C	74	SER	2.3

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Mol	Chain	Res	Type	RSRZ
2	D	90	GLU	2.3
2	B	13	LYS	2.3
2	D	10	GLU	2.3
1	A	77	ALA	2.2
1	A	228	THR	2.2
1	A	84	LYS	2.1
1	C	237	PRO	2.1
2	D	152	ALA	2.0
2	D	14	ARG	2.0
2	B	88	ASN	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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($\text{\AA}^2$)	Q<0.9
3	PCT	C	1312	8/8	0.81	0.18	54,64,75,87	0
3	PCT	A	1311	8/8	0.85	0.18	24,54,73,78	0
4	ZN	D	155	1/1	0.98	0.02	18,18,18,18	0
4	ZN	B	154	1/1	0.99	0.03	19,19,19,19	0

6.5 Other polymers [i](#)

There are no such residues in this entry.