



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 04:22 AM UTC

PDB ID : 3G79 / pdb_00003g79
Title : Crystal structure of NDP-N-acetyl-D-galactosaminuronic acid dehydrogenase from Methanosarcina mazei Go1
Authors : Malashkevich, V.N.; Toro, R.; Sauder, J.M.; Burley, S.K.; Almo, S.C.; New York SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on : 2009-02-09
Resolution : 2.40 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
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

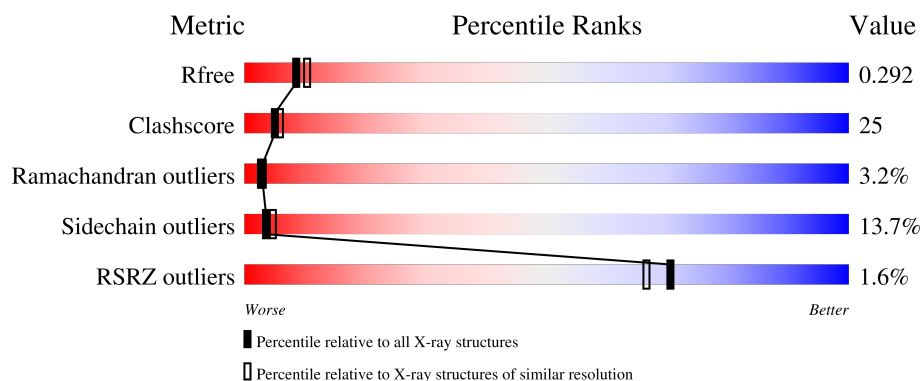
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	478	2% 60% 29% 9% ..
1	B	478	% 63% 25% 9% ..

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7421 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 NDP-N-acetyl-D-galactosaminuronic acid dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	475	Total	C	N	O	S	0	0	0
			3621	2293	627	683	18			
1	B	475	Total	C	N	O	S	0	0	0
			3621	2293	627	683	18			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	expression tag	UNP Q8PXR2
A	2	SER	-	expression tag	UNP Q8PXR2
A	3	LEU	-	expression tag	UNP Q8PXR2
A	471	GLU	-	expression tag	UNP Q8PXR2
A	472	GLY	-	expression tag	UNP Q8PXR2
A	473	HIS	-	expression tag	UNP Q8PXR2
A	474	HIS	-	expression tag	UNP Q8PXR2
A	475	HIS	-	expression tag	UNP Q8PXR2
A	476	HIS	-	expression tag	UNP Q8PXR2
A	477	HIS	-	expression tag	UNP Q8PXR2
A	478	HIS	-	expression tag	UNP Q8PXR2
B	1	MET	-	expression tag	UNP Q8PXR2
B	2	SER	-	expression tag	UNP Q8PXR2
B	3	LEU	-	expression tag	UNP Q8PXR2
B	471	GLU	-	expression tag	UNP Q8PXR2
B	472	GLY	-	expression tag	UNP Q8PXR2
B	473	HIS	-	expression tag	UNP Q8PXR2
B	474	HIS	-	expression tag	UNP Q8PXR2
B	475	HIS	-	expression tag	UNP Q8PXR2
B	476	HIS	-	expression tag	UNP Q8PXR2
B	477	HIS	-	expression tag	UNP Q8PXR2
B	478	HIS	-	expression tag	UNP Q8PXR2

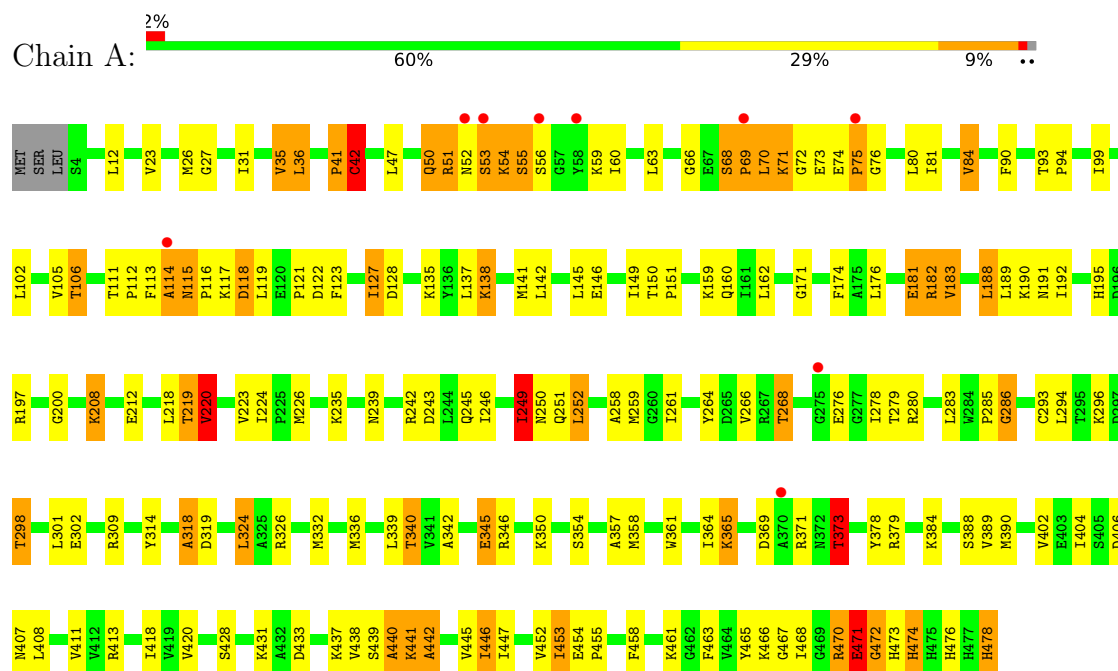
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	179	Total 179	O 179	0	0

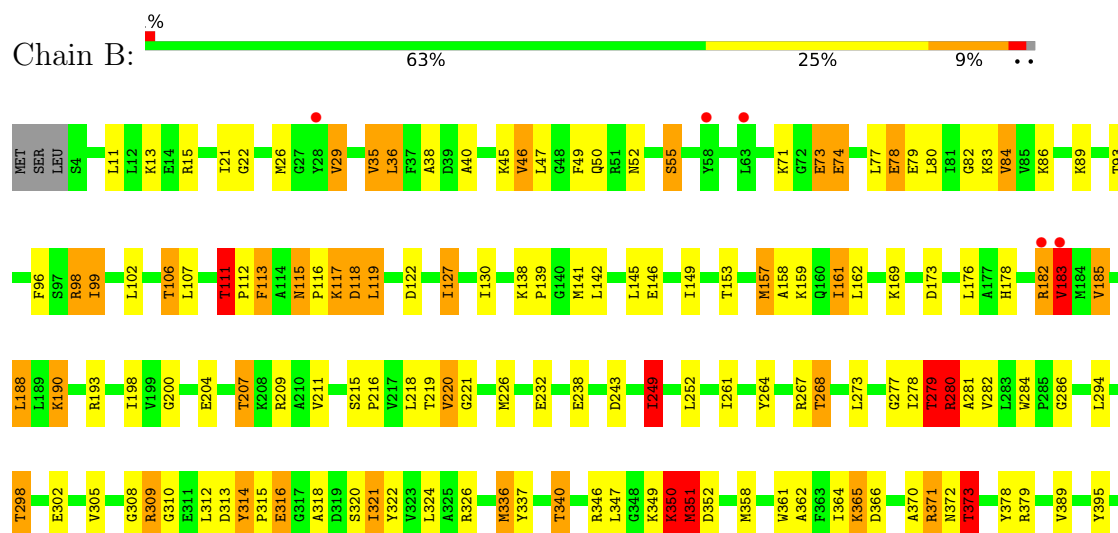
3 Residue-property plots

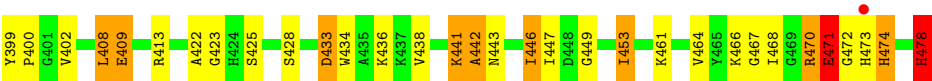
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: NDP-N-acetyl-D-galactosaminuronic acid dehydrogenase



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4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	78.83Å 88.72Å 151.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.71 – 2.40 19.71 – 2.40	Depositor EDS
% Data completeness (in resolution range)	95.4 (19.71-2.40) 95.1 (19.71-2.40)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.29 (at 2.41Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.222 , 0.296 0.218 , 0.292	Depositor DCC
R_{free} test set	2038 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	44.2	Xtriage
Anisotropy	0.144	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 24.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7421	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 19.64% 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

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	0.99	1/3690 (0.0%)	1.23	19/4986 (0.4%)
1	B	0.97	3/3690 (0.1%)	1.23	25/4986 (0.5%)
All	All	0.98	4/7380 (0.1%)	1.23	44/9972 (0.4%)

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	2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	127	ILE	CA-CB	5.55	1.61	1.54
1	B	364	ILE	CA-CB	5.37	1.60	1.54
1	A	478	HIS	C-OXT	5.24	1.34	1.23
1	B	478	HIS	C-OXT	5.16	1.33	1.23

All (44) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	314	TYR	CA-C-N	-9.81	109.94	119.85
1	A	314	TYR	C-N-CA	-9.81	109.94	119.85
1	B	111	THR	CA-C-N	9.69	131.95	119.84
1	B	111	THR	C-N-CA	9.69	131.95	119.84
1	B	98	ARG	N-CA-C	-9.58	96.99	110.50
1	A	219	THR	CB-CA-C	-7.94	100.73	112.09
1	A	41	PRO	N-CA-C	-7.26	100.52	111.41
1	B	349	LYS	N-CA-C	7.18	121.75	112.41
1	B	474	HIS	N-CA-C	7.07	121.73	113.18
1	A	93	THR	CA-C-N	6.81	128.01	120.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	93	THR	C-N-CA	6.81	128.01	120.45
1	B	119	LEU	N-CA-C	6.71	119.59	111.40
1	B	115	ASN	CA-C-N	-6.67	111.50	119.84
1	B	115	ASN	C-N-CA	-6.67	111.50	119.84
1	A	474	HIS	N-CA-C	6.39	120.67	113.01
1	A	115	ASN	CA-C-N	-6.31	111.95	119.84
1	A	115	ASN	C-N-CA	-6.31	111.95	119.84
1	A	373	THR	CB-CA-C	-6.15	99.96	109.62
1	B	249	ILE	CB-CA-C	-6.15	104.00	112.24
1	B	336	MET	CG-SD-CE	-6.12	87.43	100.90
1	B	198	ILE	CB-CA-C	-6.08	103.25	111.15
1	A	470	ARG	N-CA-C	5.84	118.18	109.25
1	B	470	ARG	N-CA-C	5.78	118.09	109.25
1	B	278	ILE	N-CA-C	5.76	116.96	112.12
1	B	40	ALA	CA-C-N	5.67	126.93	119.84
1	B	40	ALA	C-N-CA	5.67	126.93	119.84
1	A	266	VAL	N-CA-C	-5.58	105.06	110.42
1	B	183	VAL	N-CA-C	5.53	115.64	108.35
1	B	279	THR	N-CA-C	5.52	122.57	110.80
1	A	249	ILE	CB-CA-C	-5.51	104.85	112.24
1	A	53	SER	N-CA-C	-5.50	99.84	108.63
1	A	286	GLY	N-CA-C	5.46	118.55	110.42
1	B	314	TYR	N-CA-C	-5.44	101.10	108.11
1	B	373	THR	CB-CA-C	-5.39	101.16	109.62
1	A	171	GLY	N-CA-C	-5.38	107.90	115.32
1	A	54	LYS	N-CA-C	-5.30	102.79	110.64
1	B	443	ASN	CA-C-N	-5.17	114.63	119.85
1	B	443	ASN	C-N-CA	-5.17	114.63	119.85
1	B	249	ILE	N-CA-CB	5.11	119.09	110.56
1	B	45	LYS	CA-C-N	-5.05	116.53	123.14
1	B	45	LYS	C-N-CA	-5.05	116.53	123.14
1	A	252	LEU	N-CA-C	-5.04	105.97	111.82
1	B	127	ILE	N-CA-CB	5.04	117.40	110.54
1	A	70	LEU	N-CA-C	5.04	116.98	108.96

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	112	PRO	Peptide
1	A	472	GLY	Peptide

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3621	0	3655	215	0
1	B	3621	0	3655	170	0
2	A	179	0	0	10	0
All	All	7421	0	7310	362	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 25.

All (362) 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:B:471:GLU:CB	1:B:472:GLY:HA3	1.25	1.54
1:B:471:GLU:CB	1:B:472:GLY:CA	1.87	1.51
1:B:471:GLU:HB2	1:B:472:GLY:C	1.38	1.48
1:A:471:GLU:CB	1:A:472:GLY:CA	2.01	1.39
1:A:471:GLU:HB2	1:A:472:GLY:C	1.43	1.39
1:A:471:GLU:CB	1:A:472:GLY:HA3	1.42	1.35
1:B:471:GLU:HB3	1:B:472:GLY:CA	1.50	1.35
1:A:471:GLU:HB2	1:A:472:GLY:CA	1.62	1.29
1:A:342:ALA:O	1:A:345:GLU:HG3	1.31	1.27
1:A:138:LYS:H	1:A:141:MET:HE2	1.06	1.16
1:A:358:MET:HE1	1:A:379:ARG:HA	1.26	1.15
1:A:219:THR:O	1:A:220:VAL:HB	1.43	1.11
1:B:336:MET:HE3	1:B:468:ILE:HD11	1.28	1.11
1:A:250:ASN:HB3	1:A:332:MET:HE3	1.31	1.09
1:A:440:ALA:O	1:A:441:LYS:HB2	1.45	1.08
1:B:471:GLU:HB2	1:B:472:GLY:CA	1.63	1.08
1:A:74:GLU:O	1:A:76:GLY:N	1.88	1.07
1:B:358:MET:HE1	1:B:379:ARG:HA	1.36	1.07
1:B:115:ASN:C	1:B:117:LYS:H	1.62	1.06
1:A:342:ALA:O	1:A:345:GLU:CG	2.03	1.06
1:A:361:TRP:O	1:A:373:THR:HG21	1.55	1.06
1:A:138:LYS:N	1:A:141:MET:HE2	1.71	1.04
1:B:361:TRP:O	1:B:373:THR:HG21	1.58	1.03
1:B:471:GLU:CB	1:B:472:GLY:C	2.24	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:114:ALA:HB1	1:A:115:ASN:HA	1.40	1.02
1:A:358:MET:HE3	1:A:389:VAL:HG11	1.43	1.01
2:A:643:HOH:O	1:B:313:ASP:HB2	1.61	1.00
1:B:115:ASN:O	1:B:117:LYS:N	1.94	0.99
1:A:182:ARG:NE	1:B:273:LEU:HD21	1.79	0.98
1:A:113:PHE:HB3	1:A:114:ALA:C	1.91	0.96
1:A:471:GLU:HB3	1:A:472:GLY:CA	1.73	0.96
1:A:113:PHE:HA	1:A:114:ALA:HB3	1.44	0.95
1:A:358:MET:HE1	1:A:379:ARG:CA	1.98	0.93
1:A:137:LEU:HD12	1:A:141:MET:HE3	1.51	0.92
1:B:471:GLU:HB2	1:B:473:HIS:N	1.85	0.91
1:A:471:GLU:CB	1:A:472:GLY:C	2.34	0.91
1:A:219:THR:O	1:A:219:THR:OG1	1.85	0.90
1:A:251:GLN:OE1	1:B:314:TYR:CE1	2.26	0.89
1:A:324:LEU:CD2	1:B:321:ILE:HG22	2.00	0.89
1:B:336:MET:HE1	1:B:468:ILE:CG1	2.02	0.89
1:B:478:HIS:ND1	1:B:478:HIS:N	2.22	0.88
1:A:219:THR:O	1:A:220:VAL:CB	2.21	0.87
1:B:215:SER:HB2	1:B:216:PRO:HD3	1.57	0.87
1:A:342:ALA:HA	1:A:345:GLU:HG2	1.57	0.85
1:B:336:MET:HE3	1:B:468:ILE:CD1	2.06	0.85
1:B:358:MET:HE3	1:B:389:VAL:HG11	1.57	0.85
1:A:324:LEU:HD21	1:B:321:ILE:HG22	1.57	0.84
1:A:54:LYS:O	1:A:55:SER:HB3	1.76	0.84
1:A:138:LYS:H	1:A:141:MET:CE	1.90	0.84
1:B:115:ASN:C	1:B:117:LYS:N	2.26	0.83
1:A:441:LYS:O	1:A:442:ALA:CB	2.25	0.82
1:A:26:MET:HE1	1:A:90:PHE:HZ	1.42	0.81
1:A:340:THR:HG21	1:A:378:TYR:OH	1.80	0.81
2:A:482:HOH:O	1:B:268:THR:HG22	1.79	0.81
1:A:467:GLY:O	1:A:474:HIS:CE1	2.34	0.81
1:A:471:GLU:HB2	1:A:473:HIS:N	1.95	0.81
1:B:138:LYS:HB2	1:B:141:MET:HE3	1.63	0.81
1:A:336:MET:CE	1:A:468:ILE:HG13	2.11	0.80
1:A:441:LYS:O	1:A:442:ALA:HB3	1.81	0.80
1:A:471:GLU:HB3	1:A:472:GLY:HA3	0.81	0.80
1:A:346:ARG:HH21	1:A:346:ARG:HG2	1.47	0.80
1:B:99:ILE:HA	1:B:102:LEU:HD12	1.63	0.80
1:A:235:LYS:NZ	1:A:293:CYS:SG	2.54	0.80
1:B:408:LEU:O	1:B:409:GLU:CB	2.27	0.79
1:A:137:LEU:HA	1:A:141:MET:CE	2.12	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:114:ALA:HB1	1:A:115:ASN:CA	2.14	0.78
1:A:113:PHE:HB2	1:A:122:ASP:HB3	1.66	0.78
1:B:106:THR:HG21	1:B:146:GLU:OE1	1.84	0.78
1:B:408:LEU:O	1:B:409:GLU:HB3	1.81	0.78
1:B:358:MET:HE1	1:B:379:ARG:CA	2.12	0.78
1:A:336:MET:HE3	1:A:468:ILE:HG13	1.65	0.77
1:B:340:THR:HG21	1:B:378:TYR:OH	1.85	0.77
1:B:366:ASP:HA	1:B:395:TYR:CE2	2.19	0.77
1:A:361:TRP:O	1:A:373:THR:CG2	2.32	0.76
1:B:336:MET:CE	1:B:468:ILE:CG1	2.63	0.76
1:B:157:MET:O	1:B:161:ILE:HG23	1.86	0.76
1:A:358:MET:HE3	1:A:389:VAL:CG1	2.16	0.75
1:B:361:TRP:O	1:B:373:THR:CG2	2.33	0.75
1:B:264:TYR:O	1:B:268:THR:HG23	1.86	0.75
1:A:467:GLY:O	1:A:474:HIS:HE1	1.70	0.75
1:B:261:ILE:C	1:B:471:GLU:HA	2.12	0.74
1:A:113:PHE:HB3	1:A:114:ALA:O	1.87	0.74
1:B:336:MET:CE	1:B:468:ILE:HD11	2.15	0.73
1:B:200:GLY:HA2	1:B:226:MET:O	1.87	0.73
1:B:467:GLY:O	1:B:474:HIS:CE1	2.41	0.72
1:B:80:LEU:O	1:B:84:VAL:HG23	1.89	0.72
1:A:251:GLN:OE1	1:B:314:TYR:HE1	1.71	0.72
1:B:471:GLU:OE1	1:B:471:GLU:N	2.22	0.72
1:A:84:VAL:HG13	1:A:90:PHE:HB3	1.71	0.72
1:B:182:ARG:NH2	1:B:238:GLU:OE1	2.23	0.72
1:A:440:ALA:O	1:A:441:LYS:CB	2.28	0.71
1:B:336:MET:HE1	1:B:468:ILE:HG12	1.69	0.71
1:A:324:LEU:HD22	1:B:324:LEU:HD23	1.73	0.71
1:A:466:LYS:HA	1:A:474:HIS:CD2	2.26	0.71
1:B:79:GLU:OE1	1:B:79:GLU:N	2.15	0.71
1:B:112:PRO:O	1:B:113:PHE:HB2	1.89	0.71
1:A:114:ALA:CB	1:A:115:ASN:HA	2.20	0.70
1:A:243:ASP:OD2	1:A:326:ARG:HD2	1.92	0.70
1:B:38:ALA:CB	1:B:84:VAL:HG11	2.22	0.70
1:A:261:ILE:C	1:A:471:GLU:HA	2.17	0.70
1:A:113:PHE:CA	1:A:114:ALA:HB3	2.20	0.70
1:A:113:PHE:O	1:A:121:PRO:HA	1.92	0.69
1:A:113:PHE:CD1	1:A:114:ALA:HB3	2.27	0.69
1:A:358:MET:CE	1:A:379:ARG:HA	2.13	0.69
1:A:358:MET:HE1	1:A:379:ARG:CB	2.22	0.69
1:B:336:MET:HE1	1:B:468:ILE:HG13	1.73	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:50:GLN:NE2	1:A:51:ARG:O	2.26	0.69
1:B:38:ALA:HB3	1:B:84:VAL:HG11	1.75	0.68
1:A:245:GLN:HG3	1:A:283:LEU:CD1	2.24	0.68
1:A:26:MET:HE3	1:A:63:LEU:HD13	1.74	0.68
1:A:74:GLU:C	1:A:76:GLY:H	2.00	0.68
1:A:183:VAL:HG13	1:A:188:LEU:HD12	1.75	0.68
1:A:26:MET:HE1	1:A:90:PHE:CZ	2.27	0.68
1:B:467:GLY:N	1:B:474:HIS:NE2	2.32	0.67
1:A:54:LYS:O	1:A:55:SER:CB	2.43	0.67
1:A:471:GLU:N	1:A:471:GLU:OE1	2.28	0.67
1:B:340:THR:HB	1:B:447:ILE:HG13	1.77	0.67
1:A:245:GLN:HG3	1:A:283:LEU:HD12	1.77	0.66
1:A:319:ASP:O	1:B:324:LEU:HD21	1.96	0.66
1:B:219:THR:O	1:B:219:THR:OG1	2.11	0.65
1:A:218:LEU:CD1	1:A:223:VAL:HG23	2.26	0.65
1:A:336:MET:HE3	1:A:468:ILE:CG1	2.26	0.65
1:A:35:VAL:CG1	1:A:80:LEU:HG	2.26	0.65
1:B:111:THR:HG23	1:B:111:THR:O	1.95	0.65
1:A:102:LEU:HD12	1:A:105:VAL:HG22	1.79	0.65
1:A:470:ARG:HB2	1:A:474:HIS:NE2	2.13	0.64
1:B:169:LYS:N	1:B:173:ASP:OD2	2.21	0.64
1:A:35:VAL:HG13	1:A:80:LEU:HG	1.78	0.64
1:A:50:GLN:O	1:A:94:PRO:HA	1.97	0.64
1:A:66:GLY:HA2	1:A:81:ILE:HG22	1.80	0.64
1:A:242:ARG:HG2	1:A:294:LEU:HD21	1.78	0.64
1:B:35:VAL:CG1	1:B:80:LEU:HG	2.27	0.64
1:A:26:MET:HE3	1:A:63:LEU:CD1	2.28	0.63
1:B:106:THR:CG2	1:B:146:GLU:OE1	2.46	0.63
1:A:324:LEU:HD21	1:B:321:ILE:HA	1.79	0.63
1:A:200:GLY:HA2	1:A:226:MET:O	1.99	0.63
1:A:324:LEU:HD21	1:B:321:ILE:CG2	2.28	0.62
1:A:113:PHE:HA	1:A:114:ALA:CB	2.25	0.62
1:A:342:ALA:HA	1:A:345:GLU:CG	2.30	0.62
1:A:73:GLU:O	1:A:74:GLU:C	2.43	0.62
1:B:470:ARG:HB2	1:B:474:HIS:NE2	2.15	0.62
1:B:107:LEU:HD13	1:B:145:LEU:HD23	1.81	0.61
1:B:185:VAL:HA	1:B:188:LEU:HD13	1.80	0.61
1:B:336:MET:O	1:B:340:THR:HG22	2.01	0.61
1:B:314:TYR:CG	1:B:315:PRO:HD2	2.36	0.60
1:B:336:MET:HE2	1:B:336:MET:HA	1.84	0.60
1:B:157:MET:HG3	1:B:158:ALA:N	2.17	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:79:GLU:H	1:B:79:GLU:CD	2.05	0.59
1:A:70:LEU:O	1:A:71:LYS:HB2	2.02	0.59
1:A:342:ALA:C	1:A:345:GLU:CG	2.74	0.59
1:A:52:ASN:HB2	2:A:636:HOH:O	2.02	0.59
1:A:36:LEU:HD13	1:A:80:LEU:HD21	1.84	0.59
1:A:123:PHE:O	1:A:127:ILE:HG23	2.02	0.59
1:A:467:GLY:N	1:A:474:HIS:NE2	2.37	0.59
1:B:130:ILE:HB	1:B:161:ILE:HD11	1.85	0.59
1:B:466:LYS:HA	1:B:474:HIS:CD2	2.38	0.58
1:A:84:VAL:HG13	1:A:90:PHE:CB	2.33	0.58
1:B:358:MET:HE3	1:B:389:VAL:CG1	2.30	0.58
1:A:218:LEU:HD11	1:A:223:VAL:HG23	1.84	0.58
1:A:114:ALA:HA	1:A:117:LYS:H	1.69	0.58
1:A:182:ARG:CZ	1:B:273:LEU:HD21	2.33	0.58
1:A:298:THR:O	1:A:302:GLU:HG2	2.03	0.58
1:B:99:ILE:HA	1:B:102:LEU:CD1	2.33	0.57
1:B:279:THR:O	1:B:280:ARG:HB2	2.04	0.57
1:A:68:SER:HB2	1:A:69:PRO:HD3	1.85	0.57
1:A:111:THR:HG23	1:A:111:THR:O	2.03	0.57
1:B:111:THR:O	1:B:111:THR:CG2	2.51	0.57
1:B:207:THR:O	1:B:211:VAL:HG23	2.05	0.57
1:A:318:ALA:O	1:A:319:ASP:HB2	2.04	0.57
1:A:336:MET:HE1	1:A:468:ILE:HG13	1.87	0.56
1:A:342:ALA:O	1:A:345:GLU:CD	2.48	0.56
1:A:342:ALA:C	1:A:345:GLU:HG3	2.21	0.56
1:B:11:LEU:O	1:B:15:ARG:HG2	2.06	0.56
1:B:350:LYS:O	1:B:351:MET:HB2	2.05	0.56
1:B:347:LEU:HD21	1:B:464:VAL:HG21	1.87	0.56
1:A:182:ARG:HE	1:B:273:LEU:HD21	1.66	0.56
1:A:208:LYS:O	1:A:212:GLU:HG3	2.06	0.56
1:A:251:GLN:HE22	1:B:320:SER:HB2	1.71	0.55
1:A:74:GLU:HG3	1:A:189:LEU:H	1.71	0.55
1:B:336:MET:CE	1:B:468:ILE:HG12	2.33	0.55
1:B:470:ARG:O	1:B:471:GLU:C	2.50	0.55
1:A:470:ARG:O	1:A:471:GLU:C	2.49	0.55
1:B:441:LYS:O	1:B:442:ALA:CB	2.54	0.55
1:A:390:MET:HE2	1:A:411:VAL:HA	1.89	0.55
1:A:439:SER:C	1:A:440:ALA:O	2.44	0.55
1:B:219:THR:O	1:B:220:VAL:CB	2.55	0.54
1:A:41:PRO:O	1:A:42:CYS:HB3	2.06	0.54
1:A:84:VAL:CG1	1:A:90:PHE:HB3	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:470:ARG:O	1:A:471:GLU:O	2.25	0.54
1:A:53:SER:O	1:A:54:LYS:C	2.51	0.54
1:A:116:PRO:C	1:A:117:LYS:HD2	2.32	0.54
1:A:26:MET:CE	1:A:90:PHE:HZ	2.15	0.54
1:A:251:GLN:HG2	1:B:322:TYR:CZ	2.42	0.54
1:A:68:SER:HB2	1:A:69:PRO:CD	2.37	0.54
1:A:56:SER:O	1:A:59:LYS:HG3	2.08	0.54
1:A:68:SER:CB	1:A:69:PRO:CD	2.86	0.54
1:B:98:ARG:O	1:B:99:ILE:HG13	2.07	0.54
1:B:219:THR:O	1:B:220:VAL:HB	2.08	0.54
1:B:215:SER:HB2	1:B:216:PRO:CD	2.35	0.53
1:B:336:MET:CE	1:B:468:ILE:CD1	2.78	0.53
1:B:467:GLY:O	1:B:474:HIS:HE1	1.88	0.53
1:B:102:LEU:O	1:B:141:MET:HE2	2.08	0.53
1:A:324:LEU:HD22	1:B:324:LEU:CD2	2.38	0.53
2:A:585:HOH:O	1:B:55:SER:HB2	2.08	0.53
1:A:116:PRO:O	1:A:117:LYS:HB2	2.09	0.53
1:A:336:MET:HE2	1:A:339:LEU:HD12	1.90	0.52
1:A:74:GLU:C	1:A:76:GLY:N	2.64	0.52
1:A:418:ILE:CG2	1:A:446:ILE:HD12	2.40	0.52
1:A:258:ALA:O	1:B:310:GLY:HA3	2.10	0.51
1:A:41:PRO:O	1:A:42:CYS:CB	2.58	0.51
1:A:324:LEU:CD2	1:B:321:ILE:CG2	2.82	0.51
1:A:182:ARG:CZ	1:B:273:LEU:CD2	2.89	0.51
1:B:117:LYS:O	1:B:118:ASP:C	2.53	0.51
1:A:111:THR:HG22	2:A:645:HOH:O	2.11	0.51
1:A:191:ASN:O	1:A:195:HIS:HB2	2.10	0.51
1:B:471:GLU:HB3	1:B:472:GLY:HA3	0.54	0.51
1:B:243:ASP:OD2	1:B:326:ARG:HD2	2.11	0.51
1:A:145:LEU:HD12	1:A:149:ILE:HD13	1.93	0.51
1:A:433:ASP:OD1	1:A:461:LYS:NZ	2.38	0.51
1:A:336:MET:O	1:A:340:THR:HG22	2.11	0.50
1:B:337:TYR:HA	1:B:340:THR:HG23	1.93	0.50
1:A:31:ILE:O	1:A:35:VAL:HB	2.11	0.50
1:A:113:PHE:HB2	1:A:122:ASP:CB	2.40	0.50
1:A:259:MET:HE2	1:B:305:VAL:HG22	1.93	0.50
1:B:38:ALA:HB1	1:B:84:VAL:HG11	1.94	0.50
1:A:150:THR:O	1:A:151:PRO:C	2.51	0.50
1:B:98:ARG:O	1:B:99:ILE:CB	2.59	0.50
1:A:264:TYR:O	1:A:268:THR:CG2	2.59	0.50
1:A:336:MET:HE3	1:A:468:ILE:CD1	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:118:ASP:OD2	1:B:118:ASP:N	2.45	0.49
1:B:409:GLU:HB2	1:B:434:TRP:HZ2	1.78	0.49
1:A:23:VAL:HG13	1:A:106:THR:HG22	1.94	0.49
1:A:342:ALA:CA	1:A:345:GLU:HG2	2.33	0.49
1:A:324:LEU:HD23	1:B:321:ILE:HG22	1.91	0.49
1:A:402:VAL:HG12	1:A:404:ILE:CD1	2.43	0.49
1:B:36:LEU:HD13	1:B:80:LEU:HD21	1.93	0.49
1:A:365:LYS:NZ	2:A:514:HOH:O	2.32	0.49
1:A:418:ILE:HG22	1:A:446:ILE:HD12	1.95	0.49
1:B:82:GLY:O	1:B:86:LYS:HG3	2.13	0.48
1:A:71:LYS:HG2	2:A:610:HOH:O	2.12	0.48
1:A:138:LYS:O	1:A:141:MET:HG3	2.14	0.48
1:B:22:GLY:HA2	1:B:47:LEU:O	2.13	0.48
1:B:346:ARG:NH1	1:B:478:HIS:CE1	2.82	0.48
1:B:470:ARG:O	1:B:471:GLU:O	2.32	0.47
1:A:102:LEU:CD1	1:A:105:VAL:HG22	2.44	0.47
1:A:47:LEU:HD12	1:A:102:LEU:HD21	1.95	0.47
1:A:433:ASP:HA	1:A:461:LYS:HE2	1.95	0.47
1:B:78:GLU:N	1:B:79:GLU:OE1	2.47	0.47
1:A:239:ASN:ND2	1:A:293:CYS:HB3	2.29	0.47
1:B:218:LEU:HD13	1:B:221:GLY:C	2.40	0.47
1:A:53:SER:OG	2:A:609:HOH:O	2.19	0.47
1:A:418:ILE:O	1:A:446:ILE:HA	2.15	0.47
1:A:52:ASN:O	1:A:52:ASN:CG	2.57	0.47
1:A:251:GLN:NE2	1:B:320:SER:HB2	2.29	0.47
1:A:99:ILE:HG23	1:A:105:VAL:HG21	1.96	0.46
1:B:112:PRO:O	1:B:113:PHE:CB	2.60	0.46
1:A:250:ASN:HB3	1:A:332:MET:CE	2.23	0.46
1:A:118:ASP:HB2	1:A:119:LEU:HA	1.97	0.46
1:B:13:LYS:HA	1:B:13:LYS:HD3	1.73	0.46
1:B:96:PHE:O	1:B:98:ARG:O	2.33	0.46
1:A:113:PHE:HD1	1:A:114:ALA:HB3	1.75	0.46
1:A:264:TYR:O	1:A:268:THR:HG23	2.16	0.46
1:B:314:TYR:CD1	1:B:315:PRO:HD2	2.51	0.46
1:B:365:LYS:HD3	1:B:423:GLY:O	2.15	0.46
1:A:246:ILE:O	1:A:249:ILE:HD12	2.16	0.45
1:A:378:TYR:C	1:A:378:TYR:CD2	2.94	0.45
1:B:74:GLU:OE1	1:B:188:LEU:HB2	2.16	0.45
1:A:137:LEU:HD21	1:A:174:PHE:CD2	2.51	0.45
1:B:346:ARG:NH1	1:B:478:HIS:HE1	2.13	0.45
1:A:245:GLN:HG3	1:A:283:LEU:HD11	1.95	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:447:ILE:HG13	1:A:466:LYS:HB2	1.97	0.45
1:B:29:VAL:HG22	1:B:183:VAL:HG11	1.99	0.45
1:A:27:GLY:O	1:A:31:ILE:HG13	2.17	0.45
1:B:107:LEU:HD13	1:B:145:LEU:CD2	2.46	0.45
1:B:219:THR:O	1:B:220:VAL:HG23	2.17	0.45
1:B:409:GLU:HB2	1:B:434:TRP:CZ2	2.52	0.45
1:B:158:ALA:O	1:B:162:LEU:HB2	2.17	0.45
1:B:190:LYS:HA	1:B:193:ARG:HB2	1.98	0.45
1:B:261:ILE:O	1:B:471:GLU:HA	2.16	0.45
1:A:127:ILE:HG13	1:A:128:ASP:N	2.26	0.44
1:B:413:ARG:HA	1:B:438:VAL:O	2.18	0.44
1:A:113:PHE:HB3	1:A:114:ALA:CA	2.46	0.44
1:B:138:LYS:HB3	1:B:139:PRO:HD2	1.99	0.44
1:A:26:MET:CE	1:A:63:LEU:HD13	2.45	0.44
1:B:49:PHE:HA	1:B:93:THR:O	2.18	0.44
1:B:249:ILE:HD13	1:B:284:TRP:C	2.43	0.44
1:A:342:ALA:CA	1:A:345:GLU:CG	2.94	0.44
1:A:52:ASN:ND2	1:A:52:ASN:C	2.74	0.44
1:A:113:PHE:CB	1:A:114:ALA:C	2.77	0.44
1:A:118:ASP:HA	1:A:296:LYS:NZ	2.33	0.44
1:A:246:ILE:HA	1:A:249:ILE:HD11	1.99	0.44
1:B:351:MET:O	1:B:352:ASP:C	2.60	0.44
1:B:279:THR:HG22	1:B:281:ALA:H	1.81	0.44
1:B:464:VAL:HG22	1:B:478:HIS:CD2	2.52	0.44
1:A:36:LEU:HD13	1:A:80:LEU:CD2	2.46	0.43
1:A:420:VAL:HG21	1:A:453:ILE:CD1	2.48	0.43
1:B:38:ALA:O	1:B:89:LYS:HE2	2.18	0.43
1:A:452:VAL:HG23	1:A:453:ILE:HD12	2.00	0.43
1:A:115:ASN:O	1:A:115:ASN:ND2	2.49	0.43
1:A:242:ARG:NH2	1:B:277:GLY:O	2.52	0.43
2:A:533:HOH:O	1:B:478:HIS:HA	2.19	0.43
1:B:446:ILE:HD11	1:B:453:ILE:HD13	2.00	0.43
1:A:106:THR:CG2	1:A:146:GLU:OE1	2.66	0.43
1:A:357:ALA:HB1	1:A:411:VAL:HG12	2.01	0.43
1:A:369:ASP:HB2	1:A:371:ARG:HH11	1.84	0.43
1:A:336:MET:HE3	1:A:468:ILE:HD11	2.01	0.43
1:B:399:TYR:HA	1:B:400:PRO:HD3	1.92	0.43
1:B:80:LEU:HA	1:B:83:LYS:HG3	1.99	0.43
1:B:286:GLY:HA2	1:B:449:GLY:O	2.19	0.43
1:A:261:ILE:O	1:A:471:GLU:HA	2.19	0.43
1:A:60:ILE:HD13	1:A:94:PRO:HD3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:71:LYS:HE3	1:B:71:LYS:HB3	1.80	0.42
1:A:346:ARG:HG2	1:A:346:ARG:NH2	2.24	0.42
1:A:181:GLU:HG2	1:A:197:ARG:NE	2.34	0.42
1:B:21:ILE:O	1:B:46:VAL:HA	2.19	0.42
1:B:361:TRP:CD1	1:B:370:ALA:CB	3.03	0.42
1:B:98:ARG:O	1:B:99:ILE:CG1	2.68	0.42
1:A:69:PRO:HB2	1:A:70:LEU:H	1.64	0.42
1:B:73:GLU:O	1:B:74:GLU:C	2.62	0.42
1:A:114:ALA:HB1	1:A:115:ASN:C	2.45	0.42
1:A:183:VAL:CG1	1:A:188:LEU:HD12	2.48	0.42
1:A:433:ASP:OD1	1:A:461:LYS:CE	2.68	0.42
1:B:362:ALA:O	1:B:422:ALA:HB2	2.20	0.42
1:B:308:GLY:C	1:B:309:ARG:HG2	2.44	0.42
1:B:82:GLY:O	1:B:83:LYS:C	2.63	0.41
1:B:178:HIS:CD2	1:B:232:GLU:HG3	2.55	0.41
1:A:476:HIS:CE1	1:A:478:HIS:HB3	2.55	0.41
1:B:115:ASN:H	1:B:117:LYS:HB2	1.85	0.41
1:B:182:ARG:CZ	1:B:238:GLU:OE1	2.67	0.41
1:B:358:MET:HE1	1:B:379:ARG:CB	2.49	0.41
1:A:74:GLU:N	1:A:75:PRO:HD3	2.35	0.41
1:A:250:ASN:OD1	1:A:285:PRO:HA	2.21	0.41
1:A:264:TYR:O	1:A:268:THR:HG22	2.20	0.41
1:A:286:GLY:C	1:A:468:ILE:HD12	2.46	0.41
1:A:402:VAL:HG12	1:A:404:ILE:HD11	2.02	0.41
1:B:98:ARG:O	1:B:99:ILE:HB	2.19	0.41
1:B:267:ARG:HG3	1:B:282:VAL:HG11	2.03	0.41
1:A:74:GLU:OE2	1:A:190:LYS:HE3	2.20	0.41
1:A:137:LEU:HA	1:A:141:MET:HE2	1.98	0.41
1:A:245:GLN:OE1	1:B:280:ARG:HG3	2.21	0.41
1:A:324:LEU:HG	1:B:321:ILE:HG23	2.02	0.41
1:B:273:LEU:O	1:B:279:THR:HA	2.20	0.41
1:A:358:MET:HE1	1:A:379:ARG:HB2	2.01	0.41
1:A:420:VAL:HG21	1:A:453:ILE:HD13	2.01	0.41
1:A:458:PHE:O	1:A:463:PHE:HB2	2.21	0.41
1:A:465:TYR:OH	1:A:470:ARG:HG3	2.21	0.41
2:A:587:HOH:O	1:B:294:LEU:O	2.22	0.41
1:B:74:GLU:CD	1:B:188:LEU:HB2	2.45	0.41
1:B:142:LEU:HD22	1:B:209:ARG:HG3	2.03	0.41
1:B:145:LEU:HD12	1:B:149:ILE:HD13	2.02	0.41
1:A:454:GLU:HA	1:A:455:PRO:HD3	1.96	0.41
1:B:371:ARG:O	1:B:372:ASN:HB2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:26:MET:HA	1:B:26:MET:HE2	2.03	0.40
1:B:149:ILE:HD12	1:B:153:THR:HB	2.02	0.40
1:A:73:GLU:O	1:A:75:PRO:N	2.54	0.40
1:A:190:LYS:HB3	1:A:190:LYS:HE2	1.62	0.40
1:A:350:LYS:O	1:A:354:SER:OG	2.36	0.40
1:B:298:THR:O	1:B:302:GLU:HG3	2.21	0.40
1:A:137:LEU:HA	1:A:141:MET:HE3	2.01	0.40
1:A:181:GLU:OE2	1:A:192:ILE:HA	2.20	0.40
1:A:413:ARG:HA	1:A:438:VAL:HG12	2.02	0.40
1:B:433:ASP:OD1	1:B:461:LYS:HE3	2.21	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	473/478 (99%)	434 (92%)	23 (5%)	16 (3%)	3	2
1	B	473/478 (99%)	435 (92%)	24 (5%)	14 (3%)	3	3
All	All	946/956 (99%)	869 (92%)	47 (5%)	30 (3%)	3	3

All (30) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	68	SER
1	A	69	PRO
1	A	71	LYS
1	A	75	PRO
1	A	220	VAL
1	A	441	LYS
1	A	442	ALA
1	A	471	GLU

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Mol	Chain	Res	Type
1	B	99	ILE
1	B	220	VAL
1	B	351	MET
1	B	409	GLU
1	B	471	GLU
1	A	42	CYS
1	A	55	SER
1	A	72	GLY
1	A	114	ALA
1	A	118	ASP
1	B	117	LYS
1	B	318	ALA
1	B	442	ALA
1	A	318	ALA
1	A	365	LYS
1	B	316	GLU
1	A	440	ALA
1	B	113	PHE
1	B	116	PRO
1	B	350	LYS
1	B	280	ARG
1	B	74	GLU

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	383/387 (99%)	333 (87%)	50 (13%)	4	5
1	B	383/387 (99%)	328 (86%)	55 (14%)	3	4
All	All	766/774 (99%)	661 (86%)	105 (14%)	3	5

All (105) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	LEU

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Mol	Chain	Res	Type
1	A	35	VAL
1	A	36	LEU
1	A	42	CYS
1	A	50	GLN
1	A	51	ARG
1	A	84	VAL
1	A	106	THR
1	A	127	ILE
1	A	135	LYS
1	A	138	LYS
1	A	142	LEU
1	A	159	LYS
1	A	160	GLN
1	A	162	LEU
1	A	176	LEU
1	A	181	GLU
1	A	182	ARG
1	A	183	VAL
1	A	188	LEU
1	A	208	LYS
1	A	220	VAL
1	A	224	ILE
1	A	249	ILE
1	A	252	LEU
1	A	268	THR
1	A	276	GLU
1	A	278	ILE
1	A	279	THR
1	A	280	ARG
1	A	298	THR
1	A	301	LEU
1	A	309	ARG
1	A	324	LEU
1	A	340	THR
1	A	345	GLU
1	A	364	ILE
1	A	373	THR
1	A	384	LYS
1	A	388	SER
1	A	406	ASP
1	A	407	ASN
1	A	408	LEU

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Mol	Chain	Res	Type
1	A	428	SER
1	A	431	LYS
1	A	437	LYS
1	A	445	VAL
1	A	446	ILE
1	A	453	ILE
1	A	471	GLU
1	B	29	VAL
1	B	35	VAL
1	B	36	LEU
1	B	46	VAL
1	B	50	GLN
1	B	52	ASN
1	B	55	SER
1	B	73	GLU
1	B	77	LEU
1	B	78	GLU
1	B	84	VAL
1	B	106	THR
1	B	111	THR
1	B	118	ASP
1	B	119	LEU
1	B	122	ASP
1	B	127	ILE
1	B	157	MET
1	B	159	LYS
1	B	161	ILE
1	B	176	LEU
1	B	182	ARG
1	B	183	VAL
1	B	185	VAL
1	B	188	LEU
1	B	190	LYS
1	B	204	GLU
1	B	207	THR
1	B	249	ILE
1	B	252	LEU
1	B	268	THR
1	B	279	THR
1	B	280	ARG
1	B	298	THR
1	B	309	ARG

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Mol	Chain	Res	Type
1	B	312	LEU
1	B	316	GLU
1	B	321	ILE
1	B	340	THR
1	B	350	LYS
1	B	351	MET
1	B	365	LYS
1	B	371	ARG
1	B	373	THR
1	B	402	VAL
1	B	408	LEU
1	B	425	SER
1	B	428	SER
1	B	433	ASP
1	B	436	LYS
1	B	441	LYS
1	B	446	ILE
1	B	453	ILE
1	B	471	GLU
1	B	478	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	132	ASN
1	A	160	GLN
1	A	195	HIS
1	A	251	GLN
1	A	398	ASN
1	B	50	GLN
1	B	52	ASN
1	B	191	ASN
1	B	292	HIS

5.3.3 RNA ⓘ

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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [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	475/478 (99%)	-0.19	9 (1%) 66 62	21, 34, 60, 78	0
1	B	475/478 (99%)	-0.21	6 (1%) 75 71	20, 35, 61, 79	0
All	All	950/956 (99%)	-0.20	15 (1%) 70 66	20, 34, 61, 79	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	75	PRO	5.5
1	A	58	TYR	4.1
1	B	28	TYR	3.3
1	A	53	SER	3.0
1	A	56	SER	3.0
1	A	275	GLY	2.7
1	A	114	ALA	2.6
1	A	69	PRO	2.6
1	B	63	LEU	2.4
1	B	58	TYR	2.2
1	B	183	VAL	2.1
1	B	473	HIS	2.1
1	A	52	ASN	2.1
1	A	370	ALA	2.1
1	B	182	ARG	2.1

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.