



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 26, 2026 – 03:24 PM UTC

PDB ID : 2NLX / pdb_00002nlx
Title : Crystal structure of the apo E. coli xylulose kinase
Authors : di Luccio, E.; Voegtli, J.; Wilson, D.K.
Deposited on : 2006-10-20
Resolution : 2.70 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

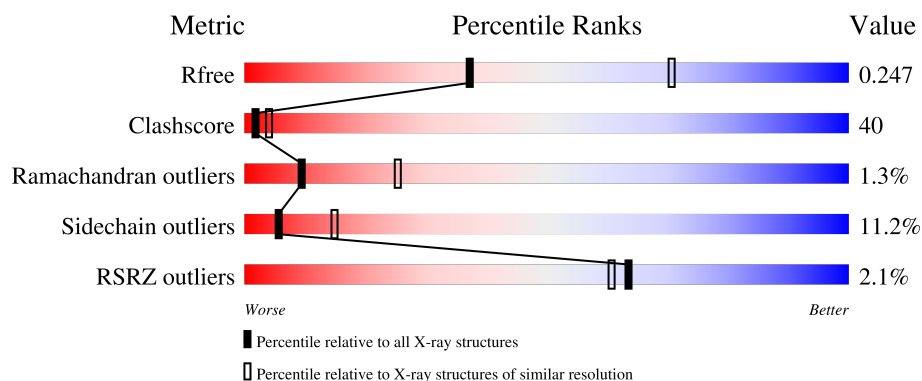
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	484	
1	B	484	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7394 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 Xylulose kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	476	Total	C	N	O	S	0	0	0
			3631	2297	637	673	24			
1	B	472	Total	C	N	O	S	0	0	0
			3605	2281	633	668	23			

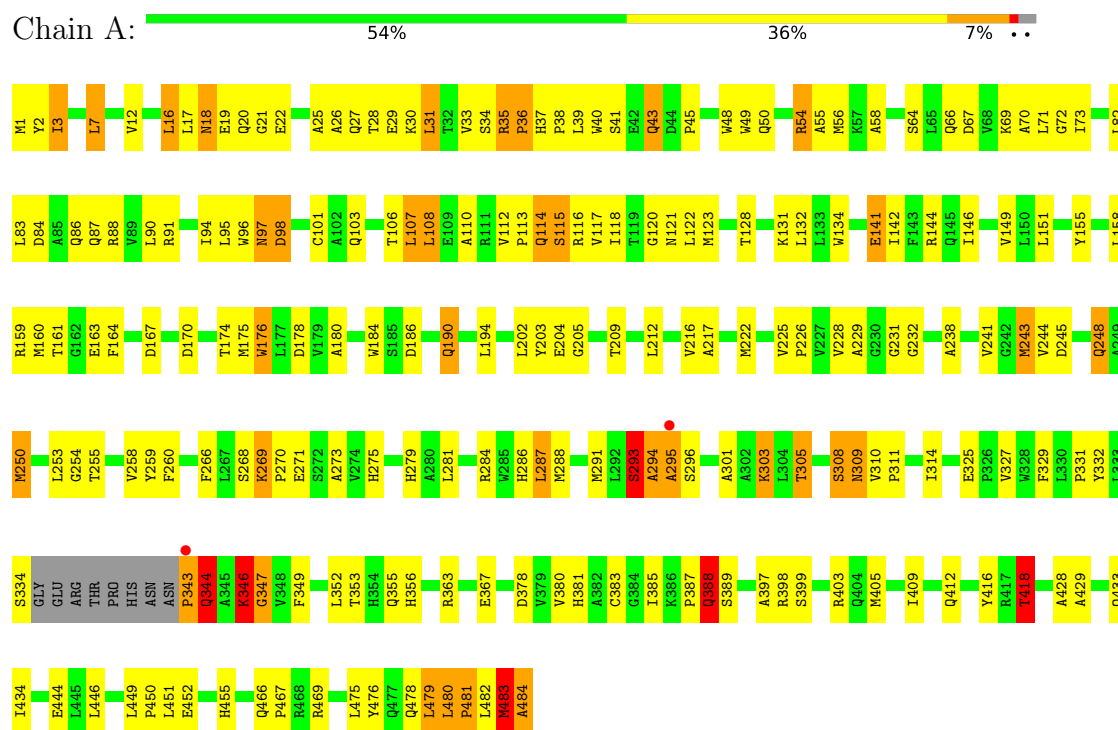
- Molecule 2 is water.

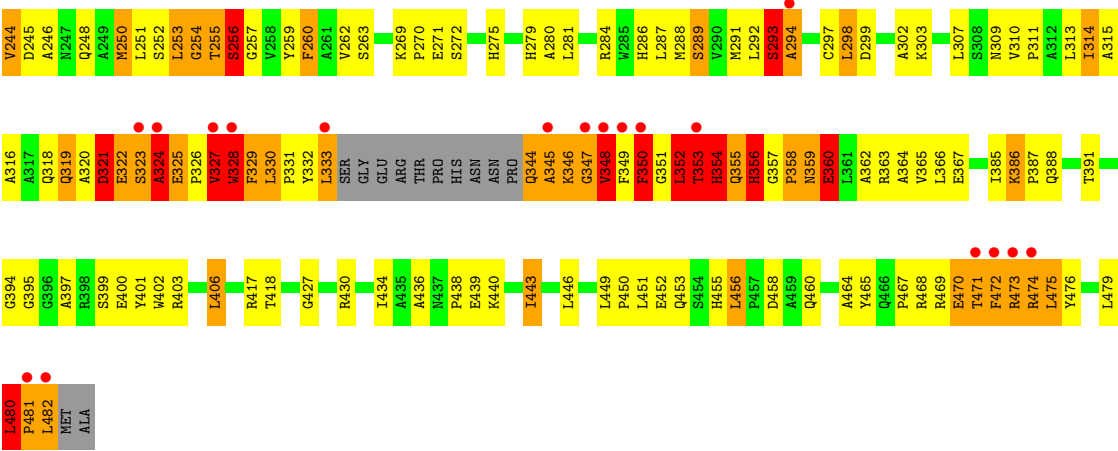
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	82	Total	O	0	0
			82	82		
2	B	76	Total	O	0	0
			76	76		

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: Xylulose kinase





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	67.78Å 112.02Å 138.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.88 – 2.70 24.88 – 2.70	Depositor EDS
% Data completeness (in resolution range)	96.8 (24.88-2.70) 96.5 (24.88-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.37 (at 2.72Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.205 , 0.254 0.201 , 0.247	Depositor DCC
R_{free} test set	1182 reflections (3.98%)	wwPDB-VP
Wilson B-factor (Å ²)	37.6	Xtriage
Anisotropy	0.181	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 45.9	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	0.93	EDS
Total number of atoms	7394	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.11% 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	0.97	8/3712 (0.2%)	1.08	20/5046 (0.4%)
1	B	0.88	12/3685 (0.3%)	1.22	40/5010 (0.8%)
All	All	0.92	20/7397 (0.3%)	1.15	60/10056 (0.6%)

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	5
1	B	1	14
All	All	1	19

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	483	MET	C-N	9.06	1.46	1.33
1	B	353	THR	CA-CB	-7.95	1.40	1.53
1	B	350	PHE	CA-C	-7.15	1.43	1.52
1	A	25	ALA	CA-CB	-7.01	1.41	1.53
1	B	112	VAL	CA-C	-6.57	1.46	1.52
1	A	106	THR	CA-CB	-6.55	1.42	1.53
1	B	25	ALA	CA-CB	-6.16	1.43	1.53
1	A	484	ALA	C-O	6.15	1.35	1.23
1	A	26	ALA	CA-CB	-5.91	1.44	1.53
1	B	110	ALA	CA-CB	-5.80	1.44	1.53
1	B	24	VAL	CA-CB	-5.61	1.46	1.54
1	B	321	ASP	C-O	-5.57	1.17	1.23
1	B	323	SER	CA-C	-5.53	1.44	1.52
1	B	27	GLN	C-O	-5.43	1.17	1.23
1	B	102	ALA	CA-CB	-5.28	1.44	1.53
1	A	110	ALA	CA-CB	-5.21	1.45	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	322	GLU	CA-C	-5.16	1.47	1.53
1	A	475	LEU	C-O	-5.13	1.18	1.24
1	A	481	PRO	C-O	-5.08	1.18	1.24
1	B	325	GLU	CD-OE1	-5.02	1.15	1.25

All (60) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	308	SER	CB-CA-C	-14.84	87.04	111.23
1	A	295	ALA	CB-CA-C	-13.26	84.04	110.42
1	B	356	HIS	CA-C-N	12.62	141.69	121.87
1	B	356	HIS	C-N-CA	12.62	141.69	121.87
1	B	256	SER	CB-CA-C	12.38	132.15	109.86
1	B	256	SER	N-CA-C	-12.04	89.05	108.55
1	B	244	VAL	N-CA-C	11.66	121.92	112.12
1	A	308	SER	N-CA-C	10.85	126.07	113.38
1	A	309	ASN	N-CA-CB	10.47	127.89	111.24
1	B	353	THR	N-CA-C	10.14	132.40	110.80
1	B	328	TRP	N-CA-C	10.04	132.18	110.80
1	B	471	THR	N-CA-C	-9.58	100.19	112.93
1	A	294	ALA	CB-CA-C	-8.67	93.17	110.42
1	B	353	THR	CA-C-N	8.47	139.05	122.03
1	B	353	THR	C-N-CA	8.47	139.05	122.03
1	B	95	LEU	N-CA-C	8.12	120.40	110.41
1	B	324	ALA	N-CA-C	8.06	127.98	110.80
1	A	204	GLU	N-CA-C	-7.93	98.75	110.48
1	B	472	PHE	N-CA-C	-7.76	102.65	113.20
1	B	350	PHE	N-CA-C	7.75	127.31	110.80
1	B	124	MET	CA-C-N	7.67	128.37	119.47
1	B	124	MET	C-N-CA	7.67	128.37	119.47
1	A	273	ALA	N-CA-C	-7.38	104.31	112.72
1	B	329	PHE	N-CA-C	7.26	121.19	110.30
1	A	155	TYR	N-CA-C	-7.17	103.55	111.36
1	B	473	ARG	N-CA-C	-7.04	98.00	108.34
1	B	101	CYS	N-CA-C	6.98	120.46	112.57
1	B	356	HIS	CB-CA-C	-6.93	97.64	111.91
1	A	128	THR	N-CA-C	6.92	118.61	111.14
1	B	256	SER	CA-C-N	6.70	134.54	121.41
1	B	256	SER	C-N-CA	6.70	134.54	121.41
1	B	204	GLU	N-CA-C	-6.65	100.64	110.48
1	B	388	GLN	N-CA-C	-6.42	105.26	113.23
1	B	293	SER	CB-CA-C	-6.37	98.00	110.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	216	VAL	N-CA-C	-6.31	104.70	110.82
1	A	176	TRP	N-CA-C	-6.27	104.90	113.30
1	A	346	LYS	CA-C-N	-6.25	116.80	121.61
1	A	346	LYS	C-N-CA	-6.25	116.80	121.61
1	B	118	ILE	N-CA-C	6.16	116.32	110.53
1	B	394	GLY	N-CA-C	5.87	118.03	112.04
1	B	128	THR	N-CA-C	5.75	117.22	111.07
1	B	480	LEU	C-N-CD	-5.67	108.13	120.60
1	A	309	ASN	N-CA-C	-5.66	99.91	108.52
1	A	101	CYS	N-CA-C	5.60	120.44	111.81
1	B	213	LEU	N-CA-C	-5.50	103.27	109.60
1	B	354	HIS	N-CA-C	5.45	118.49	110.59
1	B	360	GLU	N-CA-C	-5.43	105.79	112.90
1	A	248	GLN	N-CA-C	-5.41	100.09	108.90
1	B	323	SER	CB-CA-C	-5.39	101.46	110.56
1	B	322	GLU	N-CA-C	-5.33	102.44	110.70
1	B	176	TRP	N-CA-C	-5.32	106.73	114.12
1	B	133	LEU	N-CA-C	-5.29	105.68	111.82
1	A	388	GLN	N-CA-C	-5.25	104.99	111.40
1	A	98	ASP	N-CA-C	-5.22	101.76	110.17
1	B	28	THR	OG1-CB-CG2	-5.20	98.89	109.30
1	B	314	ILE	N-CA-C	-5.18	105.49	110.72
1	A	347	GLY	N-CA-C	5.17	119.81	111.38
1	A	232	GLY	N-CA-C	-5.14	105.96	112.54
1	B	470	GLU	N-CA-C	-5.04	107.62	112.97
1	B	106	THR	OG1-CB-CG2	-5.02	99.27	109.30

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	B	353	THR	CA

All (19) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	293	SER	Peptide
1	A	343	PRO	Peptide
1	A	344	GLN	Peptide
1	A	35	ARG	Peptide
1	A	418	THR	Peptide
1	B	253	LEU	Peptide
1	B	254	GLY	Peptide

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Mol	Chain	Res	Type	Group
1	B	255	THR	Peptide
1	B	256	SER	Peptide
1	B	294	ALA	Peptide
1	B	324	ALA	Peptide
1	B	327	VAL	Mainchain
1	B	345	ALA	Peptide
1	B	347	GLY	Peptide
1	B	348	VAL	Peptide
1	B	353	THR	Peptide
1	B	354	HIS	Peptide
1	B	356	HIS	Peptide
1	B	480	LEU	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	3631	0	3607	221	1
1	B	3605	0	3580	372	0
2	A	82	0	0	11	0
2	B	76	0	0	11	1
All	All	7394	0	7187	576	1

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 40.

All (576) 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:344:GLN:HG3	1:B:345:ALA:CA	1.25	1.61
1:B:351:GLY:C	1:B:352:LEU:HD22	1.40	1.43
1:B:344:GLN:CG	1:B:345:ALA:HA	1.51	1.40
1:B:344:GLN:CG	1:B:345:ALA:CA	2.01	1.39
1:B:327:VAL:HG11	1:B:364:ALA:CB	1.55	1.36
1:B:292:LEU:CA	1:B:293:SER:HB2	1.47	1.35
1:A:349:PHE:O	1:B:351:GLY:CA	1.93	1.16

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:344:GLN:HG3	1:B:345:ALA:N	1.34	1.15
1:B:347:GLY:CA	1:B:349:PHE:CD1	2.30	1.15
1:B:327:VAL:CG1	1:B:364:ALA:CB	2.24	1.15
1:A:478:GLN:C	1:A:479:LEU:HD23	1.72	1.14
1:B:347:GLY:CA	1:B:349:PHE:CE1	2.30	1.14
1:B:347:GLY:HA3	1:B:349:PHE:CE1	1.86	1.11
1:B:292:LEU:HA	1:B:293:SER:CB	1.81	1.10
1:B:108:LEU:HD13	1:B:123:MET:HE3	1.20	1.10
1:A:479:LEU:HD23	1:A:479:LEU:N	1.53	1.09
1:A:35:ARG:N	1:A:36:PRO:HD3	1.67	1.08
1:B:351:GLY:C	1:B:352:LEU:CD2	2.28	1.06
1:B:332:TYR:CZ	1:B:348:VAL:HG21	1.92	1.04
1:B:327:VAL:CB	1:B:364:ALA:HB2	1.87	1.03
1:B:347:GLY:C	1:B:349:PHE:CD1	2.37	1.03
1:B:324:ALA:O	1:B:325:GLU:C	1.98	1.02
1:A:352:LEU:O	1:B:349:PHE:HB2	1.61	1.01
1:A:113:PRO:O	2:A:531:HOH:O	1.77	1.00
1:A:190:GLN:HA	1:A:190:GLN:HE21	1.26	0.99
1:B:292:LEU:CB	1:B:293:SER:HB2	1.92	0.99
1:B:347:GLY:HA2	1:B:349:PHE:CE1	1.98	0.98
1:B:344:GLN:HG3	1:B:345:ALA:C	1.89	0.97
1:B:344:GLN:HG2	1:B:346:LYS:CB	1.93	0.97
1:B:352:LEU:HD22	1:B:352:LEU:N	1.77	0.97
1:B:309:ASN:HB3	1:B:311:PRO:HD2	1.47	0.96
1:A:346:LYS:HG3	1:B:353:THR:O	1.64	0.96
1:B:327:VAL:CG1	1:B:364:ALA:HB2	1.95	0.96
1:A:18:ASN:HD21	1:A:22:GLU:H	1.04	0.96
1:B:351:GLY:O	1:B:352:LEU:HD13	1.65	0.95
1:B:332:TYR:CE2	1:B:348:VAL:HG21	1.58	0.95
1:B:344:GLN:CB	1:B:345:ALA:HA	1.95	0.95
1:B:292:LEU:CA	1:B:293:SER:CB	2.36	0.95
1:B:292:LEU:HA	1:B:293:SER:HB2	0.97	0.95
1:B:443:ILE:HD12	1:B:443:ILE:H	1.30	0.95
1:B:327:VAL:CG1	1:B:364:ALA:HB1	1.96	0.94
1:B:19:GLU:HG3	2:B:490:HOH:O	1.66	0.94
1:B:344:GLN:HG2	1:B:346:LYS:CG	1.97	0.94
1:A:18:ASN:ND2	1:A:22:GLU:H	1.67	0.93
1:B:327:VAL:HG11	1:B:364:ALA:HB2	1.48	0.93
1:A:349:PHE:O	1:B:351:GLY:HA3	1.66	0.92
1:B:302:ALA:HB2	1:B:313:LEU:HD22	1.49	0.92
1:A:349:PHE:O	1:B:351:GLY:HA2	1.68	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:352:LEU:O	1:B:349:PHE:CB	2.18	0.90
1:A:385:ILE:HG22	1:A:387:PRO:HD3	1.54	0.90
1:B:347:GLY:O	1:B:349:PHE:HB2	1.72	0.90
1:B:324:ALA:O	1:B:326:PRO:N	2.04	0.89
1:B:344:GLN:HG2	1:B:345:ALA:HA	1.54	0.89
1:B:357:GLY:H	1:B:360:GLU:HG3	1.37	0.88
1:B:327:VAL:O	1:B:328:TRP:HB2	1.72	0.88
1:B:327:VAL:HG11	1:B:364:ALA:HB3	1.56	0.88
1:B:353:THR:O	1:B:353:THR:CG2	2.21	0.88
1:B:332:TYR:CE1	1:B:348:VAL:CG2	2.49	0.87
1:B:344:GLN:CG	1:B:345:ALA:N	2.22	0.87
1:B:108:LEU:HD13	1:B:123:MET:CE	2.05	0.86
1:B:480:LEU:HA	1:B:481:PRO:C	2.01	0.86
1:B:332:TYR:N	1:B:348:VAL:O	2.09	0.86
1:A:269:LYS:HG2	1:A:383:CYS:SG	2.16	0.85
1:B:471:THR:C	1:B:473:ARG:H	1.80	0.85
1:A:352:LEU:O	1:B:347:GLY:O	1.94	0.85
1:A:480:LEU:HB3	1:A:481:PRO:CD	2.05	0.85
1:B:347:GLY:O	1:B:349:PHE:CD1	2.30	0.85
1:B:347:GLY:O	1:B:349:PHE:CG	2.30	0.84
1:B:257:GLY:HA3	1:B:292:LEU:O	1.78	0.84
1:A:325:GLU:O	1:A:356:HIS:HE1	1.59	0.83
1:A:380:VAL:O	1:A:383:CYS:HB2	1.77	0.83
1:B:238:ALA:HB1	1:B:243:MET:HB3	1.60	0.83
1:A:54:ARG:HH11	1:A:54:ARG:HB3	1.42	0.83
1:B:292:LEU:HB3	1:B:293:SER:C	2.04	0.83
1:B:352:LEU:CD2	1:B:352:LEU:N	2.39	0.82
1:A:352:LEU:HB2	1:B:349:PHE:HB3	1.61	0.82
1:B:332:TYR:HB3	1:B:348:VAL:O	1.76	0.81
1:B:332:TYR:CB	1:B:348:VAL:O	2.28	0.81
1:A:303:LYS:HD2	1:A:303:LYS:O	1.80	0.81
1:A:269:LYS:HE3	1:A:383:CYS:HA	1.63	0.81
1:B:344:GLN:HG2	1:B:346:LYS:HG2	1.61	0.81
1:A:303:LYS:O	1:A:303:LYS:CD	2.30	0.80
1:B:351:GLY:O	1:B:352:LEU:CG	2.29	0.80
1:B:351:GLY:O	1:B:352:LEU:CD1	2.29	0.80
1:B:344:GLN:HG2	1:B:346:LYS:HB3	1.63	0.80
1:B:347:GLY:O	1:B:349:PHE:CB	2.30	0.80
1:A:268:SER:CB	2:A:650:HOH:O	2.29	0.80
1:B:473:ARG:HE	1:B:474:ARG:HG2	1.46	0.80
1:B:11:GLY:HA2	1:B:31:LEU:HB2	1.63	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:293:SER:O	1:B:297:CYS:HB2	1.83	0.79
1:B:351:GLY:CA	1:B:352:LEU:HD22	2.13	0.79
1:B:168:MET:HE3	1:B:182:ARG:HB3	1.63	0.79
1:B:355:GLN:N	1:B:355:GLN:CD	2.41	0.78
1:B:139:GLU:HB3	1:B:142:ILE:HD13	1.63	0.78
1:A:480:LEU:HB3	1:A:481:PRO:HD3	1.65	0.78
1:A:132:LEU:HD23	1:A:194:LEU:HD11	1.65	0.78
1:B:269:LYS:HZ2	1:B:272:SER:HB3	1.48	0.78
1:A:268:SER:HB2	2:A:650:HOH:O	1.85	0.77
1:B:18:ASN:HD21	1:B:22:GLU:H	1.32	0.77
1:B:327:VAL:HB	1:B:364:ALA:HB2	1.63	0.77
1:A:132:LEU:HD22	1:A:176:TRP:CH2	2.19	0.77
1:B:212:LEU:HD11	1:B:222:MET:HE2	1.66	0.77
1:A:54:ARG:HB3	1:A:54:ARG:NH1	2.00	0.77
1:B:332:TYR:CZ	1:B:348:VAL:CG2	2.68	0.77
1:B:344:GLN:CG	1:B:345:ALA:C	2.49	0.77
1:A:353:THR:OG1	1:A:355:GLN:HG2	1.86	0.76
1:B:347:GLY:HA3	1:B:349:PHE:CD1	2.09	0.76
1:A:132:LEU:HD21	1:A:149:VAL:HG21	1.65	0.76
1:B:332:TYR:CE1	1:B:348:VAL:HG23	2.01	0.75
1:B:18:ASN:ND2	1:B:22:GLU:H	1.84	0.75
1:B:359:ASN:N	1:B:359:ASN:HD22	1.80	0.75
1:B:443:ILE:H	1:B:443:ILE:CD1	2.00	0.75
1:B:84:ASP:OD2	1:B:88:ARG:HB2	1.87	0.75
1:A:121:ASN:HB2	1:A:175:MET:HE1	1.69	0.75
1:B:302:ALA:O	1:B:307:LEU:O	2.03	0.75
1:A:405:MET:O	1:A:409:ILE:HG13	1.87	0.74
1:B:321:ASP:C	1:B:321:ASP:OD1	2.29	0.74
1:A:35:ARG:N	1:A:36:PRO:CD	2.49	0.74
1:B:470:GLU:OE2	1:B:470:GLU:HA	1.85	0.74
1:B:344:GLN:CB	1:B:346:LYS:HD2	2.18	0.74
1:A:34:SER:C	1:A:36:PRO:HD3	2.11	0.74
1:B:480:LEU:HA	1:B:482:LEU:N	2.03	0.74
1:A:353:THR:H	1:A:356:HIS:HD2	1.35	0.74
1:A:295:ALA:HA	2:A:573:HOH:O	1.88	0.73
1:A:141:GLU:HA	1:A:144:ARG:HH12	1.54	0.73
1:B:344:GLN:HB3	1:B:346:LYS:HD2	1.71	0.73
1:A:112:VAL:O	1:A:115:SER:HB3	1.88	0.73
1:A:190:GLN:HE21	1:A:190:GLN:CA	1.99	0.73
1:B:321:ASP:CG	1:B:323:SER:HB3	2.14	0.73
1:B:440:LYS:HE2	1:B:440:LYS:HA	1.69	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:359:ASN:HD22	1:B:359:ASN:H	1.37	0.72
1:A:352:LEU:O	1:B:349:PHE:CG	2.42	0.72
1:B:314:ILE:O	1:B:318:GLN:HG3	1.88	0.72
1:B:43:GLN:HE22	1:B:76:GLN:HE22	1.37	0.72
1:B:316:ALA:O	1:B:359:ASN:HB2	1.89	0.72
1:A:190:GLN:HA	1:A:190:GLN:NE2	2.03	0.72
1:A:91:ARG:HG3	1:A:91:ARG:HH11	1.55	0.71
1:B:64:SER:OG	1:B:66:GLN:HG2	1.90	0.71
1:B:325:GLU:OE2	1:B:356:HIS:HB2	1.90	0.71
1:B:351:GLY:O	1:B:352:LEU:HD22	1.88	0.71
1:B:310:VAL:N	1:B:311:PRO:CD	2.53	0.71
1:B:400:GLU:HG3	1:B:403:ARG:NH2	2.06	0.71
1:B:473:ARG:HG2	1:B:474:ARG:CZ	2.19	0.71
1:B:470:GLU:HA	1:B:473:ARG:HB2	1.70	0.71
1:A:43:GLN:HE21	1:A:95:LEU:HD21	1.55	0.71
1:B:18:ASN:C	1:B:18:ASN:HD22	1.98	0.71
1:B:327:VAL:CG2	1:B:364:ALA:HB2	2.21	0.71
1:A:294:ALA:O	1:A:295:ALA:CB	2.38	0.71
1:B:353:THR:O	1:B:353:THR:HG23	1.90	0.71
1:B:481:PRO:O	2:B:511:HOH:O	2.09	0.70
1:A:212:LEU:HD11	1:A:222:MET:HE2	1.73	0.70
1:A:303:LYS:CD	1:A:303:LYS:C	2.64	0.70
1:B:348:VAL:O	1:B:349:PHE:HD1	1.75	0.70
1:B:353:THR:O	1:B:353:THR:HG22	1.90	0.70
1:B:470:GLU:HB3	1:B:473:ARG:CZ	2.22	0.70
1:B:215:GLU:H	1:B:215:GLU:CD	2.00	0.70
1:B:325:GLU:N	1:B:326:PRO:HA	2.06	0.69
1:B:456:LEU:N	1:B:456:LEU:HD12	2.07	0.69
1:A:310:VAL:N	1:A:311:PRO:CD	2.54	0.69
1:B:443:ILE:HD12	1:B:443:ILE:N	2.06	0.69
1:B:156:LEU:O	1:B:160:MET:HG3	1.92	0.69
1:B:327:VAL:HG11	1:B:364:ALA:HB1	1.55	0.69
1:B:327:VAL:CB	1:B:364:ALA:CB	2.62	0.69
1:B:292:LEU:CB	1:B:293:SER:CB	2.68	0.69
1:A:325:GLU:O	1:A:356:HIS:CE1	2.45	0.69
1:B:328:TRP:CE2	1:B:471:THR:HG21	2.28	0.69
1:B:356:HIS:ND1	2:B:553:HOH:O	2.11	0.69
1:B:468:ARG:O	1:B:471:THR:HG23	1.93	0.68
1:B:351:GLY:O	1:B:352:LEU:CB	2.40	0.68
1:B:345:ALA:HA	1:B:346:LYS:HG2	1.76	0.68
1:B:386:LYS:HE3	1:B:386:LYS:HA	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:319:GLN:O	1:B:320:ALA:C	2.35	0.67
1:B:347:GLY:C	1:B:349:PHE:HD1	1.99	0.67
1:B:470:GLU:OE2	1:B:473:ARG:HD3	1.94	0.67
1:A:38:PRO:O	1:A:39:LEU:HB2	1.94	0.67
1:A:308:SER:O	1:A:308:SER:OG	2.08	0.67
1:A:1:MET:HE3	1:A:16:LEU:HD22	1.74	0.67
1:A:353:THR:OG1	1:A:355:GLN:CG	2.42	0.67
1:B:292:LEU:HB3	1:B:293:SER:CB	2.24	0.67
1:A:403:ARG:HE	1:A:455:HIS:HE2	1.41	0.67
1:B:310:VAL:HA	1:B:313:LEU:CD2	2.25	0.67
1:A:64:SER:OG	1:A:66:GLN:HG2	1.95	0.66
1:B:359:ASN:H	1:B:359:ASN:ND2	1.93	0.66
1:A:70:ALA:HA	1:A:225:VAL:HG13	1.77	0.66
1:B:269:LYS:NZ	1:B:272:SER:HB3	2.10	0.66
1:B:355:GLN:O	2:B:553:HOH:O	2.12	0.66
1:A:186:ASP:O	1:A:190:GLN:HG2	1.95	0.66
1:B:321:ASP:OD1	1:B:323:SER:N	2.29	0.66
1:B:148:LYS:HG2	1:B:164:PHE:CD2	2.31	0.65
1:A:480:LEU:CB	1:A:481:PRO:CD	2.71	0.65
1:B:321:ASP:OD1	1:B:322:GLU:N	2.30	0.65
1:B:347:GLY:HA2	1:B:349:PHE:HE1	1.61	0.65
1:B:114:GLN:O	1:B:118:ILE:HG13	1.97	0.65
1:B:330:LEU:HD23	1:B:330:LEU:N	2.12	0.65
1:A:327:VAL:HG23	1:A:356:HIS:CE1	2.32	0.65
1:B:355:GLN:CD	1:B:355:GLN:H	2.04	0.65
1:B:355:GLN:O	1:B:356:HIS:ND1	2.30	0.65
1:B:286:HIS:O	1:B:287:LEU:HD12	1.97	0.65
1:A:7:LEU:HA	1:A:12:VAL:HG12	1.79	0.64
1:A:70:ALA:HA	1:A:225:VAL:CG1	2.27	0.64
1:A:243:MET:SD	1:A:250:MET:HB3	2.37	0.64
1:A:349:PHE:HB2	1:B:352:LEU:HD21	1.79	0.64
1:B:90:LEU:HB3	1:B:142:ILE:HG23	1.79	0.64
1:B:471:THR:C	1:B:473:ARG:N	2.51	0.64
1:A:20:GLN:HB2	1:A:22:GLU:HG3	1.79	0.64
1:B:5:ILE:HB	1:B:73:ILE:HG22	1.78	0.64
1:B:302:ALA:CB	1:B:313:LEU:HD22	2.25	0.64
1:B:327:VAL:HG21	1:B:364:ALA:HB2	1.80	0.64
1:A:268:SER:HB3	2:A:650:HOH:O	1.91	0.64
1:B:244:VAL:HG21	1:B:446:LEU:HD13	1.79	0.63
1:B:330:LEU:HB2	1:B:350:PHE:HB2	1.78	0.63
1:B:257:GLY:O	1:B:291:MET:N	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:440:LYS:HE2	1:B:440:LYS:CA	2.28	0.63
1:B:97:ASN:H	1:B:97:ASN:HD22	1.43	0.63
1:B:321:ASP:O	1:B:323:SER:N	2.29	0.63
1:B:330:LEU:HD11	1:B:475:LEU:HD22	1.81	0.63
1:B:400:GLU:HG3	1:B:403:ARG:HH22	1.64	0.63
1:B:54:ARG:HD3	2:B:505:HOH:O	1.99	0.63
1:B:351:GLY:C	1:B:352:LEU:CG	2.71	0.63
1:B:97:ASN:H	1:B:97:ASN:ND2	1.96	0.63
1:B:329:PHE:CE2	1:B:331:PRO:HG3	2.34	0.63
1:A:132:LEU:HD22	1:A:176:TRP:CZ2	2.33	0.62
1:A:388:GLN:HG3	1:A:389:SER:N	2.13	0.62
1:A:343:PRO:N	2:A:526:HOH:O	2.31	0.62
1:B:347:GLY:HA2	1:B:349:PHE:CD1	2.19	0.62
1:A:141:GLU:OE2	1:A:142:ILE:HG12	2.00	0.62
1:A:381:HIS:C	1:A:383:CYS:H	2.08	0.62
1:B:467:PRO:HA	1:B:470:GLU:HG2	1.81	0.62
1:A:363:ARG:O	1:A:367:GLU:HG3	2.00	0.61
1:B:124:MET:HE1	1:B:275:HIS:CE1	2.36	0.61
1:B:252:SER:O	1:B:257:GLY:HA2	2.00	0.61
1:B:238:ALA:HA	1:B:241:VAL:HG12	1.82	0.61
1:B:327:VAL:HB	1:B:364:ALA:CB	2.29	0.61
1:B:302:ALA:HB2	1:B:313:LEU:CD2	2.27	0.61
1:A:244:VAL:HG23	1:A:281:LEU:HD13	1.83	0.61
1:A:303:LYS:O	1:A:303:LYS:HD3	2.00	0.61
1:B:66:GLN:HA	1:B:66:GLN:HE21	1.65	0.61
1:B:351:GLY:O	1:B:352:LEU:CD2	2.45	0.61
1:A:254:GLY:O	1:A:293:SER:HB3	2.01	0.60
1:B:115:SER:OG	2:B:516:HOH:O	2.16	0.60
1:A:416:TYR:CE2	1:A:452:GLU:HG2	2.35	0.60
1:B:357:GLY:N	1:B:360:GLU:HG3	2.12	0.60
1:B:319:GLN:C	1:B:320:ALA:O	2.41	0.60
1:B:348:VAL:HG13	1:B:350:PHE:CZ	2.35	0.60
1:A:97:ASN:H	1:A:97:ASN:ND2	1.98	0.60
1:A:346:LYS:HG2	1:A:483:MET:CE	2.31	0.60
1:B:257:GLY:CA	1:B:292:LEU:O	2.50	0.60
1:B:473:ARG:HG2	1:B:474:ARG:NE	2.17	0.60
1:B:328:TRP:HE3	1:B:328:TRP:HA	1.67	0.59
1:B:481:PRO:C	2:B:511:HOH:O	2.44	0.59
1:B:328:TRP:HH2	1:B:468:ARG:HD2	1.67	0.59
1:A:378:ASP:OD2	1:A:469:ARG:NH2	2.36	0.59
1:B:153:LYS:HE2	1:B:170:ASP:OD1	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:344:GLN:HG2	1:B:345:ALA:CA	2.17	0.59
1:B:321:ASP:OD1	1:B:322:GLU:C	2.46	0.59
1:B:328:TRP:HA	1:B:328:TRP:CE3	2.36	0.59
1:A:97:ASN:H	1:A:97:ASN:HD22	1.50	0.59
1:B:310:VAL:HA	1:B:313:LEU:HD21	1.85	0.59
1:A:349:PHE:HB2	1:B:352:LEU:CD2	2.32	0.58
1:A:71:LEU:HD23	1:A:71:LEU:C	2.28	0.58
1:A:50:GLN:HE21	1:A:50:GLN:HA	1.68	0.58
1:B:235:ALA:O	1:B:239:VAL:HG23	2.03	0.58
1:B:281:LEU:HB2	1:B:284:ARG:HD2	1.85	0.58
1:B:482:LEU:HD13	1:B:482:LEU:H	1.69	0.58
1:A:294:ALA:O	1:A:295:ALA:HB2	2.03	0.58
1:B:254:GLY:HA3	1:B:256:SER:O	2.04	0.58
1:A:190:GLN:CA	1:A:190:GLN:NE2	2.63	0.58
1:A:346:LYS:HG2	1:A:483:MET:HE1	1.85	0.58
1:B:251:LEU:CD2	1:B:253:LEU:HD21	2.33	0.58
1:A:258:VAL:HG13	1:A:288:MET:HE2	1.86	0.58
1:A:309:ASN:HB2	1:A:311:PRO:HD2	1.84	0.58
1:B:143:PHE:O	1:B:146:ILE:HG12	2.03	0.58
1:A:260:PHE:CE1	1:A:286:HIS:CD2	2.92	0.57
1:B:243:MET:HG2	1:B:250:MET:HG2	1.85	0.57
1:B:403:ARG:HE	1:B:455:HIS:HE2	1.52	0.57
1:B:418:THR:O	1:B:449:LEU:HB3	2.03	0.57
1:B:14:VAL:HG22	1:B:27:GLN:HB3	1.86	0.57
1:A:49:TRP:CD1	1:A:159:ARG:HH21	2.22	0.57
1:B:321:ASP:OD2	1:B:323:SER:HB3	2.03	0.57
1:B:365:VAL:HG13	1:B:366:LEU:N	2.20	0.57
1:A:158:LEU:HD22	1:A:164:PHE:HE2	1.70	0.56
1:A:212:LEU:CD1	1:A:222:MET:HE2	2.34	0.56
1:A:275:HIS:O	1:A:287:LEU:HA	2.05	0.56
1:B:328:TRP:CH2	1:B:468:ARG:HD2	2.40	0.56
1:B:329:PHE:C	1:B:330:LEU:HD23	2.30	0.56
1:A:18:ASN:HD21	1:A:22:GLU:N	1.88	0.56
1:A:217:ALA:HB1	1:A:222:MET:O	2.06	0.56
1:B:213:LEU:HB3	1:B:215:GLU:OE1	2.06	0.56
1:B:344:GLN:HB3	1:B:346:LYS:CD	2.36	0.56
1:B:18:ASN:ND2	1:B:18:ASN:C	2.63	0.56
1:B:97:ASN:HD22	1:B:97:ASN:N	1.98	0.56
1:B:148:LYS:HG2	1:B:164:PHE:CE2	2.40	0.56
1:B:153:LYS:NZ	1:B:167:ASP:OD2	2.37	0.56
1:B:70:ALA:HA	1:B:225:VAL:HG13	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:315:ALA:O	1:B:318:GLN:HB2	2.05	0.56
1:B:327:VAL:O	1:B:328:TRP:CB	2.48	0.56
1:A:82:LEU:HD13	1:A:146:ILE:CD1	2.36	0.56
1:A:116:ARG:O	1:A:120:GLY:HA2	2.05	0.56
1:B:418:THR:OG1	1:B:450:PRO:HG2	2.06	0.55
1:A:353:THR:H	1:A:356:HIS:CD2	2.21	0.55
1:A:353:THR:N	1:A:356:HIS:HD2	2.04	0.55
1:A:132:LEU:CD2	1:A:149:VAL:HG21	2.36	0.55
1:B:234:ASN:ND2	1:B:288:MET:HE1	2.20	0.55
1:A:19:GLU:CD	1:A:19:GLU:H	2.14	0.55
1:A:347:GLY:O	1:B:353:THR:HA	2.07	0.55
1:A:18:ASN:ND2	1:A:22:GLU:N	2.48	0.55
1:A:141:GLU:HA	1:A:144:ARG:NH1	2.21	0.55
1:A:269:LYS:CG	1:A:383:CYS:SG	2.93	0.55
1:A:479:LEU:N	1:A:479:LEU:CD2	2.35	0.55
1:A:132:LEU:CD2	1:A:194:LEU:HD11	2.35	0.55
1:B:321:ASP:C	1:B:323:SER:N	2.65	0.55
1:A:303:LYS:C	1:A:303:LYS:HD3	2.31	0.55
1:A:38:PRO:O	1:A:39:LEU:CB	2.55	0.55
1:A:174:THR:O	1:A:175:MET:HB2	2.06	0.55
1:A:480:LEU:O	1:A:483:MET:HB2	2.06	0.55
1:B:333:LEU:N	1:B:333:LEU:HD23	2.22	0.55
1:A:478:GLN:O	1:A:479:LEU:HD23	2.06	0.54
1:B:74:ALA:HA	1:B:231:GLY:O	2.06	0.54
1:B:452:GLU:O	1:B:453:GLN:HB2	2.06	0.54
1:B:327:VAL:HG12	1:B:364:ALA:HB1	1.84	0.54
1:A:238:ALA:HA	1:A:250:MET:HE1	1.88	0.54
1:B:468:ARG:C	1:B:470:GLU:H	2.16	0.54
1:A:481:PRO:C	1:A:483:MET:H	2.16	0.54
1:A:349:PHE:C	1:B:351:GLY:HA3	2.32	0.54
1:B:38:PRO:O	1:B:39:LEU:HB2	2.07	0.54
1:A:18:ASN:ND2	1:A:21:GLY:H	2.05	0.54
1:A:480:LEU:CB	1:A:481:PRO:HD2	2.37	0.54
1:A:82:LEU:HD13	1:A:146:ILE:HD12	1.89	0.54
1:B:73:ILE:HD11	1:B:157:ARG:NH1	2.23	0.53
1:B:82:LEU:CD2	1:B:132:LEU:HD21	2.37	0.53
1:B:124:MET:HE1	1:B:275:HIS:NE2	2.23	0.53
1:B:328:TRP:CE3	1:B:328:TRP:CA	2.91	0.53
1:B:153:LYS:HE3	1:B:154:ASP:OD1	2.08	0.53
1:A:225:VAL:HG13	1:A:226:PRO:HD2	1.91	0.53
1:B:222:MET:HB2	2:B:491:HOH:O	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:471:THR:O	1:B:475:LEU:CB	2.55	0.53
1:A:84:ASP:OD2	1:A:88:ARG:HB2	2.09	0.53
1:A:310:VAL:N	1:A:311:PRO:HD2	2.24	0.53
1:B:71:LEU:C	1:B:71:LEU:HD23	2.33	0.52
1:B:82:LEU:HD22	1:B:132:LEU:HD21	1.91	0.52
1:A:114:GLN:O	1:A:117:VAL:HB	2.09	0.52
1:B:325:GLU:OE1	1:B:354:HIS:CB	2.58	0.52
1:B:344:GLN:HG2	1:B:345:ALA:C	2.30	0.52
1:A:132:LEU:HD22	1:A:176:TRP:HH2	1.70	0.52
1:B:213:LEU:HB2	1:B:216:VAL:HG23	1.91	0.52
1:B:467:PRO:O	1:B:470:GLU:HB2	2.10	0.52
1:B:482:LEU:N	1:B:482:LEU:HD13	2.23	0.52
1:B:82:LEU:HB3	1:B:146:ILE:HD12	1.91	0.52
1:A:203:TYR:CG	1:A:209:THR:HG22	2.45	0.51
1:B:344:GLN:CG	1:B:346:LYS:HG2	2.37	0.51
1:B:470:GLU:HB3	1:B:473:ARG:NH1	2.25	0.51
1:A:399:SER:O	1:A:403:ARG:HG3	2.11	0.51
1:B:344:GLN:CG	1:B:346:LYS:HB3	2.35	0.51
1:B:453:GLN:NE2	1:B:455:HIS:CE1	2.79	0.51
1:B:402:TRP:O	1:B:406:LEU:HD22	2.11	0.51
1:B:60:GLY:HA2	1:B:63:HIS:O	2.10	0.51
1:A:2:TYR:CE1	1:A:433:GLN:HG2	2.46	0.51
1:A:346:LYS:CG	1:B:353:THR:O	2.50	0.51
1:B:91:ARG:HG3	1:B:91:ARG:HH11	1.76	0.51
1:B:260:PHE:C	1:B:260:PHE:CD2	2.89	0.51
1:B:236:ALA:O	1:B:427:GLY:HA3	2.08	0.51
1:A:43:GLN:NE2	1:A:95:LEU:HD21	2.26	0.50
1:B:244:VAL:HG13	1:B:281:LEU:HD12	1.92	0.50
1:B:430:ARG:O	1:B:434:ILE:HD13	2.10	0.50
1:A:103:GLN:NE2	1:A:107:LEU:HD22	2.25	0.50
1:A:97:ASN:HD22	1:A:97:ASN:N	2.05	0.50
1:B:151:LEU:HD21	1:B:174:THR:HG22	1.92	0.50
1:B:252:SER:C	1:B:253:LEU:HD23	2.37	0.50
1:A:331:PRO:O	2:A:632:HOH:O	2.19	0.50
1:B:204:GLU:OE1	1:B:204:GLU:HA	2.12	0.50
1:B:251:LEU:HD21	1:B:253:LEU:HD21	1.91	0.50
1:A:253:LEU:HD12	1:A:397:ALA:HB2	1.93	0.50
1:B:319:GLN:O	1:B:320:ALA:O	2.30	0.50
1:A:35:ARG:NH1	2:A:653:HOH:O	2.43	0.50
1:B:132:LEU:HD13	1:B:176:TRP:HH2	1.76	0.50
1:B:470:GLU:CD	1:B:473:ARG:HD3	2.38	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:243:MET:HE2	1:B:243:MET:HA	1.94	0.49
1:B:314:ILE:HD13	1:B:399:SER:HB2	1.94	0.49
1:A:303:LYS:HD2	1:B:358:PRO:HG3	1.94	0.49
1:B:124:MET:CE	2:B:549:HOH:O	2.60	0.49
1:A:91:ARG:HH11	1:A:91:ARG:CG	2.25	0.49
1:B:418:THR:HG23	1:B:452:GLU:HB2	1.93	0.49
1:A:37:HIS:O	1:A:40:TRP:HB2	2.13	0.49
1:A:27:GLN:HG2	1:A:58:ALA:HB3	1.95	0.49
1:A:301:ALA:O	1:A:305:THR:OG1	2.22	0.49
1:A:73:ILE:HG21	1:A:160:MET:HE1	1.95	0.49
1:A:96:TRP:CD1	1:A:96:TRP:H	2.31	0.49
1:B:194:LEU:HA	1:B:198:GLN:OE1	2.13	0.49
1:A:131:LYS:O	1:A:134:TRP:HB3	2.13	0.49
1:B:436:ALA:C	1:B:438:PRO:HD3	2.38	0.48
1:B:259:TYR:O	1:B:288:MET:HA	2.13	0.48
1:B:302:ALA:O	1:B:307:LEU:C	2.56	0.48
1:B:356:HIS:CE1	2:B:553:HOH:O	2.62	0.48
1:A:50:GLN:O	1:A:54:ARG:HG3	2.13	0.48
1:B:481:PRO:O	1:B:482:LEU:C	2.57	0.48
1:B:186:ASP:OD2	1:B:196:ARG:NH1	2.47	0.48
1:B:212:LEU:CD1	1:B:222:MET:HE2	2.40	0.48
1:B:328:TRP:CE3	1:B:328:TRP:N	2.81	0.48
1:B:316:ALA:HB1	1:B:359:ASN:HB3	1.95	0.48
1:A:1:MET:HE3	1:A:16:LEU:CD2	2.41	0.48
1:A:18:ASN:C	1:A:18:ASN:HD22	2.22	0.48
1:A:43:GLN:HB2	1:A:95:LEU:HD21	1.96	0.48
1:A:72:GLY:C	1:A:428:ALA:HB1	2.39	0.48
1:A:167:ASP:CG	1:A:231:GLY:HA2	2.39	0.48
1:B:363:ARG:O	1:B:367:GLU:HG3	2.13	0.48
1:A:167:ASP:OD2	1:A:231:GLY:HA2	2.14	0.47
1:A:329:PHE:O	1:A:331:PRO:HD3	2.14	0.47
1:A:381:HIS:C	1:A:383:CYS:N	2.68	0.47
1:B:348:VAL:O	1:B:349:PHE:CD1	2.63	0.47
1:B:321:ASP:OD2	1:B:323:SER:CB	2.63	0.47
1:B:243:MET:HE2	1:B:243:MET:CA	2.45	0.47
1:B:293:SER:O	1:B:297:CYS:CB	2.58	0.47
1:B:310:VAL:N	1:B:311:PRO:HD2	2.30	0.47
1:A:481:PRO:C	1:A:483:MET:N	2.72	0.47
1:B:73:ILE:HD13	1:B:73:ILE:N	2.30	0.47
1:B:263:SER:HB3	1:B:385:ILE:HD11	1.96	0.47
1:B:303:LYS:HA	1:B:307:LEU:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:294:ALA:HB1	1:B:402:TRP:CH2	2.50	0.47
1:B:471:THR:O	1:B:473:ARG:N	2.42	0.47
1:B:298:LEU:HD21	1:B:366:LEU:CD2	2.45	0.47
1:B:403:ARG:HH21	1:B:455:HIS:HE2	1.63	0.47
1:B:348:VAL:C	1:B:349:PHE:HD1	2.22	0.46
1:A:293:SER:HB2	1:A:296:SER:HB2	1.96	0.46
1:A:303:LYS:HD2	1:A:303:LYS:C	2.35	0.46
1:A:83:LEU:HA	1:A:88:ARG:O	2.15	0.46
1:A:27:GLN:HG3	1:A:28:THR:N	2.31	0.46
1:B:245:ASP:N	1:B:248:GLN:OE1	2.45	0.46
1:A:67:ASP:O	1:A:69:LYS:HD3	2.16	0.46
1:B:324:ALA:C	1:B:326:PRO:N	2.68	0.46
1:B:439:GLU:HG2	1:B:440:LYS:H	1.79	0.46
1:B:456:LEU:N	1:B:456:LEU:CD1	2.78	0.46
1:A:29:GLU:OE1	1:A:54:ARG:NH1	2.48	0.46
1:A:29:GLU:HG2	1:A:55:ALA:HB2	1.97	0.46
1:A:69:LYS:O	1:A:225:VAL:HG13	2.14	0.46
1:A:241:VAL:HG22	1:A:449:LEU:HD11	1.97	0.46
1:A:94:ILE:HD12	1:A:94:ILE:N	2.30	0.46
1:B:153:LYS:HE2	1:B:153:LYS:HB3	1.79	0.46
1:B:327:VAL:HG21	1:B:360:GLU:O	2.15	0.46
1:A:132:LEU:HD21	1:A:149:VAL:CG2	2.42	0.46
1:B:43:GLN:NE2	1:B:76:GLN:HE22	2.08	0.46
1:B:70:ALA:HA	1:B:225:VAL:CG1	2.45	0.46
1:A:484:ALA:HA	2:A:635:HOH:O	2.14	0.45
1:B:479:LEU:HD23	1:B:479:LEU:HA	1.80	0.45
1:A:334:SER:HB2	1:A:344:GLN:NE2	2.31	0.45
1:B:395:GLY:C	1:B:397:ALA:H	2.25	0.45
1:A:90:LEU:HB3	1:A:142:ILE:HG23	1.99	0.45
1:A:151:LEU:HD13	1:A:170:ASP:CG	2.42	0.45
1:A:259:TYR:HB2	1:A:291:MET:HE2	1.98	0.45
1:A:174:THR:O	1:A:175:MET:CB	2.65	0.45
1:B:252:SER:O	1:B:253:LEU:HD23	2.16	0.45
1:B:332:TYR:HE1	1:B:346:LYS:HD3	1.81	0.45
1:B:352:LEU:O	1:B:353:THR:OG1	2.29	0.45
1:B:34:SER:C	1:B:36:PRO:HD3	2.42	0.45
1:A:95:LEU:O	1:A:131:LYS:NZ	2.44	0.45
1:B:313:LEU:HA	1:B:316:ALA:HB3	1.98	0.45
1:B:71:LEU:HD22	1:B:160:MET:HE1	1.98	0.45
1:B:346:LYS:HG3	1:B:347:GLY:H	1.82	0.45
1:B:352:LEU:O	1:B:353:THR:CB	2.64	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:470:GLU:OE2	1:B:470:GLU:CA	2.59	0.45
1:A:18:ASN:O	1:A:21:GLY:N	2.47	0.45
1:A:86:GLN:O	1:A:87:GLN:HB2	2.17	0.45
1:A:167:ASP:OD2	1:A:170:ASP:HB2	2.17	0.45
1:B:332:TYR:CA	1:B:348:VAL:O	2.64	0.45
1:A:416:TYR:CD2	1:A:452:GLU:HG2	2.52	0.45
1:B:174:THR:O	1:B:175:MET:HB2	2.15	0.45
1:B:355:GLN:N	1:B:355:GLN:NE2	2.65	0.45
1:A:480:LEU:N	1:A:481:PRO:HD2	2.32	0.45
1:B:3:ILE:HG12	1:B:68:VAL:HG21	1.99	0.45
1:B:294:ALA:CB	1:B:402:TRP:HH2	2.30	0.45
1:B:344:GLN:HB3	1:B:345:ALA:HA	1.92	0.45
1:B:468:ARG:C	1:B:470:GLU:N	2.75	0.45
1:A:3:ILE:HD12	1:A:56:MET:HE1	1.98	0.44
1:A:31:LEU:HD12	1:A:31:LEU:N	2.33	0.44
1:A:205:GLY:HA2	1:A:229:ALA:HB3	2.00	0.44
1:B:439:GLU:O	1:B:440:LYS:C	2.60	0.44
1:B:46:GLU:O	1:B:50:GLN:HG2	2.17	0.44
1:B:464:ALA:O	1:B:467:PRO:HD2	2.17	0.44
1:B:142:ILE:N	1:B:142:ILE:HD12	2.32	0.44
1:B:310:VAL:HA	1:B:313:LEU:HD23	1.99	0.44
1:A:332:TYR:OH	1:A:476:TYR:O	2.30	0.44
1:B:365:VAL:HG13	1:B:366:LEU:H	1.82	0.44
1:A:184:TRP:CZ2	1:A:202:LEU:HD21	2.53	0.44
1:A:303:LYS:HD3	1:A:303:LYS:HA	1.64	0.44
1:A:334:SER:HB2	1:A:344:GLN:HE22	1.83	0.44
1:B:328:TRP:HE3	1:B:328:TRP:N	2.16	0.44
1:B:471:THR:OG1	1:B:472:PHE:N	2.50	0.44
1:A:50:GLN:HA	1:A:50:GLN:NE2	2.32	0.44
1:B:103:GLN:HB3	2:B:542:HOH:O	2.17	0.44
1:B:172:ALA:HA	1:B:177:LEU:HB3	2.00	0.44
1:A:346:LYS:HG2	1:A:483:MET:HE3	1.99	0.44
1:B:53:ASP:OD2	1:B:57:LYS:HE3	2.17	0.44
1:B:122:LEU:HD23	1:B:123:MET:N	2.33	0.44
1:B:465:TYR:O	1:B:468:ARG:HB2	2.18	0.43
1:A:94:ILE:HG23	1:A:98:ASP:CG	2.43	0.43
1:A:244:VAL:HG23	1:A:281:LEU:CD1	2.48	0.43
1:B:71:LEU:CD2	1:B:160:MET:HE1	2.48	0.43
1:B:73:ILE:HD11	1:B:157:ARG:HH12	1.83	0.43
1:B:132:LEU:HD13	1:B:176:TRP:CH2	2.53	0.43
1:B:456:LEU:HD12	1:B:456:LEU:H	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:309:ASN:CB	1:B:311:PRO:HD2	2.32	0.43
1:A:41:SER:OG	1:A:97:ASN:ND2	2.52	0.43
1:A:418:THR:O	1:A:450:PRO:HD2	2.17	0.43
1:B:344:GLN:HG2	1:B:346:LYS:CA	2.47	0.43
1:B:465:TYR:O	1:B:468:ARG:N	2.52	0.43
1:A:17:LEU:HD12	1:A:429:ALA:HB1	1.99	0.43
1:A:434:ILE:HD11	1:A:446:LEU:HD21	2.00	0.43
1:A:18:ASN:CG	1:A:20:GLN:HG2	2.43	0.43
1:A:33:VAL:HG12	1:A:34:SER:N	2.34	0.43
1:A:349:PHE:O	1:B:351:GLY:N	2.48	0.43
1:B:302:ALA:O	1:B:307:LEU:HB2	2.18	0.43
1:A:30:LYS:C	1:A:31:LEU:HD12	2.44	0.43
1:A:116:ARG:CZ	1:A:122:LEU:HD12	2.48	0.43
1:A:270:PRO:HG2	1:A:271:GLU:OE1	2.19	0.43
1:B:386:LYS:HE3	1:B:387:PRO:HD2	1.99	0.43
1:B:27:GLN:HG2	1:B:58:ALA:HB3	2.00	0.43
1:B:279:HIS:ND1	1:B:280:ALA:N	2.61	0.42
1:B:458:ASP:OD2	1:B:460:GLN:HB2	2.20	0.42
1:A:45:PRO:HA	1:A:48:TRP:CE3	2.54	0.42
1:B:168:MET:HE3	1:B:182:ARG:CB	2.42	0.42
1:B:473:ARG:HE	1:B:474:ARG:CG	2.24	0.42
1:A:385:ILE:CG2	1:A:387:PRO:HD3	2.36	0.42
1:B:50:GLN:O	1:B:54:ARG:HG3	2.19	0.42
1:B:289:SER:HB3	1:B:291:MET:HE2	2.01	0.42
1:A:18:ASN:HD22	1:A:18:ASN:N	2.17	0.42
1:A:118:ILE:HG22	1:A:178:ASP:HA	2.00	0.42
1:A:225:VAL:HG13	1:A:226:PRO:CD	2.50	0.42
1:A:352:LEU:CB	1:B:349:PHE:HB3	2.42	0.42
1:B:238:ALA:O	1:B:241:VAL:HG12	2.20	0.42
1:B:470:GLU:CA	1:B:473:ARG:HB2	2.46	0.42
1:B:476:TYR:CD2	1:B:476:TYR:O	2.73	0.42
1:A:158:LEU:HD22	1:A:164:PHE:CE2	2.51	0.42
1:B:286:HIS:C	1:B:287:LEU:HD12	2.44	0.42
1:B:391:THR:HG23	1:B:417:ARG:HD2	2.01	0.42
1:B:467:PRO:O	1:B:470:GLU:HG2	2.20	0.42
1:B:326:PRO:O	1:B:326:PRO:CD	2.67	0.42
1:B:348:VAL:CG1	1:B:350:PHE:CZ	3.02	0.42
1:B:480:LEU:H	1:B:480:LEU:HG	1.60	0.42
1:A:245:ASP:O	1:A:248:GLN:HB2	2.20	0.41
1:B:469:ARG:C	1:B:471:THR:H	2.28	0.41
1:A:29:GLU:OE1	1:A:54:ARG:CZ	2.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:480:LEU:C	1:A:480:LEU:CD2	2.91	0.41
1:A:484:ALA:HB1	2:A:635:HOH:O	2.20	0.41
1:B:73:ILE:HD13	1:B:73:ILE:H	1.83	0.41
1:B:77:MET:O	1:B:96:TRP:HB3	2.20	0.41
1:B:246:ALA:HA	1:B:262:VAL:HG12	2.02	0.41
1:B:470:GLU:HB3	1:B:473:ARG:NE	2.36	0.41
1:A:113:PRO:C	1:A:115:SER:H	2.28	0.41
1:B:362:ALA:O	1:B:365:VAL:HG12	2.21	0.41
1:B:400:GLU:HA	1:B:403:ARG:CZ	2.50	0.41
1:A:87:GLN:HE21	1:A:164:PHE:HZ	1.68	0.41
1:A:108:LEU:HD13	1:A:123:MET:HE3	2.01	0.41
1:A:288:MET:HE2	1:A:288:MET:HB2	1.96	0.41
1:A:466:GLN:N	1:A:467:PRO:HD2	2.35	0.41
1:B:325:GLU:N	1:B:326:PRO:CA	2.70	0.41
1:A:161:THR:OG1	1:A:163:GLU:HG2	2.21	0.41
1:B:131:LYS:O	1:B:134:TRP:HB3	2.21	0.41
1:B:270:PRO:C	1:B:272:SER:H	2.29	0.41
1:B:471:THR:OG1	1:B:472:PHE:HD1	2.04	0.41
1:B:167:ASP:OD2	1:B:231:GLY:HA2	2.20	0.41
1:B:329:PHE:CD2	1:B:365:VAL:HA	2.55	0.41
1:B:314:ILE:HG23	1:B:401:TYR:HD2	1.85	0.41
1:B:367:GLU:OE1	1:B:465:TYR:HE2	2.03	0.41
1:A:91:ARG:CG	1:A:91:ARG:NH1	2.83	0.41
1:A:484:ALA:CB	2:A:635:HOH:O	2.69	0.41
1:A:180:ALA:HB2	1:A:266:PHE:CD2	2.56	0.41
1:A:353:THR:OG1	1:A:355:GLN:HG3	2.19	0.41
1:A:18:ASN:ND2	1:A:18:ASN:C	2.79	0.40
1:B:168:MET:HE1	1:B:182:ARG:O	2.20	0.40
1:B:292:LEU:HB3	1:B:293:SER:O	2.20	0.40
1:B:313:LEU:HD23	1:B:313:LEU:H	1.84	0.40
1:A:479:LEU:O	1:A:480:LEU:C	2.64	0.40
1:A:482:LEU:N	1:A:482:LEU:CD1	2.84	0.40
1:B:102:ALA:O	1:B:105:CYS:HB2	2.21	0.40
1:A:72:GLY:HA2	1:A:228:VAL:HG22	2.03	0.40
1:B:43:GLN:NE2	1:B:48:TRP:HE1	2.20	0.40
1:A:18:ASN:C	1:A:20:GLN:N	2.78	0.40

All (1) 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)
1:A:484:ALA:O	2:B:543:HOH:O[4_445]	1.20	1.00

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	472/484 (98%)	440 (93%)	31 (7%)	1 (0%)	43	68
1	B	468/484 (97%)	413 (88%)	44 (9%)	11 (2%)	4	12
All	All	940/968 (97%)	853 (91%)	75 (8%)	12 (1%)	9	25

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	328	TRP
1	B	350	PHE
1	B	352	LEU
1	B	353	THR
1	B	481	PRO
1	B	327	VAL
1	B	348	VAL
1	A	36	PRO
1	B	271	GLU
1	B	293	SER
1	B	324	ALA
1	B	358	PRO

5.3.2 Protein sidechains [i](#)

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	375/382 (98%)	339 (90%)	36 (10%)	8	20
1	B	372/382 (97%)	324 (87%)	48 (13%)	4	10
All	All	747/764 (98%)	663 (89%)	84 (11%)	6	15

All (84) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	ILE
1	A	7	LEU
1	A	16	LEU
1	A	18	ASN
1	A	31	LEU
1	A	43	GLN
1	A	54	ARG
1	A	97	ASN
1	A	107	LEU
1	A	108	LEU
1	A	114	GLN
1	A	115	SER
1	A	141	GLU
1	A	190	GLN
1	A	243	MET
1	A	250	MET
1	A	255	THR
1	A	269	LYS
1	A	279	HIS
1	A	284	ARG
1	A	287	LEU
1	A	293	SER
1	A	303	LYS
1	A	305	THR
1	A	314	ILE
1	A	344	GLN
1	A	346	LYS
1	A	388	GLN
1	A	398	ARG
1	A	412	GLN
1	A	418	THR
1	A	444	GLU
1	A	451	LEU
1	A	479	LEU

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Mol	Chain	Res	Type
1	A	480	LEU
1	A	483	MET
1	B	7	LEU
1	B	12	VAL
1	B	16	LEU
1	B	18	ASN
1	B	20	GLN
1	B	24	VAL
1	B	31	LEU
1	B	43	GLN
1	B	73	ILE
1	B	90	LEU
1	B	97	ASN
1	B	107	LEU
1	B	108	LEU
1	B	115	SER
1	B	132	LEU
1	B	133	LEU
1	B	144	ARG
1	B	190	GLN
1	B	197	ASP
1	B	250	MET
1	B	255	THR
1	B	256	SER
1	B	260	PHE
1	B	289	SER
1	B	293	SER
1	B	298	LEU
1	B	299	ASP
1	B	319	GLN
1	B	321	ASP
1	B	328	TRP
1	B	330	LEU
1	B	333	LEU
1	B	344	GLN
1	B	346	LYS
1	B	352	LEU
1	B	354	HIS
1	B	355	GLN
1	B	359	ASN
1	B	360	GLU
1	B	386	LYS

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Mol	Chain	Res	Type
1	B	406	LEU
1	B	443	ILE
1	B	451	LEU
1	B	456	LEU
1	B	474	ARG
1	B	475	LEU
1	B	480	LEU
1	B	482	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (38) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	18	ASN
1	A	43	GLN
1	A	47	GLN
1	A	50	GLN
1	A	62	GLN
1	A	63	HIS
1	A	66	GLN
1	A	87	GLN
1	A	97	ASN
1	A	103	GLN
1	A	121	ASN
1	A	136	GLN
1	A	190	GLN
1	A	275	HIS
1	A	286	HIS
1	A	344	GLN
1	A	356	HIS
1	A	404	GLN
1	A	413	GLN
1	B	18	ASN
1	B	43	GLN
1	B	47	GLN
1	B	50	GLN
1	B	63	HIS
1	B	66	GLN
1	B	97	ASN
1	B	136	GLN
1	B	234	ASN
1	B	247	ASN
1	B	286	HIS

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Mol	Chain	Res	Type
1	B	355	GLN
1	B	359	ASN
1	B	404	GLN
1	B	412	GLN
1	B	413	GLN
1	B	433	GLN
1	B	453	GLN
1	B	460	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](#)

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

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	476/484 (98%)	-0.44	2 (0%) 88 87	9, 28, 54, 85	0
1	B	472/484 (97%)	-0.17	18 (3%) 44 40	8, 32, 67, 92	0
All	All	948/968 (97%)	-0.31	20 (2%) 63 61	8, 30, 61, 92	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	353	THR	7.0
1	B	348	VAL	4.0
1	B	324	ALA	3.7
1	B	472	PHE	3.5
1	B	350	PHE	3.5
1	B	473	ARG	3.3
1	B	328	TRP	3.3
1	B	294	ALA	3.3
1	B	345	ALA	3.3
1	B	471	THR	3.2
1	B	327	VAL	3.2
1	A	295	ALA	3.1
1	B	323	SER	2.9
1	B	474	ARG	2.7
1	B	347	GLY	2.6
1	B	482	LEU	2.4
1	B	333	LEU	2.4
1	B	349	PHE	2.4
1	B	481	PRO	2.4
1	A	343	PRO	2.3

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.