



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 01:17 AM UTC

PDB ID : 3K5O / pdb_00003k5o
Title : Crystal structure of E.coli Pol II
Authors : Yang, W.; Wang, F.
Deposited on : 2009-10-07
Resolution : 2.20 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

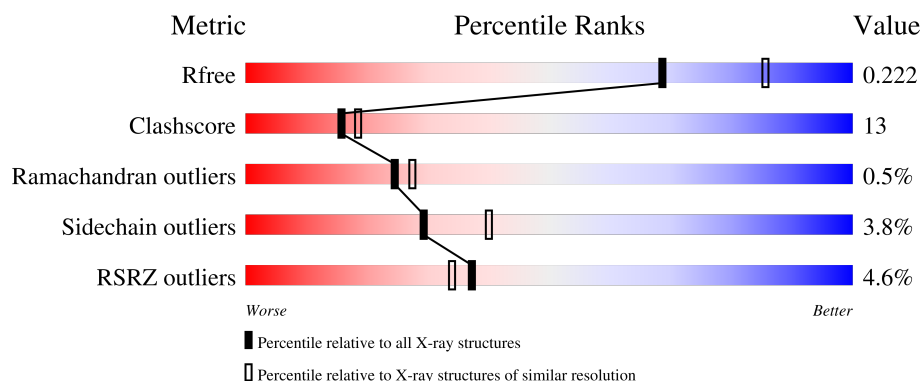
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	786	4% 73% 22% • •
1	B	786	5% 67% 24% • 5%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 12674 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 DNA polymerase II.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	758	Total	C	N	O	S	0	0	0
			6137	3918	1087	1109	23			
1	B	744	Total	C	N	O	S	0	0	0
			6015	3847	1056	1089	23			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP P21189
A	-1	PRO	-	expression tag	UNP P21189
A	0	HIS	-	expression tag	UNP P21189
A	335	ASN	ASP	engineered mutation	UNP P21189
B	-2	GLY	-	expression tag	UNP P21189
B	-1	PRO	-	expression tag	UNP P21189
B	0	HIS	-	expression tag	UNP P21189
B	335	ASN	ASP	engineered mutation	UNP P21189

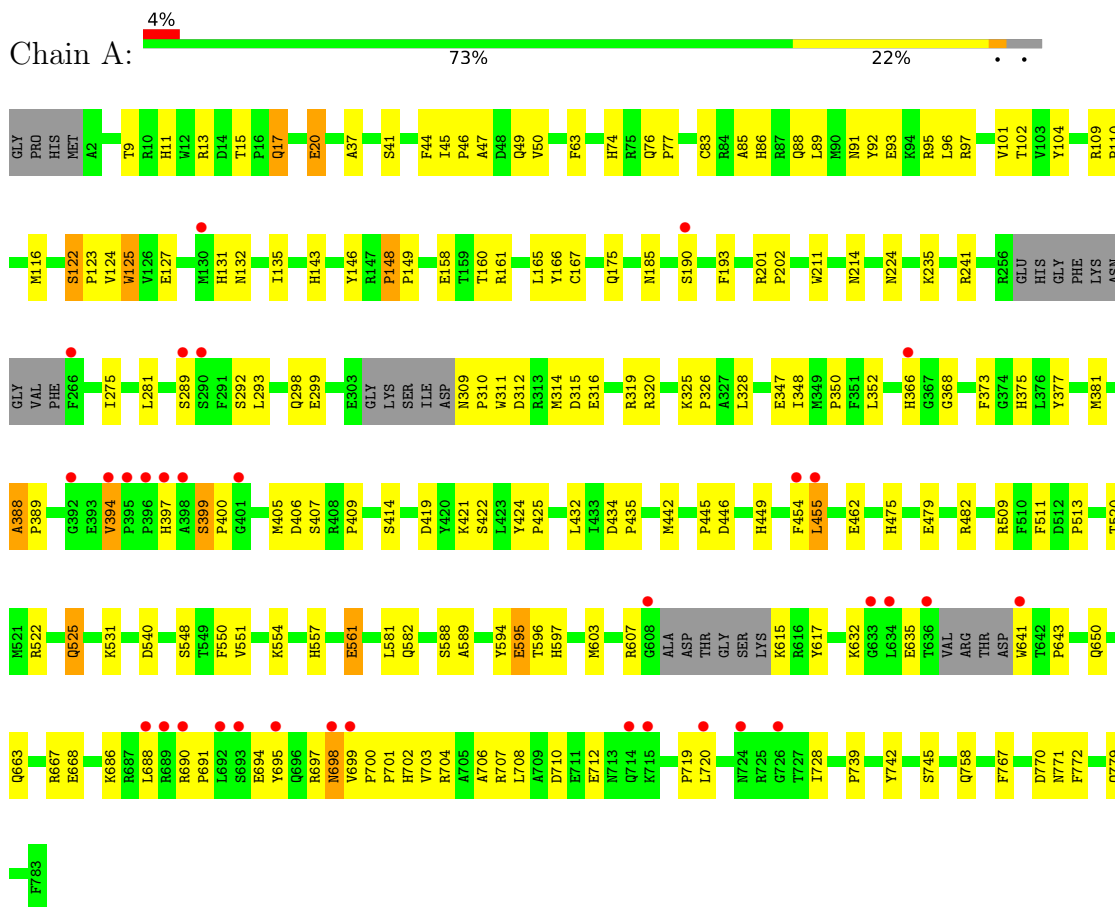
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	250	Total	O	0	0
			250	250		
2	B	272	Total	O	0	0
			272	272		

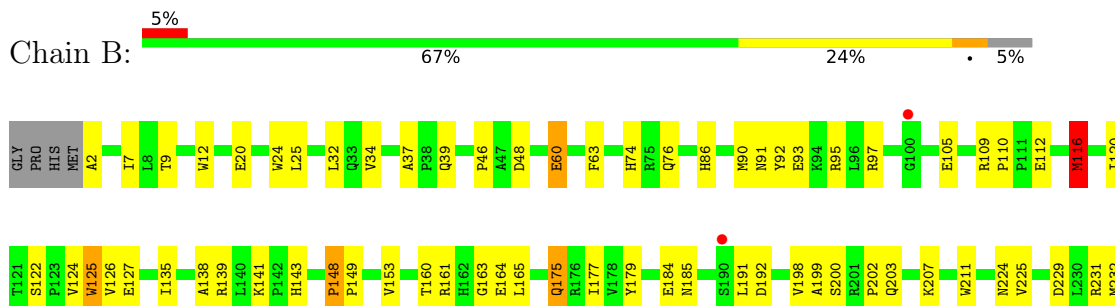
3 Residue-property plots [i](#)

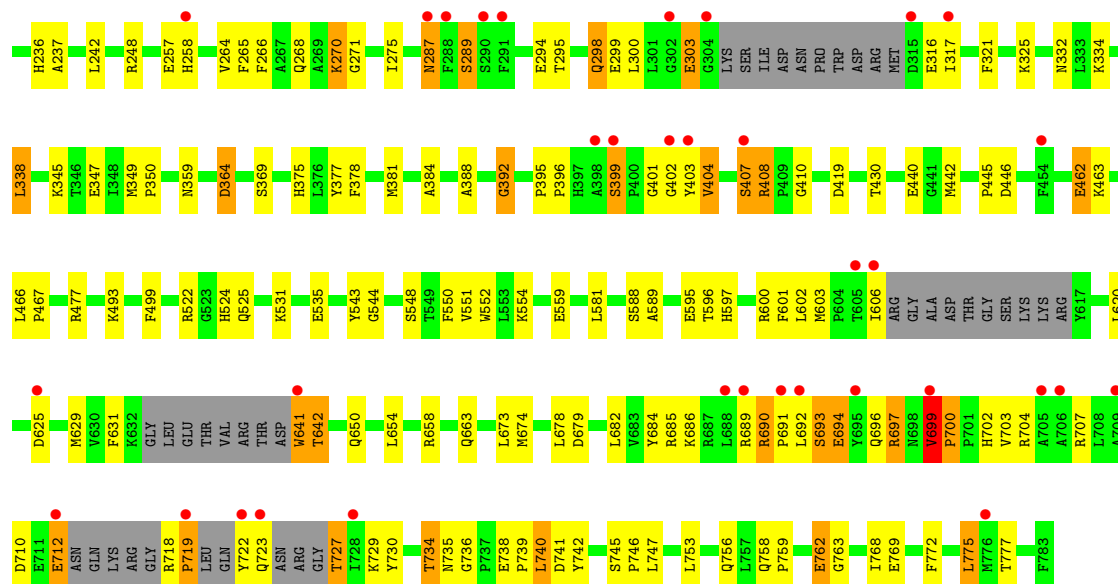
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

• Molecule 1: DNA polymerase II



• Molecule 1: DNA polymerase II





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	92.85Å 116.82Å 163.46Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.20 50.00 – 2.20	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-2.20) 91.1 (50.00-2.20)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.78 (at 2.20Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.218 , 0.223 0.218 , 0.222	Depositor DCC
R_{free} test set	2225 reflections (2.47%)	wwPDB-VP
Wilson B-factor (Å ²)	31.2	Xtriage
Anisotropy	0.163	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 38.1	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	0.95	EDS
Total number of atoms	12674	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 73.70 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.7531e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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	0.47	0/6299	1.04	35/8546 (0.4%)
1	B	0.47	1/6175 (0.0%)	1.07	42/8376 (0.5%)
All	All	0.47	1/12474 (0.0%)	1.06	77/16922 (0.5%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	116	MET	SD-CE	-7.52	1.60	1.79

All (77) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	734	THR	N-CA-C	-11.88	93.75	110.50
1	B	694	GLU	N-CA-C	-11.32	98.69	111.71
1	A	399	SER	N-CA-C	9.13	121.93	109.24
1	A	694	GLU	N-CA-C	8.94	121.10	111.36
1	B	60	GLU	N-CA-C	8.02	121.11	110.53
1	A	699	VAL	N-CA-C	7.97	117.65	108.96
1	B	148	PRO	N-CA-C	7.57	119.93	110.70
1	A	165	LEU	N-CA-C	7.55	121.17	110.23
1	B	225	VAL	N-CA-C	7.50	118.27	110.62
1	B	392	GLY	N-CA-C	7.47	124.38	113.48
1	A	148	PRO	N-CA-C	7.43	119.76	110.70
1	B	388	ALA	N-CA-C	7.25	119.04	109.83
1	B	191	LEU	N-CA-C	7.24	120.89	110.24
1	B	110	PRO	N-CA-C	7.21	119.50	110.70
1	A	368	GLY	N-CA-C	7.07	125.12	115.30
1	B	125	TRP	N-CA-C	-7.00	97.81	109.07
1	A	292	SER	N-CA-C	-6.85	100.84	110.50
1	B	736	GLY	CA-C-N	6.85	126.61	119.76
1	B	736	GLY	C-N-CA	6.85	126.61	119.76
1	A	125	TRP	N-CA-C	-6.76	98.19	109.07
1	A	399	SER	CA-C-N	6.71	126.67	119.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	399	SER	C-N-CA	6.71	126.67	119.76
1	B	736	GLY	N-CA-C	6.67	125.95	112.34
1	B	446	ASP	CA-C-N	6.58	126.28	119.56
1	B	446	ASP	C-N-CA	6.58	126.28	119.56
1	B	399	SER	N-CA-C	6.47	119.75	109.40
1	B	74	HIS	N-CA-C	-6.30	105.23	113.17
1	B	224	ASN	N-CA-C	-6.24	103.32	111.74
1	B	149	PRO	N-CA-C	-6.15	99.57	111.69
1	B	287	ASN	N-CA-C	6.13	119.22	108.56
1	A	275	ILE	N-CA-C	6.13	117.02	107.28
1	A	691	PRO	N-CA-C	-6.12	101.59	111.14
1	A	149	PRO	N-CA-C	-6.12	100.85	111.32
1	B	37	ALA	N-CA-C	-6.10	101.25	110.39
1	B	589	ALA	N-CA-C	-6.09	104.47	113.61
1	B	402	GLY	N-CA-C	6.06	118.89	111.93
1	A	37	ALA	N-CA-C	-6.04	101.50	110.20
1	A	589	ALA	N-CA-C	-6.04	105.09	112.88
1	A	377	TYR	N-CA-C	5.99	117.61	111.14
1	B	359	ASN	N-CA-C	5.87	120.44	113.28
1	B	689	ARG	N-CA-C	5.77	117.37	111.14
1	B	408	ARG	N-CA-C	-5.73	96.75	108.21
1	A	366	HIS	N-CA-C	5.72	117.38	111.03
1	A	643	PRO	N-CA-C	-5.71	106.09	113.57
1	A	595	GLU	N-CA-C	5.67	120.20	112.04
1	B	699	VAL	N-CA-C	5.64	121.05	108.88
1	B	316	GLU	N-CA-C	-5.61	105.70	112.54
1	B	499	PHE	N-CA-C	5.57	117.36	111.28
1	A	388	ALA	N-CA-C	5.56	116.89	109.83
1	B	763	GLY	N-CA-C	-5.56	107.77	114.66
1	A	745	SER	CA-C-N	5.55	125.48	119.76
1	A	745	SER	C-N-CA	5.55	125.48	119.76
1	A	110	PRO	N-CA-C	5.52	117.44	110.70
1	A	394	VAL	CA-C-N	5.48	123.60	119.66
1	A	394	VAL	C-N-CA	5.48	123.60	119.66
1	B	399	SER	CA-C-N	5.47	125.40	119.76
1	B	399	SER	C-N-CA	5.47	125.40	119.76
1	B	377	TYR	N-CA-C	5.40	116.97	111.14
1	B	105	GLU	N-CA-C	5.38	119.13	112.24
1	A	146	TYR	N-CA-C	5.35	118.07	110.10
1	A	74	HIS	N-CA-C	-5.33	106.36	112.92
1	A	663	GLN	N-CA-C	5.30	117.47	111.11
1	A	462	GLU	N-CA-C	5.30	118.20	111.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	229	ASP	N-CA-C	5.24	117.41	111.02
1	B	124	VAL	N-CA-C	5.24	116.56	108.44
1	B	430	THR	N-CA-C	5.24	117.07	111.36
1	B	275	ILE	N-CA-C	5.19	115.05	107.37
1	B	642	THR	N-CA-C	-5.19	102.73	110.20
1	B	551	VAL	N-CA-C	5.18	115.42	108.17
1	A	293	LEU	N-CA-C	5.17	116.91	111.28
1	A	224	ASN	N-CA-C	-5.15	104.78	111.74
1	B	663	GLN	N-CA-C	5.12	117.25	111.11
1	A	214	ASN	N-CA-C	5.09	116.91	111.36
1	B	700	PRO	N-CA-C	-5.08	104.50	110.70
1	A	551	VAL	N-CA-C	5.04	115.11	107.80
1	A	432	LEU	N-CA-C	5.04	118.55	111.90
1	A	124	VAL	N-CA-C	5.03	116.24	108.44

There are no chirality outliers.

There are no planarity outliers.

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	6137	0	5992	124	0
1	B	6015	0	5849	198	0
2	A	250	0	0	3	0
2	B	272	0	0	8	0
All	All	12674	0	11841	319	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 13.

All (319) 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:116:MET:HE2	1:B:378:PHE:HB2	1.32	1.12
1:A:522:ARG:NH1	1:A:525:GLN:HE22	1.49	1.10

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:86:HIS:CE1	1:B:90:MET:HE1	1.91	1.04
1:A:522:ARG:HH11	1:A:525:GLN:NE2	1.56	1.02
1:B:674:MET:HE1	1:B:753:LEU:HB2	1.40	1.01
1:A:311:TRP:CZ2	1:B:696:GLN:HB2	2.00	0.95
1:B:258:HIS:HD2	1:B:266:PHE:HD2	1.10	0.95
1:A:49:GLN:HE22	1:A:102:THR:H	1.04	0.95
1:B:685:ARG:HD2	1:B:727:THR:HG21	1.53	0.91
1:B:692:LEU:O	1:B:693:SER:HB3	1.70	0.91
1:B:258:HIS:HD2	1:B:266:PHE:CD2	1.89	0.90
1:B:674:MET:HE3	1:B:753:LEU:HD22	1.52	0.89
1:B:86:HIS:ND1	1:B:90:MET:HE1	1.89	0.87
1:A:712:GLU:HG2	1:A:742:TYR:CD1	2.11	0.86
1:A:49:GLN:NE2	1:A:102:THR:H	1.75	0.85
1:B:685:ARG:CD	1:B:727:THR:HG21	2.07	0.84
1:A:405:MET:HE3	1:A:531:LYS:HE3	1.60	0.83
1:B:199:ALA:H	1:B:203:GLN:NE2	1.77	0.82
1:B:674:MET:CE	1:B:753:LEU:HB2	2.10	0.82
1:B:116:MET:HE2	1:B:378:PHE:CB	2.10	0.82
1:A:522:ARG:HH11	1:A:525:GLN:HE22	0.86	0.81
1:B:258:HIS:CD2	1:B:266:PHE:HD2	1.97	0.80
1:A:83:CYS:HB3	1:A:88:GLN:HE21	1.47	0.80
1:B:93:GLU:O	1:B:97:ARG:HG2	1.82	0.80
1:B:758:GLN:HG3	1:B:772:PHE:CD2	2.16	0.80
1:B:477:ARG:HE	1:B:493:LYS:HB2	1.45	0.79
1:B:673:LEU:HD23	1:B:674:MET:HE2	1.64	0.79
1:B:642:THR:H	1:B:756:GLN:HE22	1.27	0.78
1:B:294:GLU:O	1:B:298:GLN:HG2	1.85	0.76
1:A:49:GLN:HE22	1:A:102:THR:N	1.83	0.75
1:A:91:ASN:HB2	2:A:1051:HOH:O	1.87	0.75
1:A:85:ALA:O	1:A:88:GLN:HG2	1.87	0.75
1:B:699:VAL:CG1	1:B:704:ARG:HG3	2.17	0.73
1:B:116:MET:CE	1:B:378:PHE:HB2	2.16	0.73
1:B:745:SER:HB3	1:B:746:PRO:HD2	1.70	0.72
1:A:311:TRP:CE2	1:B:696:GLN:HB2	2.25	0.72
1:A:389:PRO:O	1:A:509:ARG:HD3	1.89	0.72
1:B:696:GLN:HG2	1:B:697:ARG:H	1.56	0.71
1:B:654:LEU:O	1:B:658:ARG:HG3	1.92	0.70
1:A:710:ASP:HB3	1:A:720:LEU:HD22	1.74	0.70
1:A:116:MET:HE2	1:A:375:HIS:HA	1.75	0.69
1:B:375:HIS:HD2	2:B:808:HOH:O	1.74	0.69
1:B:722:TYR:HE1	1:B:727:THR:O	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:642:THR:H	1:B:756:GLN:NE2	1.90	0.68
1:B:258:HIS:CD2	1:B:266:PHE:CD2	2.78	0.68
1:A:758:GLN:HG3	1:A:772:PHE:CD2	2.28	0.68
1:B:160:THR:CG2	1:B:164:GLU:HB2	2.23	0.68
1:B:116:MET:HE3	1:B:375:HIS:HA	1.74	0.68
1:A:309:ASN:OD1	1:A:719:PRO:HG2	1.94	0.67
1:B:175:GLN:NE2	1:B:211:TRP:HE1	1.92	0.67
1:A:131:HIS:CE1	1:A:132:ASN:ND2	2.63	0.66
1:A:540:ASP:OD1	1:A:554:LYS:HE3	1.97	0.65
1:B:768:ILE:O	1:B:769:GLU:HB2	1.97	0.64
1:B:700:PRO:HD2	1:B:703:VAL:CG2	2.27	0.64
1:A:615:LYS:HG3	1:A:615:LYS:O	1.97	0.64
1:B:772:PHE:O	1:B:775:LEU:HD22	1.97	0.64
1:A:581:LEU:HD12	1:A:588:SER:HB2	1.79	0.64
1:B:303:GLU:HG3	1:B:303:GLU:O	1.96	0.64
1:B:629:MET:HE1	1:B:654:LEU:HB2	1.80	0.63
1:B:693:SER:HA	1:B:707:ARG:HH21	1.63	0.63
1:B:699:VAL:HG11	1:B:704:ARG:HG3	1.79	0.63
1:B:522:ARG:HH22	1:B:525:GLN:HE22	1.45	0.63
1:B:543:TYR:HB2	1:B:603:MET:HE3	1.78	0.63
1:B:696:GLN:CG	1:B:697:ARG:H	2.11	0.63
1:B:718:ARG:CA	1:B:719:PRO:C	2.71	0.63
1:B:192:ASP:OD1	1:B:192:ASP:C	2.42	0.62
1:B:762:GLU:OE1	1:B:772:PHE:HB3	2.00	0.62
1:A:394:VAL:HG11	1:A:511:PHE:O	2.00	0.62
1:B:2:ALA:HB2	1:B:127:GLU:HG2	1.82	0.62
1:B:175:GLN:HE22	1:B:177:ILE:HG22	1.63	0.62
1:B:559:GLU:OE1	1:B:597:HIS:HD2	1.83	0.62
1:A:405:MET:CE	1:A:531:LYS:HE3	2.29	0.61
1:B:699:VAL:HG12	1:B:704:ARG:HG3	1.82	0.61
1:A:131:HIS:CE1	1:A:132:ASN:HD21	2.19	0.61
1:B:734:THR:O	1:B:735:ASN:HB2	1.99	0.61
1:A:697:ARG:O	1:A:698:ASN:C	2.44	0.61
1:A:635:GLU:HG2	1:A:641:TRP:CD2	2.36	0.60
1:B:740:LEU:HD12	1:B:740:LEU:O	2.01	0.60
1:A:706:ALA:HA	1:A:728:ILE:CD1	2.32	0.60
1:B:629:MET:HE1	1:B:654:LEU:HD13	1.83	0.60
1:B:522:ARG:NH2	1:B:525:GLN:NE2	2.50	0.60
1:B:679:ASP:HA	1:B:682:LEU:HD22	1.84	0.59
1:B:692:LEU:O	1:B:693:SER:CB	2.46	0.59
1:B:696:GLN:CG	1:B:697:ARG:N	2.66	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:650:GLN:HB3	2:B:1187:HOH:O	2.03	0.59
1:B:718:ARG:N	1:B:719:PRO:C	2.61	0.59
1:B:522:ARG:NH2	1:B:525:GLN:HE22	2.00	0.58
1:B:199:ALA:H	1:B:203:GLN:HE22	1.50	0.58
1:A:706:ALA:HA	1:A:728:ILE:HD12	1.85	0.58
1:B:34:VAL:HG13	1:B:138:ALA:CB	2.34	0.58
1:B:364:ASP:OD1	1:B:364:ASP:N	2.36	0.58
1:B:758:GLN:HG3	1:B:772:PHE:HD2	1.66	0.58
1:B:32:LEU:HD21	1:B:135:ILE:CD1	2.34	0.58
1:B:163:GLY:HA3	1:B:232:MET:HE1	1.85	0.58
1:B:739:PRO:HG2	1:B:741:ASP:O	2.03	0.58
1:B:691:PRO:HG2	1:B:694:GLU:OE1	2.04	0.57
1:A:388:ALA:HB1	1:A:509:ARG:HD2	1.85	0.57
1:B:116:MET:HE1	1:B:378:PHE:CG	2.40	0.57
1:B:198:VAL:HB	1:B:203:GLN:HE21	1.69	0.57
1:B:685:ARG:CG	1:B:727:THR:CG2	2.82	0.57
1:A:49:GLN:NE2	1:A:101:VAL:HA	2.20	0.57
1:A:442:MET:O	1:A:445:PRO:HD3	2.04	0.57
1:B:690:ARG:HD2	1:B:694:GLU:HG2	1.86	0.57
1:A:316:GLU:OE2	1:A:319:ARG:NH1	2.37	0.57
1:A:85:ALA:HB3	1:A:88:GLN:CD	2.30	0.56
1:B:127:GLU:OE1	1:B:139:ARG:NH1	2.39	0.56
1:A:49:GLN:HE21	1:A:101:VAL:HA	1.70	0.56
1:A:86:HIS:HE1	1:A:109:ARG:NH1	2.02	0.56
1:B:34:VAL:HG22	1:B:135:ILE:HB	1.86	0.56
1:B:758:GLN:HB3	1:B:759:PRO:HD3	1.88	0.56
1:B:32:LEU:HD21	1:B:135:ILE:HD12	1.88	0.56
1:B:384:ALA:O	1:B:463:LYS:HE3	2.06	0.56
1:B:629:MET:HE1	1:B:654:LEU:CB	2.35	0.56
1:A:400:PRO:HB2	1:A:520:THR:HG21	1.87	0.56
1:B:641:TRP:HA	1:B:641:TRP:CE3	2.40	0.56
1:A:13:ARG:NE	1:A:20:GLU:OE2	2.35	0.55
1:A:686:LYS:HD3	1:A:702:HIS:CG	2.41	0.55
1:A:309:ASN:HD22	1:A:312:ASP:H	1.54	0.55
1:B:642:THR:HG23	1:B:756:GLN:NE2	2.22	0.55
1:A:557:HIS:HD2	1:A:561:GLU:OE2	1.89	0.55
1:B:641:TRP:HA	1:B:641:TRP:HE3	1.71	0.55
1:A:407:SER:CB	1:A:603:MET:HE2	2.37	0.54
1:A:617:TYR:CZ	1:A:632:LYS:HG3	2.43	0.54
1:A:706:ALA:CA	1:A:728:ILE:CD1	2.85	0.54
1:B:710:ASP:C	1:B:712:GLU:H	2.15	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:160:THR:HG23	1:B:164:GLU:HB2	1.89	0.54
1:B:710:ASP:C	1:B:712:GLU:N	2.60	0.54
1:A:47:ALA:O	1:A:50:VAL:HG23	2.08	0.54
1:A:712:GLU:HG2	1:A:742:TYR:CE1	2.43	0.54
1:A:63:PHE:CD1	1:A:63:PHE:C	2.86	0.53
1:A:394:VAL:O	1:A:394:VAL:HG13	2.07	0.53
1:B:125:TRP:HB2	1:B:141:LYS:HG2	1.90	0.53
1:B:407:SER:HB2	1:B:606:ILE:HB	1.89	0.53
1:B:700:PRO:HD2	1:B:703:VAL:HB	1.90	0.53
1:A:175:GLN:NE2	1:A:211:TRP:HZ2	2.06	0.52
1:A:161:ARG:HG3	1:A:314:MET:HE2	1.91	0.52
1:A:522:ARG:NH1	1:A:525:GLN:NE2	2.29	0.52
1:A:557:HIS:CD2	1:A:561:GLU:OE2	2.63	0.52
1:B:347:GLU:C	1:B:350:PRO:HD2	2.35	0.52
1:A:405:MET:HE3	1:A:531:LYS:CE	2.38	0.51
1:B:347:GLU:O	1:B:350:PRO:HD2	2.10	0.51
1:A:690:ARG:HB2	1:A:695:TYR:CE2	2.46	0.51
1:B:522:ARG:HH21	1:B:525:GLN:CD	2.17	0.51
1:A:407:SER:HB2	1:A:603:MET:HE2	1.92	0.51
1:B:442:MET:O	1:B:445:PRO:HD3	2.11	0.51
1:B:477:ARG:NE	1:B:493:LYS:HB2	2.19	0.51
1:B:686:LYS:HE2	1:B:702:HIS:CE1	2.46	0.51
1:A:454:PHE:HB3	1:A:455:LEU:CD1	2.41	0.51
1:B:334:LYS:HE3	1:B:338:LEU:HD13	1.93	0.50
1:A:201:ARG:HB2	1:A:202:PRO:HD3	1.93	0.50
1:A:315:ASP:OD2	1:B:697:ARG:NH2	2.44	0.50
1:A:700:PRO:HG2	1:A:703:VAL:CG2	2.41	0.50
1:B:710:ASP:O	1:B:712:GLU:N	2.44	0.50
1:B:112:GLU:O	1:B:116:MET:HB2	2.11	0.50
1:B:2:ALA:HA	1:B:126:VAL:O	2.12	0.50
1:B:440:GLU:HG3	1:B:463:LYS:HD3	1.93	0.50
1:B:700:PRO:HD2	1:B:703:VAL:HG21	1.92	0.50
1:A:690:ARG:HD2	1:A:695:TYR:CZ	2.47	0.49
1:B:86:HIS:CE1	1:B:109:ARG:NH1	2.81	0.49
1:B:730:TYR:HB2	1:B:738:GLU:O	2.12	0.49
1:B:629:MET:HG2	1:B:631:PHE:CZ	2.47	0.49
1:A:381:MET:HE1	1:A:388:ALA:HB2	1.95	0.49
1:B:289:SER:HB3	1:B:299:GLU:OE2	2.13	0.49
1:A:701:PRO:HA	1:A:704:ARG:HG2	1.95	0.48
1:A:122:SER:HB2	1:A:123:PRO:HD3	1.95	0.48
1:B:248:ARG:NH1	1:B:271:GLY:O	2.45	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:86:HIS:HE1	1:B:109:ARG:NH1	2.11	0.48
1:B:116:MET:CE	1:B:378:PHE:CG	2.96	0.48
1:A:347:GLU:O	1:A:350:PRO:HD2	2.14	0.48
1:A:397:HIS:HB2	1:A:513:PRO:HB3	1.95	0.48
1:B:601:PHE:HE2	1:B:603:MET:HE2	1.79	0.48
1:B:629:MET:CE	1:B:654:LEU:HB2	2.43	0.48
1:A:160:THR:HG22	1:A:166:TYR:CZ	2.49	0.48
1:B:200:SER:HB2	1:B:202:PRO:HD2	1.96	0.48
1:B:295:THR:HA	1:B:298:GLN:CG	2.44	0.48
1:B:403:TYR:HB2	1:B:524:HIS:CD2	2.49	0.48
1:B:700:PRO:HD2	1:B:703:VAL:CB	2.44	0.48
1:B:734:THR:CG2	1:B:746:PRO:HG2	2.44	0.48
1:A:175:GLN:NE2	1:A:175:GLN:O	2.48	0.47
1:A:289:SER:HB3	1:A:299:GLU:OE2	2.14	0.47
1:A:596:THR:HG22	1:A:597:HIS:N	2.28	0.47
1:B:462:GLU:HB2	2:B:1275:HOH:O	2.14	0.47
1:A:45:ILE:HG22	1:A:46:PRO:O	2.14	0.47
1:B:410:GLY:O	1:B:602:LEU:HD12	2.15	0.47
1:B:116:MET:CE	1:B:378:PHE:CB	2.84	0.47
1:B:690:ARG:CB	1:B:691:PRO:CD	2.92	0.47
1:B:39:GLN:HG2	2:B:1039:HOH:O	2.15	0.47
1:B:419:ASP:HB3	1:B:548:SER:OG	2.14	0.47
1:B:185:ASN:OD1	1:B:185:ASN:C	2.58	0.47
1:B:685:ARG:CG	1:B:727:THR:HG23	2.45	0.47
1:A:399:SER:HA	1:A:400:PRO:HD3	1.78	0.47
1:A:455:LEU:N	1:A:455:LEU:HD12	2.30	0.47
1:B:685:ARG:HD2	1:B:727:THR:CG2	2.36	0.47
1:A:175:GLN:HB3	2:A:1133:HOH:O	2.14	0.46
1:A:550:PHE:N	1:A:550:PHE:CD2	2.83	0.46
1:B:543:TYR:CB	1:B:603:MET:HE3	2.43	0.46
1:B:257:GLU:HB2	1:B:265:PHE:CE1	2.51	0.46
1:B:401:GLY:O	1:B:524:HIS:NE2	2.47	0.46
1:A:690:ARG:HD2	1:A:695:TYR:CE1	2.50	0.46
1:B:91:ASN:HD21	1:B:95:ARG:HH11	1.63	0.46
1:B:550:PHE:N	1:B:550:PHE:CD2	2.84	0.46
1:A:475:HIS:HD2	2:A:999:HOH:O	1.98	0.46
1:B:199:ALA:N	1:B:203:GLN:NE2	2.56	0.46
1:A:89:LEU:O	1:A:93:GLU:HG3	2.16	0.46
1:A:158:GLU:HB2	1:A:167:CYS:SG	2.56	0.46
1:A:594:TYR:OH	1:A:597:HIS:HB2	2.16	0.46
1:B:91:ASN:ND2	1:B:95:ARG:HH11	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:294:GLU:CD	1:B:294:GLU:H	2.23	0.46
1:A:770:ASP:OD1	1:A:771:ASN:N	2.46	0.46
1:B:160:THR:HG21	1:B:164:GLU:HB2	1.95	0.46
1:B:522:ARG:NH2	1:B:525:GLN:CD	2.74	0.46
1:A:309:ASN:HB3	1:A:312:ASP:HB2	1.98	0.45
1:A:235:LYS:HA	1:A:235:LYS:HD3	1.63	0.45
1:B:46:PRO:HB3	1:B:76:GLN:HG2	1.98	0.45
1:B:349:MET:HB2	1:B:350:PRO:HD3	1.97	0.45
1:B:300:LEU:HG	1:B:345:LYS:HG2	1.98	0.45
1:B:544:GLY:HA2	1:B:548:SER:O	2.16	0.45
1:B:595:GLU:HG3	2:B:1061:HOH:O	2.15	0.45
1:A:419:ASP:OD2	1:A:595:GLU:OE1	2.35	0.45
1:A:706:ALA:CA	1:A:728:ILE:HD12	2.47	0.45
1:B:581:LEU:HD12	1:B:588:SER:HB2	1.99	0.45
1:B:741:ASP:O	1:B:742:TYR:CD2	2.70	0.45
1:A:309:ASN:CG	1:A:719:PRO:HG2	2.41	0.45
1:B:298:GLN:HB3	1:B:303:GLU:O	2.16	0.45
1:B:741:ASP:O	1:B:742:TYR:CB	2.63	0.45
1:B:179:TYR:CE1	1:B:207:LYS:HE2	2.52	0.45
1:B:7:ILE:HG12	1:B:25:LEU:CD2	2.46	0.45
1:B:258:HIS:O	1:B:264:VAL:HG22	2.17	0.45
1:B:90:MET:HE2	1:B:90:MET:HB2	1.74	0.44
1:A:406:ASP:OD1	1:A:607:ARG:HA	2.17	0.44
1:B:684:TYR:O	1:B:729:LYS:HA	2.17	0.44
1:A:434:ASP:OD1	1:A:435:PRO:HD2	2.18	0.44
1:A:419:ASP:HB3	1:A:548:SER:OG	2.18	0.44
1:B:120:ILE:O	1:B:375:HIS:HE1	2.00	0.44
1:B:600:ARG:HB2	1:B:620:LEU:HB3	2.00	0.44
1:B:678:LEU:O	1:B:682:LEU:HD13	2.17	0.44
1:B:691:PRO:HD2	1:B:694:GLU:HB2	2.00	0.44
1:A:455:LEU:CD1	1:A:455:LEU:N	2.81	0.44
1:A:479:GLU:OE2	1:A:482:ARG:NH2	2.50	0.44
1:A:185:ASN:OD1	1:A:185:ASN:C	2.61	0.44
1:A:325:LYS:N	1:A:326:PRO:CD	2.80	0.44
1:B:237:ALA:HB1	1:B:242:LEU:O	2.18	0.44
1:A:424:TYR:HB2	1:A:425:PRO:HD3	2.00	0.44
1:B:332:ASN:OD1	1:B:332:ASN:C	2.60	0.44
1:B:699:VAL:HA	1:B:700:PRO:HD3	1.78	0.44
1:B:24:TRP:HE1	1:B:270:LYS:HE3	1.83	0.43
1:B:403:TYR:HB2	1:B:524:HIS:HD2	1.83	0.43
1:B:531:LYS:O	1:B:535:GLU:HG3	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:690:ARG:HB3	1:B:691:PRO:CD	2.48	0.43
1:B:522:ARG:NH2	1:B:525:GLN:OE1	2.47	0.43
1:B:231:ARG:HG2	1:B:231:ARG:HH11	1.83	0.43
1:B:395:PRO:HA	1:B:396:PRO:HD2	1.92	0.43
1:A:320:ARG:HB3	1:A:328:LEU:HB2	2.00	0.43
1:B:674:MET:CE	1:B:753:LEU:HD22	2.36	0.43
1:B:408:ARG:HE	1:B:408:ARG:HB3	1.67	0.43
1:B:596:THR:HG22	1:B:597:HIS:N	2.33	0.43
1:A:421:LYS:O	1:A:422:SER:C	2.61	0.43
1:A:161:ARG:HG3	1:A:314:MET:CE	2.49	0.43
1:A:41:SER:OG	1:A:86:HIS:HD2	2.02	0.43
1:A:131:HIS:ND1	1:A:132:ASN:ND2	2.66	0.43
1:A:348:ILE:O	1:A:352:LEU:HG	2.19	0.43
1:A:690:ARG:HB2	1:A:695:TYR:CZ	2.54	0.43
1:B:86:HIS:CE1	1:B:109:ARG:HD3	2.53	0.43
1:B:97:ARG:NE	2:B:1132:HOH:O	2.52	0.43
1:B:153:VAL:O	1:B:153:VAL:HG13	2.19	0.43
1:B:740:LEU:HD12	1:B:740:LEU:C	2.43	0.43
1:A:76:GLN:HA	1:A:77:PRO:HD3	1.92	0.42
1:B:165:LEU:HB2	1:B:236:HIS:NE2	2.33	0.42
1:B:741:ASP:O	1:B:742:TYR:HB2	2.19	0.42
1:A:690:ARG:HG3	1:A:690:ARG:HH11	1.84	0.42
1:B:691:PRO:HA	1:B:723:GLN:O	2.19	0.42
1:A:454:PHE:C	1:A:455:LEU:HD13	2.44	0.42
1:B:48:ASP:H	1:B:76:GLN:NE2	2.18	0.42
1:B:334:LYS:HA	1:B:334:LYS:HD2	1.81	0.42
1:B:403:TYR:O	1:B:404:VAL:CG2	2.68	0.42
1:A:405:MET:CE	1:A:531:LYS:CE	2.97	0.42
1:A:175:GLN:CD	1:A:175:GLN:C	2.87	0.42
1:B:63:PHE:CD1	1:B:63:PHE:C	2.97	0.42
1:B:287:ASN:ND2	1:B:287:ASN:H	2.17	0.42
1:B:86:HIS:CE1	1:B:109:ARG:HH11	2.37	0.42
1:B:125:TRP:CE2	1:B:143:HIS:CD2	3.07	0.42
1:A:241:ARG:HA	1:A:241:ARG:HD2	1.85	0.42
1:B:629:MET:CE	1:B:654:LEU:HD13	2.49	0.42
1:A:44:PHE:HB2	1:A:104:TYR:HB2	2.00	0.42
1:B:466:LEU:N	1:B:467:PRO:CD	2.83	0.42
1:B:699:VAL:HG11	1:B:704:ARG:CG	2.46	0.42
1:A:9:THR:OG1	1:A:11:HIS:HE1	2.02	0.41
1:B:9:THR:HA	2:B:838:HOH:O	2.19	0.41
1:A:86:HIS:CE1	1:A:109:ARG:NH1	2.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:92:TYR:O	1:A:96:LEU:HG	2.21	0.41
1:B:34:VAL:HG21	1:B:126:VAL:HG21	2.02	0.41
1:B:321:PHE:CE1	1:B:325:LYS:HE2	2.56	0.41
1:A:289:SER:CB	1:A:299:GLU:OE2	2.69	0.41
1:A:373:PHE:CD2	1:A:373:PHE:C	2.98	0.41
1:B:86:HIS:CE1	1:B:90:MET:CE	2.82	0.41
1:B:543:TYR:CG	1:B:544:GLY:N	2.88	0.41
1:A:522:ARG:HD3	1:A:522:ARG:HA	1.88	0.41
1:A:700:PRO:HG2	1:A:703:VAL:HG23	2.02	0.41
1:A:739:PRO:HG2	1:A:742:TYR:HB2	2.03	0.41
1:B:381:MET:HE2	1:B:381:MET:HB3	1.99	0.41
1:A:446:ASP:OD1	1:A:449:HIS:HD2	2.04	0.41
1:A:667:ARG:HB3	1:A:779:GLN:OE1	2.20	0.41
1:A:706:ALA:HB2	1:A:728:ILE:CD1	2.51	0.41
1:B:32:LEU:HD21	1:B:135:ILE:HD11	2.03	0.41
1:B:543:TYR:HB2	1:B:603:MET:CE	2.50	0.41
1:A:15:THR:C	1:A:17:GLN:N	2.78	0.40
1:B:552:TRP:CE2	1:B:554:LYS:HA	2.56	0.40
1:B:60:GLU:HB3	1:B:92:TYR:OH	2.22	0.40
1:B:403:TYR:C	1:B:404:VAL:HG23	2.46	0.40
1:A:125:TRP:CE2	1:A:143:HIS:CD2	3.08	0.40
1:A:668:GLU:OE1	1:A:668:GLU:HA	2.22	0.40
1:B:12:TRP:HA	1:B:20:GLU:O	2.21	0.40
1:A:85:ALA:HB3	1:A:88:GLN:CG	2.51	0.40
1:A:193:PHE:CD2	1:A:193:PHE:N	2.89	0.40
1:B:392:GLY:HA2	2:B:1106:HOH:O	2.20	0.40
1:A:409:PRO:HB2	1:A:767:PHE:CZ	2.56	0.40
1:B:629:MET:HE1	1:B:654:LEU:CD1	2.52	0.40
1:B:685:ARG:HG3	1:B:727:THR:CG2	2.51	0.40
1:B:693:SER:O	1:B:693:SER:OG	2.39	0.40

There are no symmetry-related clashes.

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	748/786 (95%)	733 (98%)	12 (2%)	3 (0%)	30	34
1	B	730/786 (93%)	709 (97%)	17 (2%)	4 (0%)	24	27
All	All	1478/1572 (94%)	1442 (98%)	29 (2%)	7 (0%)	24	27

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	693	SER
1	A	698	ASN
1	B	122	SER
1	B	699	VAL
1	A	122	SER
1	A	414	SER
1	B	404	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	642/672 (96%)	623 (97%)	19 (3%)	36	49
1	B	629/672 (94%)	600 (95%)	29 (5%)	24	32
All	All	1271/1344 (95%)	1223 (96%)	48 (4%)	29	40

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	GLN
1	A	20	GLU
1	A	95	ARG
1	A	97	ARG
1	A	127	GLU
1	A	135	ILE

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Mol	Chain	Res	Type
1	A	148	PRO
1	A	190	SER
1	A	281	LEU
1	A	298	GLN
1	A	310	PRO
1	A	455	LEU
1	A	525	GLN
1	A	561	GLU
1	A	582	GLN
1	A	650	GLN
1	A	688	LEU
1	A	707	ARG
1	A	708	LEU
1	B	116	MET
1	B	148	PRO
1	B	161	ARG
1	B	175	GLN
1	B	184	GLU
1	B	268	GLN
1	B	270	LYS
1	B	289	SER
1	B	298	GLN
1	B	303	GLU
1	B	317	ILE
1	B	338	LEU
1	B	364	ASP
1	B	369	SER
1	B	399	SER
1	B	407	SER
1	B	462	GLU
1	B	625	ASP
1	B	641	TRP
1	B	690	ARG
1	B	697	ARG
1	B	712	GLU
1	B	719	PRO
1	B	727	THR
1	B	740	LEU
1	B	747	LEU
1	B	762	GLU
1	B	775	LEU
1	B	777	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (37) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	3	GLN
1	A	11	HIS
1	A	33	GLN
1	A	49	GLN
1	A	86	HIS
1	A	88	GLN
1	A	132	ASN
1	A	449	HIS
1	A	475	HIS
1	A	497	ASN
1	A	525	GLN
1	A	557	HIS
1	A	571	GLN
1	A	584	GLN
1	A	649	GLN
1	A	756	GLN
1	B	29	ASN
1	B	76	GLN
1	B	86	HIS
1	B	91	ASN
1	B	137	ASN
1	B	175	GLN
1	B	203	GLN
1	B	258	HIS
1	B	287	ASN
1	B	298	GLN
1	B	375	HIS
1	B	390	ASN
1	B	483	GLN
1	B	529	GLN
1	B	582	GLN
1	B	597	HIS
1	B	659	ASN
1	B	702	HIS
1	B	735	ASN
1	B	756	GLN
1	B	758	GLN

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

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	758/786 (96%)	0.14	33 (4%) 39 36	18, 35, 65, 85	0
1	B	744/786 (94%)	0.18	36 (4%) 35 32	17, 36, 67, 81	0
All	All	1502/1572 (95%)	0.16	69 (4%) 37 34	17, 36, 66, 85	0

All (69) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	705	ALA	4.4
1	A	395	PRO	4.1
1	B	287	ASN	4.0
1	A	398	ALA	3.8
1	A	608	GLY	3.7
1	A	290	SER	3.7
1	B	304	GLY	3.6
1	A	396	PRO	3.5
1	B	688	LEU	3.5
1	B	709	ALA	3.3
1	B	723	GLN	3.3
1	B	689	ARG	3.3
1	A	636	THR	3.3
1	B	605	THR	3.2
1	A	289	SER	3.2
1	B	190	SER	3.1
1	A	641	TRP	3.1
1	B	719	PRO	3.1
1	A	392	GLY	3.0
1	A	699	VAL	3.0
1	A	688	LEU	2.9
1	B	403	TYR	2.9
1	A	454	PHE	2.9
1	A	698	ASN	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	398	ALA	2.9
1	B	706	ALA	2.9
1	A	266	PHE	2.8
1	B	606	ILE	2.8
1	A	634	LEU	2.8
1	A	714	GLN	2.8
1	A	720	LEU	2.7
1	B	291	PHE	2.7
1	B	407	SER	2.7
1	B	399	SER	2.6
1	B	641	TRP	2.6
1	B	722	TYR	2.6
1	B	288	PHE	2.6
1	B	728	ILE	2.6
1	A	726	GLY	2.5
1	A	397	HIS	2.5
1	B	317	ILE	2.5
1	B	290	SER	2.4
1	A	633	GLY	2.4
1	B	454	PHE	2.4
1	B	776	MET	2.4
1	A	455	LEU	2.4
1	A	366	HIS	2.3
1	B	699	VAL	2.3
1	A	724	ASN	2.3
1	B	402	GLY	2.3
1	A	693	SER	2.3
1	A	394	VAL	2.3
1	A	190	SER	2.3
1	A	401	GLY	2.2
1	B	315	ASP	2.2
1	B	712	GLU	2.2
1	A	692	LEU	2.2
1	B	695	TYR	2.2
1	B	692	LEU	2.2
1	B	691	PRO	2.1
1	A	690	ARG	2.1
1	A	695	TYR	2.1
1	A	715	LYS	2.1
1	B	625	ASP	2.1
1	B	258	HIS	2.1
1	B	100	GLY	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	302	GLY	2.0
1	A	130	MET	2.0
1	A	689	ARG	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.