



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:13 AM UTC

PDB ID : 3C3L / pdb_00003c3l
Title : X-ray crystal structure of the N4 mini-vRNAP P2 promoter complex
Authors : Gleghorn, M.L.; Murakami, K.S.
Deposited on : 2008-01-28
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

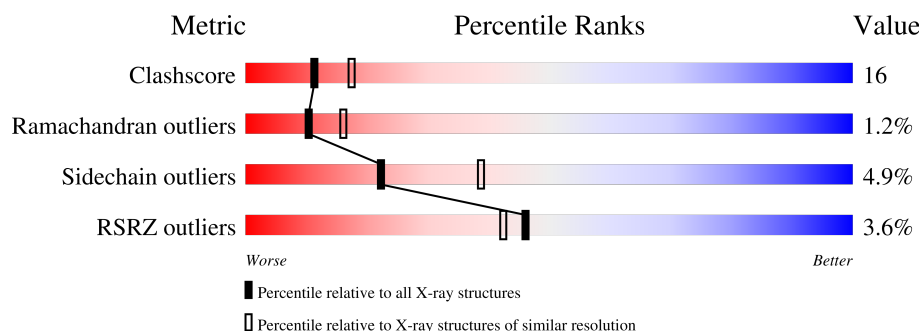
1 Overall quality at a glance

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))
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	C	33	3% 27% 27% . 42%
1	D	33	39% 15% . 42%
2	A	1117	4% 67% 26% 5% .
2	B	1117	3% 67% 26% . .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 17839 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 DNA chain called P2 Promoter DNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	19	Total	C	N	O	P	0	0	0
			390	186	78	108	18			
1	D	19	Total	C	N	O	P	0	0	0
			390	186	78	108	18			

- Molecule 2 is a protein called Virion RNA polymerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	1089	Total	C	N	O	S	0	0	0
			8401	5274	1427	1659	41			
2	B	1085	Total	C	N	O	S	0	0	0
			8367	5254	1419	1653	41			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	MET	-	expression tag	UNP Q859P9
A	-10	GLY	-	expression tag	UNP Q859P9
A	-9	GLY	-	expression tag	UNP Q859P9
A	-8	SER	-	expression tag	UNP Q859P9
A	-7	HIS	-	expression tag	UNP Q859P9
A	-6	HIS	-	expression tag	UNP Q859P9
A	-5	HIS	-	expression tag	UNP Q859P9
A	-4	HIS	-	expression tag	UNP Q859P9
A	-3	HIS	-	expression tag	UNP Q859P9
A	-2	HIS	-	expression tag	UNP Q859P9
A	-1	ARG	-	expression tag	UNP Q859P9
A	0	SER	-	expression tag	UNP Q859P9
B	-11	MET	-	expression tag	UNP Q859P9
B	-10	GLY	-	expression tag	UNP Q859P9
B	-9	GLY	-	expression tag	UNP Q859P9
B	-8	SER	-	expression tag	UNP Q859P9
B	-7	HIS	-	expression tag	UNP Q859P9

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-6	HIS	-	expression tag	UNP Q859P9
B	-5	HIS	-	expression tag	UNP Q859P9
B	-4	HIS	-	expression tag	UNP Q859P9
B	-3	HIS	-	expression tag	UNP Q859P9
B	-2	HIS	-	expression tag	UNP Q859P9
B	-1	ARG	-	expression tag	UNP Q859P9
B	0	SER	-	expression tag	UNP Q859P9

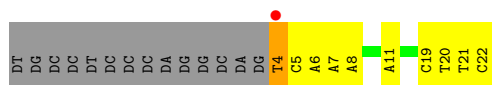
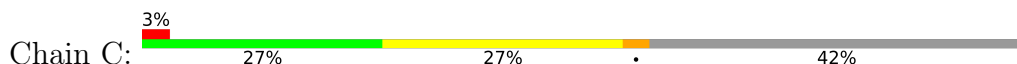
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	C	5	Total O 5 5	0	0
3	D	13	Total O 13 13	0	0
3	A	135	Total O 135 135	0	0
3	B	138	Total O 138 138	0	0

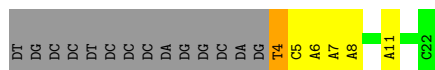
3 Residue-property plots [i](#)

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.

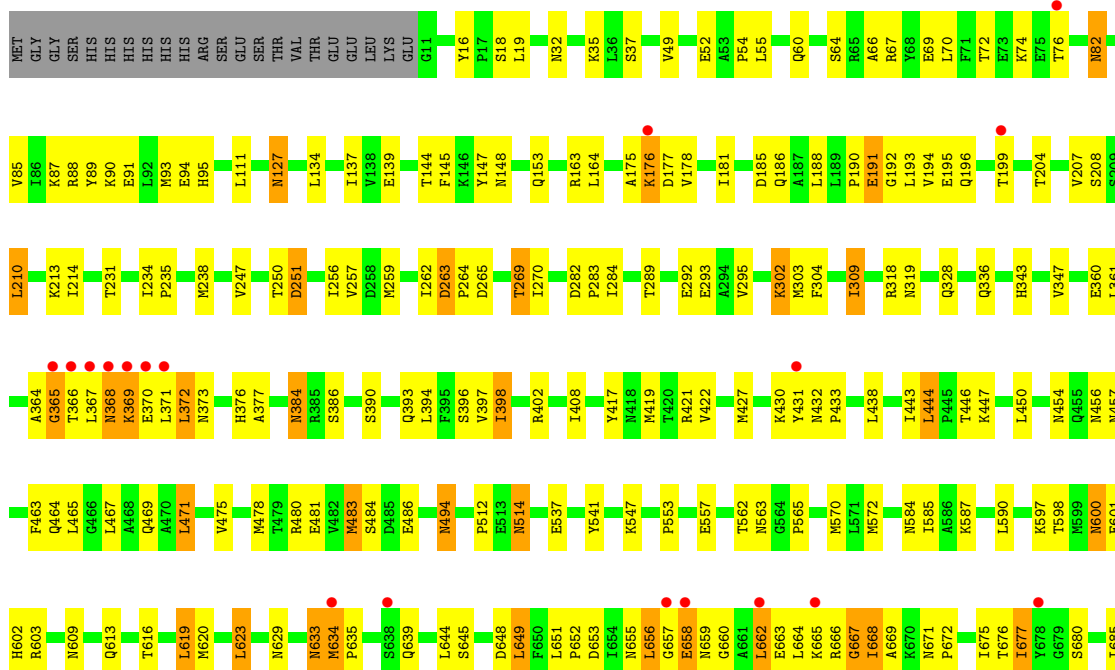
- Molecule 1: P2 Promoter DNA

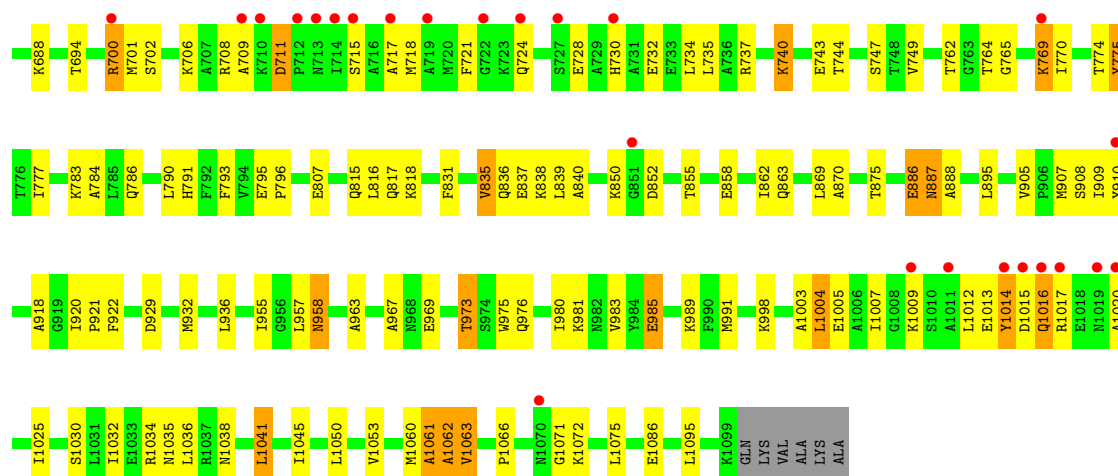


- Molecule 1: P2 Promoter DNA

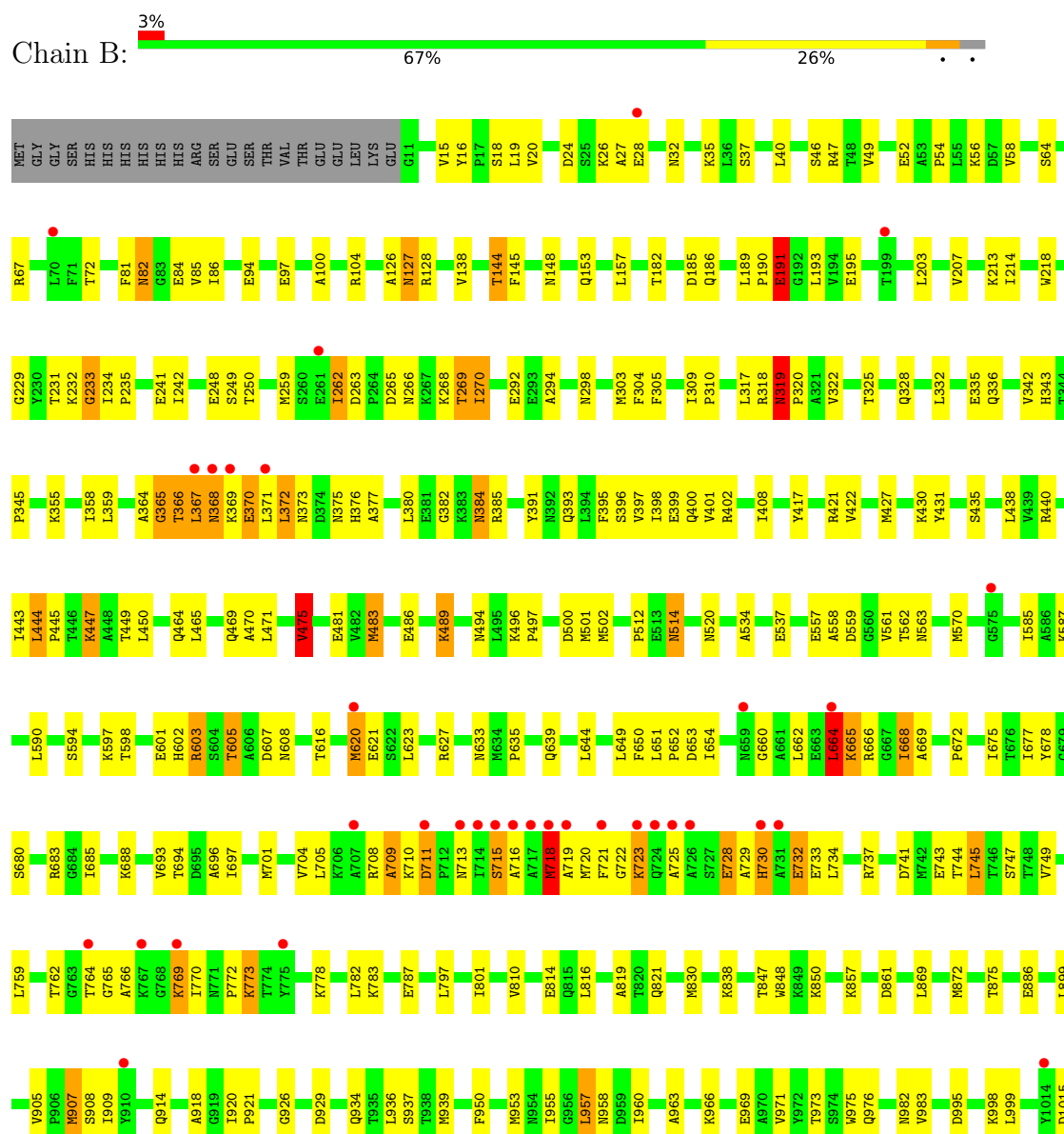


- Molecule 2: Virion RNA polymerase





• Molecule 2: Virion RNA polymerase





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	82.34Å 111.20Å 276.95Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.40 30.00 – 2.41	Depositor EDS
% Data completeness (in resolution range)	90.3 (30.00-2.40) 91.0 (30.00-2.41)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.59 (at 2.42Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.215 , 0.246 0.232 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	23.9	Xtriage
Anisotropy	0.456	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 32.7	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	0.92	EDS
Total number of atoms	17839	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.52% 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 [i](#)

5.1 Standard geometry [i](#)

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	C	0.28	0/439	0.68	1/676 (0.1%)
1	D	0.28	0/439	0.70	1/676 (0.1%)
2	A	0.43	0/8530	0.92	23/11539 (0.2%)
2	B	0.43	0/8496	0.95	36/11495 (0.3%)
All	All	0.42	0/17904	0.92	61/24386 (0.3%)

There are no bond length outliers.

All (61) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	660	GLY	N-CA-C	-10.90	99.73	115.64
2	B	558	ALA	N-CA-C	-9.45	95.54	109.15
2	B	148	ASN	N-CA-C	-8.54	97.04	109.59
2	B	475	VAL	N-CA-C	8.24	120.01	110.62
2	B	262	ILE	N-CA-C	-7.38	104.66	111.67
2	B	1061	ALA	N-CA-C	7.32	120.43	110.55
2	A	309	ILE	N-CA-C	7.28	115.79	109.02
2	A	251	ASP	N-CA-C	-7.24	103.91	112.89
2	A	148	ASN	N-CA-C	-7.12	98.35	109.25
2	B	732	GLU	N-CA-C	-7.06	105.29	114.04
2	B	396	SER	N-CA-C	-6.97	103.76	111.36
2	A	709	ALA	N-CA-C	-6.93	104.30	112.89
2	B	718	MET	N-CA-C	-6.89	104.07	113.30
2	A	1061	ALA	N-CA-C	6.70	118.65	110.41
2	A	309	ILE	CA-C-N	6.61	124.48	119.66
2	A	309	ILE	C-N-CA	6.61	124.48	119.66
2	B	1071	GLY	N-CA-C	-6.44	103.35	112.37
2	B	976	GLN	N-CA-C	-6.43	105.18	113.16
2	B	709	ALA	N-CA-C	-6.29	105.67	113.15
2	B	559	ASP	N-CA-C	6.25	119.13	109.07
2	B	957	LEU	N-CA-C	6.18	119.92	112.38
2	A	369	LYS	N-CA-C	-6.11	101.22	110.70
2	A	656	LEU	N-CA-C	-6.09	99.35	109.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	18	SER	N-CA-C	6.08	120.70	113.16
2	A	572	MET	N-CA-C	6.02	120.23	112.41
2	A	270	ILE	N-CA-C	6.01	116.58	108.17
2	A	295	VAL	N-CA-C	5.96	116.13	110.53
2	A	269	THR	N-CA-C	-5.95	98.70	108.41
2	B	319	ASN	CA-C-N	5.94	127.27	119.84
2	B	319	ASN	C-N-CA	5.94	127.27	119.84
2	B	605	THR	N-CA-C	5.80	121.24	114.04
2	B	728	GLU	N-CA-C	-5.79	105.98	113.16
2	A	396	SER	N-CA-C	-5.73	105.11	111.36
2	B	270	ILE	N-CA-C	5.70	116.09	108.11
2	A	247	VAL	N-CA-C	-5.66	105.33	110.82
1	D	4	DT	O5'-C5'-C4'	5.66	119.28	110.80
2	A	676	THR	N-CA-C	-5.63	105.90	112.89
2	B	232	LYS	N-CA-C	-5.62	106.10	113.12
2	B	298	ASN	CA-C-N	5.60	125.60	119.89
2	B	298	ASN	C-N-CA	5.60	125.60	119.89
2	A	835	VAL	N-CA-C	-5.53	104.98	111.00
2	B	770	ILE	N-CA-C	5.50	116.68	109.21
2	B	971	VAL	N-CA-C	-5.45	105.19	110.42
2	A	976	GLN	N-CA-C	-5.40	106.46	113.16
2	A	361	LEU	N-CA-C	5.38	116.95	111.14
2	A	888	ALA	N-CA-C	-5.38	106.77	113.38
2	B	745	LEU	N-CA-C	5.37	118.05	111.82
2	A	1063	VAL	N-CA-C	5.30	116.08	110.72
2	B	269	THR	N-CA-C	-5.29	99.78	108.41
2	B	1065	ALA	CA-C-N	5.24	125.14	119.85
2	B	1065	ALA	C-N-CA	5.24	125.14	119.85
2	B	367	LEU	N-CA-C	-5.18	106.96	113.28
2	B	730	HIS	N-CA-C	-5.17	106.92	113.18
2	A	667	GLY	N-CA-C	5.16	118.88	112.64
2	A	875	THR	N-CA-C	-5.14	107.68	114.31
2	B	218	TRP	N-CA-C	-5.09	106.17	112.38
2	B	233	GLY	N-CA-C	5.09	118.41	112.50
2	B	494	ASN	N-CA-C	5.04	116.77	111.28
2	B	435	SER	N-CA-C	5.04	119.55	113.41
1	C	4	DT	O5'-C5'-C4'	5.02	118.33	110.80
2	B	1063	VAL	N-CA-C	5.01	117.35	111.09

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	C	390	0	214	12	0
1	D	390	0	214	11	0
2	A	8401	0	8429	280	0
2	B	8367	0	8392	274	0
3	A	135	0	0	0	0
3	B	138	0	0	2	0
3	C	5	0	0	0	0
3	D	13	0	0	1	0
All	All	17839	0	17249	563	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 16.

All (563) 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)
2:A:469:GLN:HE22	2:A:557:GLU:H	1.01	1.00
2:A:887:ASN:H	2:A:887:ASN:HD22	1.13	0.95
2:A:144:THR:HG22	2:A:145:PHE:H	1.32	0.95
2:B:469:GLN:HE22	2:B:557:GLU:H	0.99	0.93
2:A:336:GLN:HE21	2:A:417:TYR:H	1.16	0.92
2:B:1072:LYS:HA	2:B:1072:LYS:HE2	1.52	0.91
2:B:364:ALA:H	2:B:384:ASN:HD21	1.18	0.89
2:A:1072:LYS:HE2	2:A:1072:LYS:HA	1.55	0.88
2:B:336:GLN:HE21	2:B:417:TYR:H	1.21	0.85
2:A:790:LEU:O	2:A:795:GLU:HG2	1.76	0.85
2:B:369:LYS:HE3	2:B:371:LEU:HB3	1.58	0.85
2:B:722:GLY:C	2:B:723:LYS:HZ3	1.83	0.85
2:B:718:MET:HE1	2:B:728:GLU:HG2	1.57	0.84
2:B:620:MET:HG3	2:B:664:LEU:HD23	1.59	0.84
2:A:360:GLU:HA	2:A:365:GLY:HA3	1.59	0.83
2:B:364:ALA:H	2:B:384:ASN:ND2	1.76	0.83
2:B:1059:GLN:HG3	2:B:1060:MET:HE2	1.62	0.81
2:A:259:MET:HE2	2:A:259:MET:HA	1.64	0.80
2:A:665:LYS:HG2	2:A:667:GLY:H	1.46	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:127:ASN:H	2:B:127:ASN:HD22	1.32	0.78
2:A:257:VAL:HG12	2:A:259:MET:HE3	1.67	0.77
1:C:4:DT:H5'	2:A:680:SER:HA	1.66	0.77
2:B:372:LEU:HD13	2:B:377:ALA:HB2	1.66	0.77
1:C:5:DC:H2''	1:C:6:DA:H5'	1.67	0.76
2:A:920:ILE:HB	2:A:921:PRO:HD3	1.68	0.76
2:B:701:MET:HE1	2:B:720:MET:HE2	1.66	0.76
2:A:863:GLN:HA	2:A:863:GLN:HE21	1.51	0.76
2:A:895:LEU:HD13	2:A:907:MET:HE3	1.66	0.76
2:B:598:THR:OG1	2:B:601:GLU:HG3	1.86	0.76
2:B:64:SER:OG	2:B:67:ARG:HG2	1.86	0.75
2:B:918:ALA:O	2:B:921:PRO:HD2	1.86	0.75
2:B:309:ILE:HD12	2:B:309:ILE:O	1.87	0.74
1:C:19:DC:H2''	1:C:20:DT:H5'	1.69	0.74
1:D:5:DC:H5'	2:B:921:PRO:HG2	1.68	0.74
2:A:289:THR:O	2:A:293:GLU:HG3	1.88	0.74
2:A:190:PRO:HG2	2:A:193:LEU:HB2	1.69	0.74
2:A:369:LYS:C	2:A:371:LEU:H	1.95	0.74
2:A:998:LYS:HE2	2:A:998:LYS:HA	1.70	0.73
2:A:639:GLN:HE22	2:A:744:THR:HB	1.54	0.73
2:B:725:ALA:HA	2:B:730:HIS:HD2	1.52	0.73
2:B:1078:MET:HE2	2:B:1082:GLN:HB3	1.72	0.72
2:B:816:LEU:CD1	2:B:983:VAL:HG21	2.20	0.72
2:B:627:ARG:HH21	2:B:644:LEU:HD12	1.55	0.71
1:D:4:DT:H2''	1:D:5:DC:OP2	1.89	0.71
2:B:373:ASN:HD22	2:B:376:HIS:H	1.35	0.71
2:A:887:ASN:H	2:A:887:ASN:ND2	1.88	0.70
2:B:747:SER:HB3	2:B:765:GLY:HA3	1.72	0.70
2:B:597:LYS:NZ	2:B:602:HIS:HD2	1.90	0.70
2:B:127:ASN:HD22	2:B:127:ASN:N	1.89	0.70
2:B:367:LEU:HD21	2:B:380:LEU:HB2	1.72	0.70
2:A:887:ASN:HD22	2:A:887:ASN:N	1.84	0.69
2:B:496:LYS:HB3	2:B:497:PRO:HD3	1.74	0.69
2:B:47:ARG:HD2	2:B:294:ALA:O	1.92	0.69
2:B:570:MET:HE1	2:B:1050:LEU:HD23	1.73	0.68
2:B:721:PHE:O	2:B:723:LYS:HE2	1.94	0.68
2:B:1094:GLU:O	2:B:1095:LEU:HD23	1.93	0.68
2:B:303:MET:HE1	2:B:397:VAL:HG13	1.75	0.68
2:A:1016:GLN:O	2:A:1020:ALA:HB2	1.94	0.68
1:D:5:DC:H2''	1:D:6:DA:H5'	1.75	0.68
2:B:54:PRO:HG2	2:B:153:GLN:HB2	1.74	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:88:ARG:HG3	2:A:283:PRO:HB2	1.76	0.67
2:B:322:VAL:HG22	2:B:872:MET:HE1	1.76	0.67
2:A:343:HIS:HE1	2:A:537:GLU:OE2	1.79	0.66
2:A:454:ASN:HD22	2:A:457:ASN:ND2	1.92	0.66
2:B:203:LEU:O	2:B:207:VAL:HG12	1.95	0.66
2:B:469:GLN:HE22	2:B:557:GLU:N	1.83	0.66
2:B:449:THR:H	2:B:958:ASN:HD21	1.43	0.66
2:A:213:LYS:HE3	2:A:292:GLU:OE1	1.96	0.66
2:A:700:ARG:NH1	2:A:724:GLN:NE2	2.44	0.66
2:B:266:ASN:OD1	2:B:268:LYS:HB2	1.95	0.65
2:A:675:ILE:HD11	2:A:685:ILE:HG12	1.76	0.65
2:A:87:LYS:HE2	2:A:91:GLU:OE1	1.96	0.65
2:B:469:GLN:NE2	2:B:557:GLU:H	1.83	0.65
2:A:645:SER:HA	2:A:656:LEU:HD11	1.78	0.65
2:A:190:PRO:HD2	2:A:193:LEU:HD22	1.79	0.65
2:B:401:VAL:HG12	2:B:408:ILE:HD12	1.78	0.65
2:B:46:SER:O	2:B:49:VAL:HG12	1.95	0.65
2:B:704:VAL:HG23	2:B:719:ALA:HB1	1.79	0.65
2:A:178:VAL:HG21	2:A:194:VAL:HA	1.78	0.64
2:B:501:MET:HE3	2:B:502:MET:HE3	1.78	0.64
2:A:336:GLN:HE21	2:A:417:TYR:N	1.94	0.64
2:A:633:ASN:OD1	2:A:635:PRO:HG2	1.98	0.64
2:A:454:ASN:HB3	2:A:457:ASN:ND2	2.12	0.64
2:B:710:LYS:O	2:B:711:ASP:HB2	1.96	0.64
2:A:402:ARG:HA	2:A:408:ILE:HG22	1.80	0.64
2:A:639:GLN:NE2	2:A:744:THR:HB	2.12	0.64
2:A:991:MET:HE2	2:A:1030:SER:HA	1.80	0.63
2:B:263:ASP:OD1	2:B:265:ASP:HB2	1.97	0.63
2:B:616:THR:CG2	2:B:664:LEU:HB2	2.28	0.63
2:A:469:GLN:HE22	2:A:557:GLU:N	1.86	0.63
2:A:700:ARG:HH12	2:A:724:GLN:NE2	1.96	0.63
2:B:213:LYS:HE3	2:B:292:GLU:OE2	1.96	0.63
2:B:398:ILE:C	2:B:398:ILE:HD12	2.24	0.63
2:B:1078:MET:CE	2:B:1082:GLN:HB3	2.29	0.63
2:B:190:PRO:HG2	2:B:193:LEU:HB2	1.80	0.62
2:B:332:LEU:O	2:B:336:GLN:HG3	1.98	0.62
2:A:791:HIS:HA	2:A:795:GLU:HG3	1.80	0.62
2:A:454:ASN:HD21	2:A:456:ASN:HB2	1.63	0.62
2:A:494:ASN:H	2:A:494:ASN:HD22	1.46	0.62
2:B:64:SER:HA	2:B:86:ILE:HD13	1.81	0.61
2:B:723:LYS:HZ3	2:B:723:LYS:N	1.96	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:127:ASN:N	2:A:127:ASN:HD22	1.97	0.61
2:A:176:LYS:HE3	2:A:176:LYS:HA	1.81	0.61
2:A:364:ALA:H	2:A:384:ASN:ND2	1.99	0.61
2:A:791:HIS:HA	2:A:795:GLU:CG	2.31	0.61
2:B:317:LEU:HG	2:B:318:ARG:NH1	2.16	0.61
2:B:464:GLN:HB3	2:B:483:MET:HE1	1.83	0.61
2:B:369:LYS:C	2:B:371:LEU:H	2.08	0.60
2:A:66:ALA:O	2:A:70:LEU:HD23	2.02	0.60
2:B:918:ALA:C	2:B:921:PRO:HD2	2.27	0.60
2:A:127:ASN:HD22	2:A:127:ASN:H	1.49	0.60
2:A:18:SER:HB2	2:A:139:GLU:OE2	2.02	0.60
2:A:514:ASN:HD22	2:A:514:ASN:H	1.49	0.59
2:A:1005:GLU:O	2:A:1009:LYS:HG3	2.01	0.59
2:B:907:MET:HE2	2:B:909:ILE:HD11	1.84	0.59
2:B:358:ILE:HD12	2:B:391:TYR:CE1	2.38	0.59
2:B:54:PRO:HG2	2:B:153:GLN:CB	2.32	0.59
2:B:398:ILE:HD12	2:B:399:GLU:N	2.16	0.59
2:B:715:SER:HB3	2:B:718:MET:CB	2.32	0.59
2:A:570:MET:HG2	2:A:975:TRP:CD2	2.38	0.59
2:A:1075:LEU:HD21	2:A:1086:GLU:HG2	1.85	0.59
2:B:995:ASP:CG	2:B:998:LYS:HG2	2.28	0.59
2:B:304:PHE:CG	2:B:310:PRO:HG3	2.37	0.58
2:B:810:VAL:O	2:B:814:GLU:HG3	2.02	0.58
2:B:701:MET:HE1	2:B:720:MET:CE	2.33	0.58
2:B:678:TYR:O	2:B:921:PRO:HG3	2.03	0.58
2:B:769:LYS:HB3	2:B:769:LYS:NZ	2.18	0.58
2:A:369:LYS:O	2:A:371:LEU:N	2.30	0.58
2:A:494:ASN:HD22	2:A:494:ASN:N	2.00	0.58
2:A:207:VAL:HG11	2:A:905:VAL:HG21	1.86	0.58
2:A:658:GLU:N	2:A:658:GLU:OE1	2.37	0.58
1:C:8:DA:H4'	2:A:886:GLU:O	2.04	0.58
1:D:6:DA:H5'	1:D:6:DA:H8	1.69	0.58
2:A:584:ASN:HA	2:A:587:LYS:HD2	1.86	0.58
2:A:855:THR:OG1	2:A:858:GLU:HG3	2.03	0.58
2:B:15:VAL:HG21	2:B:40:LEU:HD21	1.86	0.58
2:A:393:GLN:HG2	2:A:431:TYR:HB2	1.85	0.57
2:A:653:ASP:OD2	2:A:665:LYS:HD3	2.05	0.57
2:B:191:GLU:HG2	2:B:375:ASN:HB3	1.86	0.57
2:B:343:HIS:CD2	2:B:345:PRO:HD2	2.40	0.57
2:B:367:LEU:O	2:B:369:LYS:N	2.37	0.57
2:B:908:SER:C	2:B:909:ILE:HD12	2.28	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:815:GLN:HE21	2:A:1035:ASN:HB2	1.68	0.57
2:B:633:ASN:OD1	2:B:635:PRO:HG2	2.04	0.57
2:B:654:ILE:HD11	2:B:668:ILE:HD13	1.85	0.57
2:B:725:ALA:HB1	2:B:730:HIS:HB3	1.87	0.57
2:A:369:LYS:C	2:A:371:LEU:N	2.63	0.57
2:B:848:TRP:CH2	2:B:850:LYS:HA	2.40	0.57
2:A:563:ASN:HD21	2:A:929:ASP:HB3	1.69	0.57
2:A:980:ILE:HG23	2:A:1036:LEU:HD12	1.86	0.57
2:B:262:ILE:HD12	2:B:262:ILE:N	2.19	0.57
2:B:708:ARG:C	2:B:710:LYS:H	2.11	0.57
1:C:5:DC:H5'	2:A:921:PRO:HG2	1.87	0.57
2:A:870:ALA:HB2	2:A:989:LYS:HD3	1.87	0.57
2:A:795:GLU:HB2	2:A:796:PRO:CD	2.36	0.56
2:A:816:LEU:CD1	2:A:983:VAL:HG21	2.35	0.56
2:A:1004:LEU:HD13	2:A:1025:ILE:HD13	1.85	0.56
2:B:24:ASP:HB3	2:B:27:ALA:HB2	1.87	0.56
2:A:600:ASN:ND2	2:A:600:ASN:H	2.02	0.56
2:B:372:LEU:CD1	2:B:377:ALA:HB2	2.35	0.56
2:B:464:GLN:CB	2:B:483:MET:HE1	2.36	0.56
2:B:1059:GLN:HG3	2:B:1060:MET:CE	2.34	0.56
2:B:603:ARG:NH1	2:B:608:ASN:OD1	2.38	0.56
2:A:54:PRO:HG2	2:A:153:GLN:HB2	1.87	0.56
2:A:886:GLU:HG3	2:A:910:TYR:CE2	2.41	0.56
2:A:82:ASN:HD21	2:A:85:VAL:HG23	1.70	0.56
2:A:858:GLU:O	2:A:862:ILE:HG13	2.05	0.56
2:A:1012:LEU:HD22	2:A:1016:GLN:NE2	2.21	0.56
2:B:234:ILE:HB	2:B:235:PRO:HD3	1.88	0.56
2:B:830:MET:HA	2:B:830:MET:HE2	1.87	0.56
2:A:144:THR:HG22	2:A:145:PHE:N	2.12	0.55
2:B:704:VAL:HG13	2:B:705:LEU:H	1.71	0.55
2:A:465:LEU:HD11	2:A:475:VAL:CG1	2.35	0.55
2:A:444:LEU:N	2:A:444:LEU:HD22	2.22	0.55
2:A:613:GLN:HG2	2:A:666:ARG:HB3	1.87	0.55
2:A:762:THR:HB	2:A:764:THR:HG22	1.89	0.55
2:A:700:ARG:HG3	2:A:700:ARG:HH11	1.70	0.55
2:A:372:LEU:HD12	2:A:372:LEU:O	2.07	0.55
2:B:1072:LYS:HE2	2:B:1072:LYS:CA	2.31	0.55
1:C:11:DA:H5'	2:A:269:THR:O	2.07	0.55
2:A:454:ASN:HB3	2:A:457:ASN:HD21	1.71	0.55
2:B:704:VAL:HG23	2:B:719:ALA:CB	2.36	0.55
2:B:303:MET:HG3	2:B:400:GLN:CD	2.33	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:920:ILE:HB	2:B:921:PRO:HD3	1.90	0.54
2:B:639:GLN:NE2	2:B:744:THR:HG22	2.23	0.54
2:B:450:LEU:HD11	2:B:957:LEU:HD12	1.89	0.54
2:B:444:LEU:N	2:B:444:LEU:HD22	2.22	0.54
2:A:93:MET:HE2	2:A:93:MET:HA	1.89	0.54
2:A:740:LYS:O	2:A:743:GLU:HB3	2.07	0.54
2:A:936:LEU:HD13	2:A:967:ALA:HA	1.90	0.54
2:A:908:SER:O	2:A:909:ILE:HD12	2.07	0.54
2:A:234:ILE:HB	2:A:235:PRO:HD3	1.90	0.54
2:A:367:LEU:O	2:A:369:LYS:N	2.41	0.53
2:B:100:ALA:O	2:B:104:ARG:HG3	2.08	0.53
2:A:1032:ILE:O	2:A:1036:LEU:HD23	2.09	0.53
2:A:1061:ALA:O	2:A:1062:ALA:CB	2.56	0.53
2:B:639:GLN:NE2	2:B:744:THR:CG2	2.71	0.53
2:A:981:LYS:O	2:A:985:GLU:HG2	2.08	0.53
2:B:355:LYS:O	2:B:359:LEU:HG	2.09	0.53
2:A:422:VAL:HG12	2:A:922:PHE:HA	1.89	0.53
2:A:454:ASN:ND2	2:A:456:ASN:HB2	2.23	0.53
2:A:958:ASN:HD22	2:A:958:ASN:H	1.54	0.53
2:A:336:GLN:NE2	2:A:417:TYR:H	1.96	0.53
2:A:464:GLN:CB	2:A:483:MET:HE1	2.38	0.53
2:B:830:MET:HE3	2:B:999:LEU:HD23	1.89	0.53
2:B:1094:GLU:O	2:B:1094:GLU:HG3	2.08	0.53
1:D:4:DT:H5'	2:B:680:SER:HA	1.89	0.53
2:B:82:ASN:C	2:B:82:ASN:HD22	2.16	0.53
2:B:1086:GLU:OE1	2:B:1089:LYS:HE3	2.09	0.53
2:A:629:ASN:N	2:A:629:ASN:HD22	2.06	0.53
2:B:512:PRO:HB2	2:B:514:ASN:ND2	2.24	0.53
2:A:204:THR:O	2:A:208:SER:HB2	2.09	0.53
2:A:372:LEU:CD1	2:A:377:ALA:HB2	2.39	0.53
2:B:1094:GLU:C	2:B:1095:LEU:HD23	2.33	0.53
2:A:655:ASN:HB2	2:A:663:GLU:CG	2.39	0.52
2:B:597:LYS:HZ1	2:B:602:HIS:HD2	1.56	0.52
2:B:654:ILE:CD1	2:B:668:ILE:HD13	2.39	0.52
2:A:616:THR:O	2:A:620:MET:HG3	2.10	0.52
2:B:20:VAL:HG23	2:B:138:VAL:O	2.08	0.52
2:B:367:LEU:O	2:B:368:ASN:C	2.52	0.52
2:A:955:ILE:HD13	2:A:963:ALA:HB3	1.90	0.52
2:B:191:GLU:HB2	2:B:375:ASN:HD22	1.74	0.52
2:B:729:ALA:O	2:B:733:GLU:HG3	2.10	0.52
2:B:710:LYS:O	2:B:710:LYS:HG2	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:373:ASN:HD21	2:B:375:ASN:HB2	1.75	0.52
2:B:728:GLU:O	2:B:732:GLU:HB2	2.09	0.52
2:A:262:ILE:HG22	2:A:262:ILE:O	2.09	0.52
2:A:648:ASP:OD2	2:A:655:ASN:HA	2.10	0.52
2:B:597:LYS:HE2	2:B:602:HIS:HB2	1.92	0.52
2:B:653:ASP:O	2:B:665:LYS:HB2	2.09	0.52
2:A:343:HIS:CE1	2:A:537:GLU:OE2	2.61	0.52
2:A:597:LYS:NZ	2:A:602:HIS:HD2	2.07	0.52
2:A:669:ALA:HA	2:A:672:PRO:HG2	1.91	0.52
2:A:72:THR:O	2:A:74:LYS:HG3	2.10	0.51
1:D:6:DA:H5'	1:D:6:DA:C8	2.45	0.51
2:B:635:PRO:HB2	2:B:759:LEU:HD12	1.92	0.51
2:A:718:MET:HE1	2:A:728:GLU:HA	1.91	0.51
2:A:793:PHE:O	2:A:796:PRO:HG2	2.10	0.51
2:B:395:PHE:HA	2:B:398:ILE:HG13	1.93	0.51
2:A:37:SER:HB3	2:A:231:THR:HG22	1.93	0.51
2:B:229:GLY:O	2:B:233:GLY:HA3	2.11	0.51
2:B:250:THR:HG22	2:B:250:THR:O	2.10	0.51
2:A:210:LEU:HD22	2:A:214:ILE:HD11	1.92	0.51
2:A:465:LEU:HD11	2:A:475:VAL:HG11	1.92	0.51
2:A:715:SER:HB3	2:A:718:MET:CB	2.40	0.51
2:B:317:LEU:HG	2:B:318:ARG:HH11	1.75	0.51
2:B:367:LEU:HD21	2:B:380:LEU:CB	2.39	0.51
3:D:31:HOH:O	2:B:421:ARG:HG3	2.10	0.51
2:A:863:GLN:HA	2:A:863:GLN:NE2	2.22	0.51
2:B:97:GLU:HG3	3:B:1215:HOH:O	2.11	0.51
2:A:95:HIS:HA	2:B:248:GLU:O	2.11	0.50
2:A:185:ASP:OD2	2:A:188:LEU:HG	2.11	0.50
2:A:262:ILE:O	2:A:263:ASP:HB2	2.11	0.50
2:B:723:LYS:HZ2	2:B:723:LYS:HA	1.75	0.50
2:A:191:GLU:O	2:A:193:LEU:N	2.44	0.50
2:A:634:MET:N	2:A:635:PRO:HD2	2.26	0.50
2:B:393:GLN:HG2	2:B:431:TYR:HB2	1.93	0.50
2:A:887:ASN:ND2	2:A:887:ASN:N	2.54	0.50
1:D:8:DA:H4'	2:B:886:GLU:O	2.11	0.50
2:A:257:VAL:CG1	2:A:259:MET:HE3	2.39	0.50
2:B:382:GLY:HA2	2:B:385:ARG:HG2	1.92	0.50
2:A:303:MET:HE1	2:A:397:VAL:HG13	1.93	0.50
2:A:619:LEU:O	2:A:623:LEU:HB2	2.12	0.50
2:A:653:ASP:HB2	2:A:668:ILE:HG23	1.93	0.50
2:B:1053:VAL:HG11	2:B:1075:LEU:HD12	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:649:LEU:HD13	2:B:737:ARG:NH2	2.27	0.50
2:B:465:LEU:HD11	2:B:475:VAL:HG13	1.94	0.49
2:A:783:LYS:O	2:A:786:GLN:HB3	2.12	0.49
2:A:1061:ALA:O	2:A:1062:ALA:HB2	2.12	0.49
2:B:1048:LYS:HE3	2:B:1048:LYS:HA	1.94	0.49
2:B:81:PHE:CZ	2:B:86:ILE:HG12	2.47	0.49
2:A:88:ARG:HD3	2:A:282:ASP:OD1	2.12	0.49
2:A:717:ALA:HB2	2:A:735:LEU:CD2	2.42	0.49
2:A:1013:GLU:O	2:A:1015:ASP:N	2.46	0.49
2:B:82:ASN:ND2	2:B:85:VAL:H	2.09	0.49
2:B:765:GLY:O	2:B:766:ALA:C	2.55	0.49
2:A:835:VAL:O	2:A:839:LEU:HG	2.13	0.49
2:A:1014:TYR:HA	2:A:1017:ARG:NE	2.27	0.49
2:B:309:ILE:HD12	2:B:309:ILE:C	2.37	0.49
2:B:723:LYS:N	2:B:723:LYS:NZ	2.61	0.49
2:A:134:LEU:HD13	2:A:147:TYR:OH	2.12	0.49
2:B:342:VAL:HG21	2:B:408:ILE:HD11	1.94	0.49
2:B:587:LYS:NZ	2:B:607:ASP:OD2	2.39	0.49
2:A:715:SER:HB3	2:A:718:MET:HB2	1.95	0.49
2:A:1053:VAL:HG11	2:A:1075:LEU:HD12	1.95	0.49
2:B:486:GLU:HG2	2:B:489:LYS:NZ	2.28	0.49
2:B:82:ASN:HD21	2:B:85:VAL:HG23	1.78	0.49
2:B:675:ILE:HD11	2:B:685:ILE:HG12	1.94	0.49
1:D:11:DA:H5'	2:B:269:THR:O	2.13	0.48
2:B:186:GLN:O	2:B:189:LEU:HG	2.13	0.48
2:B:358:ILE:HD12	2:B:391:TYR:HE1	1.74	0.48
2:A:16:TYR:O	2:A:35:LYS:HE2	2.12	0.48
2:B:501:MET:HE3	2:B:502:MET:CE	2.42	0.48
2:B:694:THR:HG21	2:B:782:LEU:HD21	1.96	0.48
2:A:250:THR:O	2:A:250:THR:HG22	2.14	0.48
2:A:430:LYS:HE3	2:A:431:TYR:CE2	2.48	0.48
2:A:1012:LEU:HD11	2:A:1025:ILE:HG22	1.95	0.48
2:A:1041:LEU:O	2:A:1045:ILE:HG12	2.13	0.48
2:B:16:TYR:O	2:B:35:LYS:CE	2.61	0.48
2:B:207:VAL:HG11	2:B:905:VAL:CG2	2.43	0.48
2:B:769:LYS:HB3	2:B:769:LYS:HZ2	1.79	0.48
2:B:886:GLU:HG2	2:B:908:SER:HB3	1.96	0.48
2:A:747:SER:HB3	2:A:765:GLY:HA3	1.94	0.48
2:A:932:MET:HE1	2:A:1060:MET:HE2	1.95	0.48
2:B:127:ASN:N	2:B:127:ASN:ND2	2.61	0.48
2:A:590:LEU:HD21	2:A:1050:LEU:HD21	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:481:GLU:O	2:A:484:SER:HB3	2.13	0.48
2:B:563:ASN:HD21	2:B:929:ASP:HB3	1.78	0.48
2:B:664:LEU:O	2:B:665:LYS:CB	2.62	0.48
2:B:816:LEU:HD13	2:B:983:VAL:HG21	1.96	0.48
2:A:562:THR:O	2:A:565:PRO:HD2	2.13	0.48
2:A:478:MET:O	2:A:600:ASN:HB3	2.14	0.48
2:B:37:SER:HB3	2:B:231:THR:HG22	1.95	0.48
2:B:325:THR:OG1	2:B:328:GLN:HG3	2.14	0.48
2:A:190:PRO:HG3	2:A:262:ILE:HG21	1.95	0.47
2:B:336:GLN:HE21	2:B:417:TYR:N	2.02	0.47
2:A:191:GLU:C	2:A:193:LEU:H	2.22	0.47
2:A:629:ASN:N	2:A:629:ASN:ND2	2.63	0.47
2:B:715:SER:HB3	2:B:718:MET:HB2	1.97	0.47
2:A:467:LEU:O	2:A:471:LEU:HD22	2.15	0.47
2:A:587:LYS:HG2	2:A:609:ASN:O	2.14	0.47
2:B:127:ASN:H	2:B:127:ASN:ND2	2.07	0.47
2:B:1093:GLU:C	2:B:1095:LEU:H	2.22	0.47
2:A:256:ILE:N	2:A:256:ILE:HD12	2.29	0.47
2:A:257:VAL:HG12	2:A:259:MET:CE	2.41	0.47
2:A:164:LEU:HD22	2:A:284:ILE:HG21	1.95	0.47
2:A:367:LEU:N	2:A:367:LEU:HD12	2.29	0.47
2:B:182:THR:HA	2:B:270:ILE:CD1	2.45	0.47
2:B:1090:LEU:O	2:B:1094:GLU:HB2	2.14	0.47
2:A:671:ASN:N	2:A:672:PRO:HD2	2.28	0.47
2:B:20:VAL:O	2:B:32:ASN:HB2	2.15	0.47
2:B:126:ALA:C	2:B:128:ARG:H	2.22	0.47
2:B:821:GLN:HE22	2:B:914:GLN:NE2	2.12	0.47
2:A:364:ALA:H	2:A:384:ASN:HD21	1.61	0.47
2:A:446:THR:O	2:A:447:LYS:HB2	2.14	0.47
2:A:969:GLU:O	2:A:973:THR:HG23	2.15	0.47
2:A:1003:ALA:O	2:A:1007:ILE:HG13	2.15	0.47
2:A:1072:LYS:HE2	2:A:1072:LYS:CA	2.35	0.47
2:B:214:ILE:HD11	2:B:242:ILE:HD12	1.95	0.47
2:B:373:ASN:ND2	2:B:375:ASN:HB2	2.30	0.47
2:B:598:THR:HG1	2:B:601:GLU:HG3	1.76	0.47
2:B:650:PHE:HB3	2:B:696:ALA:CB	2.44	0.47
2:A:347:VAL:HG11	2:A:398:ILE:HD13	1.96	0.47
2:A:665:LYS:HG2	2:A:666:ARG:N	2.29	0.47
2:B:371:LEU:HG	2:B:371:LEU:O	2.15	0.47
1:D:7:DA:C5'	2:B:421:ARG:HE	2.27	0.47
2:A:82:ASN:HD22	2:A:82:ASN:C	2.21	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:190:PRO:HG3	2:A:262:ILE:CG2	2.44	0.47
2:A:600:ASN:H	2:A:600:ASN:HD22	1.63	0.47
2:A:769:LYS:HD3	2:A:770:ILE:N	2.29	0.47
2:B:259:MET:HA	2:B:262:ILE:HD13	1.96	0.47
2:B:969:GLU:HG3	2:B:1067:TYR:CE1	2.50	0.47
2:A:657:GLY:O	2:A:659:ASN:N	2.48	0.47
2:A:55:LEU:HB2	2:A:153:GLN:OE1	2.15	0.46
2:A:443:ILE:C	2:A:444:LEU:HD22	2.41	0.46
2:A:465:LEU:HD22	2:A:480:ARG:NE	2.30	0.46
2:B:304:PHE:CD2	2:B:310:PRO:HG3	2.50	0.46
2:B:501:MET:CE	2:B:502:MET:HE3	2.43	0.46
2:B:620:MET:CG	2:B:664:LEU:HD23	2.40	0.46
2:B:715:SER:HB3	2:B:718:MET:HB3	1.96	0.46
2:B:995:ASP:OD2	2:B:998:LYS:HG2	2.15	0.46
2:B:741:ASP:O	2:B:745:LEU:HG	2.16	0.46
2:A:89:TYR:O	2:A:93:MET:HG2	2.16	0.46
2:A:514:ASN:H	2:A:514:ASN:ND2	2.13	0.46
2:B:19:LEU:HB3	2:B:32:ASN:ND2	2.30	0.46
2:B:207:VAL:HG11	2:B:905:VAL:HG21	1.97	0.46
2:B:664:LEU:O	2:B:665:LYS:HB2	2.13	0.46
2:B:708:ARG:C	2:B:710:LYS:N	2.73	0.46
2:B:929:ASP:HB2	2:B:950:PHE:O	2.16	0.46
2:A:386:SER:O	2:A:390:SER:HB2	2.15	0.46
2:A:769:LYS:HD3	2:A:769:LYS:C	2.40	0.46
2:B:444:LEU:N	2:B:444:LEU:CD2	2.79	0.46
2:B:514:ASN:C	2:B:514:ASN:HD22	2.23	0.46
2:B:705:LEU:HD11	2:B:773:LYS:CA	2.45	0.46
2:B:1079:THR:O	2:B:1083:GLN:HG3	2.15	0.46
2:B:669:ALA:HA	2:B:672:PRO:HG2	1.97	0.46
2:A:69:GLU:OE2	2:A:76:THR:HA	2.16	0.46
2:A:438:LEU:HD23	2:A:438:LEU:C	2.40	0.46
2:B:443:ILE:C	2:B:444:LEU:HD22	2.41	0.46
1:D:7:DA:N6	2:B:318:ARG:HH21	2.14	0.45
2:B:704:VAL:HG13	2:B:705:LEU:N	2.30	0.45
2:A:402:ARG:HA	2:A:408:ILE:CG2	2.45	0.45
2:B:185:ASP:OD2	2:B:185:ASP:C	2.59	0.45
2:A:817:GLN:NE2	2:A:818:LYS:N	2.64	0.45
2:B:570:MET:HG2	2:B:975:TRP:CD2	2.51	0.45
2:B:594:SER:HB3	2:B:597:LYS:HB2	1.98	0.45
2:A:432:ASN:HB2	2:A:433:PRO:HD2	1.99	0.45
2:A:598:THR:HG22	2:A:1066:PRO:HD3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:440:ARG:O	2:B:444:LEU:HD13	2.17	0.45
2:B:749:VAL:HG13	2:B:762:THR:HG21	1.98	0.45
2:A:82:ASN:H	2:A:82:ASN:ND2	2.14	0.45
2:A:1053:VAL:O	2:A:1071:GLY:HA3	2.16	0.45
2:B:249:SER:O	2:B:250:THR:HB	2.16	0.45
2:B:371:LEU:HD21	2:B:709:ALA:CB	2.47	0.45
2:A:55:LEU:HG	2:A:153:GLN:HB3	1.98	0.45
2:A:469:GLN:NE2	2:A:557:GLU:H	1.87	0.45
2:A:815:GLN:HE21	2:A:1035:ASN:CB	2.30	0.45
2:B:603:ARG:HH11	2:B:603:ARG:HB3	1.80	0.45
2:B:417:TYR:OH	2:B:427:MET:HE3	2.17	0.45
2:B:195:GLU:OE2	2:B:385:ARG:HD3	2.17	0.45
1:C:19:DC:H1'	1:C:20:DT:H5''	1.99	0.45
2:A:421:ARG:HG3	2:A:421:ARG:HH11	1.82	0.45
2:A:708:ARG:HA	2:A:711:ASP:O	2.17	0.45
2:B:343:HIS:HE1	2:B:537:GLU:OE2	2.00	0.45
2:B:598:THR:HG22	2:B:1066:PRO:HD3	1.99	0.45
2:B:797:LEU:O	2:B:801:ILE:HG13	2.17	0.45
2:B:939:MET:HE2	2:B:966:LYS:HD2	1.98	0.45
2:A:918:ALA:O	2:A:921:PRO:HD2	2.17	0.44
2:B:857:LYS:HE3	2:B:861:ASP:OD2	2.17	0.44
2:A:60:GLN:OE1	2:A:60:GLN:HA	2.16	0.44
2:A:831:PHE:O	2:A:835:VAL:HG23	2.17	0.44
2:B:715:SER:O	2:B:716:ALA:HB3	2.16	0.44
2:A:367:LEU:O	2:A:368:ASN:C	2.60	0.44
2:A:541:TYR:CE1	2:A:547:LYS:HD3	2.52	0.44
2:A:367:LEU:C	2:A:369:LYS:N	2.75	0.44
2:B:328:GLN:HG2	2:B:934:GLN:OE1	2.18	0.44
2:B:72:THR:HG22	2:B:294:ALA:HA	2.00	0.44
2:B:355:LYS:HE2	2:B:355:LYS:HB3	1.75	0.44
2:B:368:ASN:HD22	2:B:368:ASN:N	2.16	0.44
2:B:570:MET:HG2	2:B:975:TRP:CG	2.53	0.44
2:B:955:ILE:HD13	2:B:963:ALA:HB3	1.98	0.44
1:C:4:DT:H2''	1:C:5:DC:OP2	2.17	0.44
2:A:657:GLY:O	2:A:660:GLY:N	2.46	0.44
2:B:561:VAL:O	2:B:562:THR:C	2.60	0.44
2:A:908:SER:C	2:A:909:ILE:HD12	2.43	0.43
2:A:343:HIS:CG	2:A:553:PRO:HG3	2.52	0.43
2:A:394:LEU:O	2:A:398:ILE:HG23	2.18	0.43
2:A:464:GLN:HB2	2:A:483:MET:HE1	2.00	0.43
2:A:598:THR:OG1	2:A:601:GLU:HG3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:645:SER:HA	2:A:656:LEU:CD1	2.46	0.43
2:A:649:LEU:HD13	2:A:737:ARG:NH2	2.32	0.43
2:A:1016:GLN:H	2:A:1016:GLN:HG3	1.59	0.43
2:B:723:LYS:NZ	2:B:723:LYS:CA	2.80	0.43
2:A:480:ARG:HH21	2:A:1063:VAL:HG13	1.83	0.43
2:A:1012:LEU:CD1	2:A:1025:ILE:HG22	2.49	0.43
2:A:95:HIS:NE2	2:A:251:ASP:OD2	2.42	0.43
2:A:895:LEU:CD1	2:A:907:MET:HE3	2.42	0.43
2:A:19:LEU:HB3	2:A:32:ASN:ND2	2.34	0.43
2:A:175:ALA:HB1	2:A:186:GLN:HG3	2.01	0.43
2:A:238:MET:HE3	2:A:238:MET:HA	2.01	0.43
2:B:185:ASP:OD2	2:B:186:GLN:N	2.52	0.43
2:B:1075:LEU:HD21	2:B:1086:GLU:HG2	2.01	0.43
2:A:64:SER:OG	2:A:67:ARG:HG3	2.19	0.43
2:A:384:ASN:HD22	2:A:384:ASN:HA	1.60	0.43
1:D:7:DA:C5	2:B:318:ARG:NE	2.87	0.43
2:A:514:ASN:HD22	2:A:514:ASN:N	2.09	0.43
2:A:694:THR:HG22	2:A:777:ILE:HD12	2.01	0.43
2:A:815:GLN:NE2	2:A:1035:ASN:HB2	2.33	0.43
2:B:319:ASN:HD22	2:B:319:ASN:HA	1.49	0.43
2:B:366:THR:O	2:B:366:THR:HG22	2.19	0.43
2:A:465:LEU:HD11	2:A:475:VAL:HG13	2.01	0.43
2:B:1061:ALA:O	2:B:1062:ALA:HB2	2.19	0.43
2:A:717:ALA:HB2	2:A:735:LEU:HD22	1.99	0.42
2:A:762:THR:CB	2:A:764:THR:HG22	2.47	0.42
2:A:795:GLU:HB2	2:A:796:PRO:HD3	2.01	0.42
2:B:369:LYS:HE3	2:B:371:LEU:HD23	2.01	0.42
2:B:376:HIS:O	2:B:380:LEU:HG	2.18	0.42
2:B:470:ALA:HB3	2:B:534:ALA:HB2	2.01	0.42
2:A:163:ARG:HD3	2:A:163:ARG:C	2.45	0.42
2:A:464:GLN:HB3	2:A:483:MET:HE1	2.00	0.42
2:A:565:PRO:HA	2:A:677:ILE:HG12	2.01	0.42
2:A:700:ARG:NH1	2:A:724:GLN:HE21	2.15	0.42
2:B:364:ALA:O	2:B:365:GLY:O	2.37	0.42
2:B:422:VAL:O	2:B:926:GLY:HA2	2.19	0.42
2:B:621:GLU:HA	2:B:621:GLU:OE1	2.19	0.42
2:B:650:PHE:HB3	2:B:696:ALA:HB1	2.00	0.42
2:A:850:LYS:HD2	2:A:850:LYS:O	2.19	0.42
2:A:1053:VAL:C	2:A:1071:GLY:HA3	2.44	0.42
2:B:335:GLU:OE2	2:B:937:SER:HB3	2.19	0.42
2:B:514:ASN:ND2	2:B:514:ASN:C	2.76	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:869:LEU:HD21	3:B:1201:HOH:O	2.19	0.42
2:A:774:THR:O	2:A:775:TYR:C	2.62	0.42
2:B:481:GLU:H	2:B:481:GLU:CD	2.27	0.42
2:A:144:THR:CG2	2:A:145:PHE:H	2.13	0.42
2:A:791:HIS:HA	2:A:795:GLU:HG2	2.01	0.42
2:B:82:ASN:C	2:B:82:ASN:ND2	2.78	0.42
2:B:438:LEU:C	2:B:438:LEU:HD23	2.44	0.42
2:B:447:LYS:HE2	2:B:447:LYS:HB3	1.80	0.42
2:B:721:PHE:HB3	2:B:734:LEU:CD1	2.49	0.42
2:A:54:PRO:HG2	2:A:153:GLN:CB	2.49	0.42
2:A:749:VAL:HG11	2:A:784:ALA:HA	2.02	0.42
2:B:58:VAL:HG21	2:B:157:LEU:HD13	2.02	0.42
2:B:319:ASN:N	2:B:320:PRO:HD3	2.33	0.42
2:A:16:TYR:O	2:A:35:LYS:CE	2.68	0.42
2:A:134:LEU:O	2:A:137:ILE:HG12	2.20	0.42
2:A:177:ASP:O	2:A:181:ILE:HG13	2.20	0.42
2:A:837:GLU:O	2:A:840:ALA:HB3	2.19	0.42
2:A:932:MET:CE	2:A:1060:MET:SD	3.07	0.42
2:A:444:LEU:N	2:A:444:LEU:CD2	2.81	0.42
2:A:651:LEU:HA	2:A:652:PRO:HD3	1.87	0.42
2:B:783:LYS:O	2:B:787:GLU:HG3	2.19	0.42
1:C:5:DC:C2'	1:C:6:DA:H5'	2.45	0.42
2:A:648:ASP:HB2	2:A:656:LEU:HG	2.01	0.42
2:A:662:LEU:HD23	2:A:662:LEU:O	2.20	0.42
2:B:144:THR:HB	2:B:145:PHE:H	1.52	0.42
2:B:651:LEU:HA	2:B:652:PRO:HD3	1.88	0.42
2:B:1015:ASP:OD1	2:B:1016:GLN:HG3	2.19	0.42
2:A:195:GLU:O	2:A:199:THR:HG22	2.19	0.42
2:A:512:PRO:HB2	2:A:514:ASN:ND2	2.35	0.42
2:A:730:HIS:C	2:A:732:GLU:N	2.78	0.42
2:B:303:MET:HE3	2:B:305:PHE:CZ	2.55	0.42
2:B:693:VAL:O	2:B:697:ILE:HG13	2.20	0.42
2:B:705:LEU:HD11	2:B:773:LYS:HA	2.01	0.42
2:A:655:ASN:HB2	2:A:663:GLU:HG3	2.02	0.41
2:B:705:LEU:HG	2:B:772:PRO:HB2	2.01	0.41
2:A:111:LEU:HD13	2:A:144:THR:HG22	2.01	0.41
2:A:196:GLN:O	2:A:199:THR:HG22	2.20	0.41
2:A:259:MET:HE1	2:A:262:ILE:HD12	2.02	0.41
2:A:585:ILE:HD12	2:A:585:ILE:HA	1.95	0.41
2:B:620:MET:HE3	2:B:620:MET:HB3	1.87	0.41
2:B:711:ASP:C	2:B:713:ASN:H	2.29	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:90:LYS:O	2:A:94:GLU:HG3	2.21	0.41
2:A:700:ARG:HH11	2:A:700:ARG:CG	2.33	0.41
2:A:815:GLN:NE2	2:A:1035:ASN:CB	2.83	0.41
2:B:496:LYS:HE2	2:B:500:ASP:OD1	2.20	0.41
2:A:372:LEU:HB2	2:A:702:SER:OG	2.21	0.41
2:B:26:LYS:HG2	2:B:847:THR:HG21	2.02	0.41
2:B:398:ILE:HD13	2:B:402:ARG:CZ	2.50	0.41
2:B:730:HIS:O	2:B:734:LEU:HG	2.20	0.41
1:C:7:DA:OP1	2:A:318:ARG:NH1	2.54	0.41
2:A:263:ASP:HA	2:A:264:PRO:HD2	1.84	0.41
2:A:450:LEU:HD11	2:A:957:LEU:HD12	2.02	0.41
2:A:463:PHE:HA	2:A:957:LEU:HD13	2.01	0.41
2:A:494:ASN:N	2:A:494:ASN:ND2	2.66	0.41
2:A:616:THR:CG2	2:A:664:LEU:HB2	2.51	0.41
2:A:644:LEU:HB3	2:A:656:LEU:HD21	2.03	0.41
2:A:706:LYS:O	2:A:706:LYS:HG3	2.19	0.41
2:B:486:GLU:HG2	2:B:489:LYS:HZ1	1.84	0.41
2:B:773:LYS:O	2:B:773:LYS:HG3	2.19	0.41
2:B:367:LEU:C	2:B:369:LYS:N	2.79	0.41
2:B:778:LYS:HA	2:B:778:LYS:HD3	1.87	0.41
2:A:88:ARG:CD	2:A:283:PRO:HD2	2.51	0.41
2:A:454:ASN:HD22	2:A:457:ASN:HD21	1.66	0.41
2:A:701:MET:HE3	2:A:775:TYR:CD2	2.55	0.41
2:B:249:SER:O	2:B:250:THR:CB	2.69	0.41
2:B:1088:ASN:O	2:B:1091:PHE:HB3	2.21	0.41
1:C:4:DT:O4	2:A:688:LYS:NZ	2.29	0.41
1:C:21:DT:C4	1:C:22:DC:N4	2.88	0.41
2:A:82:ASN:ND2	2:A:85:VAL:HG23	2.35	0.41
2:A:620:MET:HG2	2:A:664:LEU:HD12	2.02	0.41
2:A:721:PHE:HB3	2:A:734:LEU:HD12	2.03	0.41
2:A:932:MET:HE1	2:A:1060:MET:CE	2.50	0.41
2:B:875:THR:HG22	2:B:982:ASN:ND2	2.36	0.41
2:B:939:MET:HE1	2:B:969:GLU:HB3	2.01	0.41
2:B:1075:LEU:HD22	2:B:1078:MET:SD	2.61	0.41
2:A:127:ASN:H	2:A:127:ASN:ND2	2.17	0.41
2:B:797:LEU:O	2:B:797:LEU:HD12	2.21	0.41
2:B:936:LEU:HD21	2:B:953:MET:CE	2.51	0.41
2:B:241:GLU:CD	2:B:899:LEU:HG	2.46	0.40
2:A:302:LYS:HD2	2:A:304:PHE:CE1	2.56	0.40
2:A:373:ASN:HD22	2:A:376:HIS:H	1.69	0.40
2:A:134:LEU:HD23	2:A:134:LEU:HA	1.94	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:126:ALA:C	2:B:128:ARG:N	2.80	0.40
2:B:369:LYS:C	2:B:371:LEU:N	2.72	0.40
2:B:585:ILE:HG12	2:B:590:LEU:HD23	2.03	0.40
2:B:720:MET:SD	2:B:721:PHE:CE1	3.14	0.40
2:A:417:TYR:OH	2:A:427:MET:HE3	2.21	0.40
2:A:644:LEU:HD23	2:A:644:LEU:HA	1.94	0.40
2:B:819:ALA:HB2	2:B:1036:LEU:HD21	2.03	0.40
2:A:328:GLN:HB3	2:A:419:MET:HE3	2.03	0.40
2:A:918:ALA:C	2:A:921:PRO:HD2	2.47	0.40
2:B:886:GLU:HA	2:B:909:ILE:O	2.22	0.40
2:B:960:ILE:HB	2:B:1063:VAL:HG21	2.04	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	
2	A	1087/1117 (97%)	1024 (94%)	50 (5%)	13 (1%)	10	16
2	B	1083/1117 (97%)	1026 (95%)	43 (4%)	14 (1%)	9	14
All	All	2170/2234 (97%)	2050 (94%)	93 (4%)	27 (1%)	10	16

All (27) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	191	GLU
2	A	658	GLU
2	A	1014	TYR
2	A	1062	ALA
2	B	191	GLU
2	B	365	GLY
2	B	368	ASN

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Mol	Chain	Res	Type
2	B	664	LEU
2	B	665	LYS
2	B	711	ASP
2	B	1062	ALA
2	A	192	GLY
2	A	365	GLY
2	A	368	ASN
2	A	370	GLU
2	A	633	ASN
2	B	366	THR
2	B	764	THR
2	A	263	ASP
2	B	715	SER
2	A	775	TYR
2	B	666	ARG
2	B	1094	GLU
2	A	366	THR
2	B	370	GLU
2	A	711	ASP
2	B	445	PRO

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	
2	A	910/934 (97%)	863 (95%)	47 (5%)	21	36
2	B	907/934 (97%)	865 (95%)	42 (5%)	24	41
All	All	1817/1868 (97%)	1728 (95%)	89 (5%)	22	39

All (89) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	49	VAL
2	A	52	GLU
2	A	82	ASN

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Mol	Chain	Res	Type
2	A	127	ASN
2	A	176	LYS
2	A	210	LEU
2	A	265	ASP
2	A	302	LYS
2	A	309	ILE
2	A	319	ASN
2	A	372	LEU
2	A	384	ASN
2	A	398	ILE
2	A	444	LEU
2	A	471	LEU
2	A	483	MET
2	A	486	GLU
2	A	494	ASN
2	A	514	ASN
2	A	600	ASN
2	A	603	ARG
2	A	619	LEU
2	A	623	LEU
2	A	634	MET
2	A	649	LEU
2	A	662	LEU
2	A	668	ILE
2	A	677	ILE
2	A	700	ARG
2	A	740	LYS
2	A	769	LYS
2	A	807	GLU
2	A	836	GLN
2	A	838	LYS
2	A	852	ASP
2	A	869	LEU
2	A	886	GLU
2	A	887	ASN
2	A	958	ASN
2	A	973	THR
2	A	985	GLU
2	A	1004	LEU
2	A	1016	GLN
2	A	1034	ARG
2	A	1038	ASN

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Mol	Chain	Res	Type
2	A	1041	LEU
2	A	1095	LEU
2	B	28	GLU
2	B	52	GLU
2	B	56	LYS
2	B	82	ASN
2	B	84	GLU
2	B	94	GLU
2	B	127	ASN
2	B	144	THR
2	B	191	GLU
2	B	319	ASN
2	B	370	GLU
2	B	372	LEU
2	B	384	ASN
2	B	430	LYS
2	B	444	LEU
2	B	447	LYS
2	B	471	LEU
2	B	475	VAL
2	B	483	MET
2	B	489	LYS
2	B	514	ASN
2	B	520	ASN
2	B	603	ARG
2	B	605	THR
2	B	620	MET
2	B	623	LEU
2	B	662	LEU
2	B	664	LEU
2	B	668	ILE
2	B	677	ILE
2	B	683	ARG
2	B	688	LYS
2	B	718	MET
2	B	723	LYS
2	B	743	GLU
2	B	769	LYS
2	B	773	LYS
2	B	838	LYS
2	B	907	MET
2	B	973	THR

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Mol	Chain	Res	Type
2	B	1036	LEU
2	B	1041	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (103) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	82	ASN
2	A	127	ASN
2	A	150	GLN
2	A	186	GLN
2	A	196	GLN
2	A	212	GLN
2	A	255	ASN
2	A	266	ASN
2	A	298	ASN
2	A	316	GLN
2	A	319	ASN
2	A	324	ASN
2	A	336	GLN
2	A	343	HIS
2	A	348	GLN
2	A	368	ASN
2	A	373	ASN
2	A	376	HIS
2	A	384	ASN
2	A	393	GLN
2	A	414	HIS
2	A	454	ASN
2	A	455	GLN
2	A	456	ASN
2	A	457	ASN
2	A	464	GLN
2	A	469	GLN
2	A	494	ASN
2	A	506	ASN
2	A	514	ASN
2	A	563	ASN
2	A	584	ASN
2	A	600	ASN
2	A	602	HIS
2	A	629	ASN
2	A	639	GLN

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Mol	Chain	Res	Type
2	A	724	GLN
2	A	771	ASN
2	A	781	GLN
2	A	815	GLN
2	A	817	GLN
2	A	833	GLN
2	A	856	GLN
2	A	863	GLN
2	A	887	ASN
2	A	892	ASN
2	A	914	GLN
2	A	954	ASN
2	A	958	ASN
2	A	982	ASN
2	A	1016	GLN
2	A	1035	ASN
2	A	1059	GLN
2	A	1070	ASN
2	B	82	ASN
2	B	127	ASN
2	B	150	GLN
2	B	196	GLN
2	B	255	ASN
2	B	298	ASN
2	B	316	GLN
2	B	319	ASN
2	B	324	ASN
2	B	336	GLN
2	B	343	HIS
2	B	348	GLN
2	B	368	ASN
2	B	373	ASN
2	B	375	ASN
2	B	384	ASN
2	B	414	HIS
2	B	455	GLN
2	B	456	ASN
2	B	457	ASN
2	B	469	GLN
2	B	506	ASN
2	B	514	ASN
2	B	520	ASN

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Mol	Chain	Res	Type
2	B	563	ASN
2	B	602	HIS
2	B	613	GLN
2	B	629	ASN
2	B	637	GLN
2	B	639	GLN
2	B	655	ASN
2	B	724	GLN
2	B	730	HIS
2	B	771	ASN
2	B	815	GLN
2	B	817	GLN
2	B	833	GLN
2	B	878	GLN
2	B	892	ASN
2	B	893	GLN
2	B	914	GLN
2	B	954	ASN
2	B	958	ASN
2	B	982	ASN
2	B	1035	ASN
2	B	1038	ASN
2	B	1047	HIS
2	B	1059	GLN
2	B	1082	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	C	19/33 (57%)	0.40	1 (5%) 32 28	25, 31, 59, 62	0
1	D	19/33 (57%)	0.08	0 100 100	18, 28, 51, 59	0
2	A	1089/1117 (97%)	0.13	43 (3%) 43 39	8, 24, 50, 66	0
2	B	1085/1117 (97%)	0.08	36 (3%) 49 45	9, 22, 49, 67	0
All	All	2212/2300 (96%)	0.10	80 (3%) 46 42	8, 23, 50, 67	0

All (80) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	A	368	ASN	6.2
2	B	368	ASN	5.7
2	B	664	LEU	4.4
2	A	1019	ASN	4.2
2	B	724	GLN	4.2
2	B	369	LYS	4.1
2	B	659	ASN	3.7
2	A	657	GLY	3.6
2	A	365	GLY	3.6
2	B	726	ALA	3.5
2	B	719	ALA	3.4
2	A	665	LYS	3.1
1	C	4	DT	3.1
2	B	764	THR	3.1
2	A	1014	TYR	3.0
2	B	714	ILE	3.0
2	B	1070	ASN	2.9
2	B	371	LEU	2.9
2	A	1070	ASN	2.9
2	A	719	ALA	2.9
2	A	371	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
2	A	715	SER	2.8
2	B	717	ALA	2.8
2	A	712	PRO	2.8
2	A	369	LYS	2.8
2	A	851	GLY	2.8
2	A	199	THR	2.8
2	A	367	LEU	2.7
2	B	1095	LEU	2.7
2	A	713	ASN	2.6
2	A	658	GLU	2.6
2	B	716	ALA	2.6
2	A	730	HIS	2.6
2	A	714	ILE	2.5
2	B	730	HIS	2.5
2	B	199	THR	2.5
2	B	1014	TYR	2.4
2	A	634	MET	2.4
2	B	28	GLU	2.4
2	A	176	LYS	2.4
2	A	1020	ALA	2.4
2	B	725	ALA	2.4
2	A	710	LYS	2.4
2	A	662	LEU	2.4
2	B	713	ASN	2.4
2	B	70	LEU	2.4
2	A	1011	ALA	2.3
2	B	715	SER	2.3
2	A	370	GLU	2.3
2	A	709	ALA	2.3
2	B	620	MET	2.3
2	A	638	SER	2.2
2	B	367	LEU	2.2
2	A	76	THR	2.2
2	A	366	THR	2.2
2	B	775	TYR	2.2
2	A	678	TYR	2.2
2	A	910	TYR	2.2
2	A	727	SER	2.2
2	B	261	GLU	2.2
2	A	724	GLN	2.1
2	B	575	GLY	2.1
2	B	711	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
2	B	767	LYS	2.1
2	B	731	ALA	2.1
2	A	1015	ASP	2.1
2	A	1016	GLN	2.1
2	B	707	ALA	2.1
2	A	700	ARG	2.1
2	A	722	GLY	2.1
2	A	1017	ARG	2.1
2	A	1009	LYS	2.1
2	B	910	TYR	2.1
2	B	769	LYS	2.0
2	A	431	TYR	2.0
2	B	718	MET	2.0
2	B	721	PHE	2.0
2	A	717	ALA	2.0
2	A	769	LYS	2.0
2	B	723	LYS	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.