



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:15 AM UTC

PDB ID : 1PVP / pdb_00001pvp
Title : BASIS FOR A SWITCH IN SUBSTRATE SPECIFICITY: CRYSTAL STRUCTURE OF SELECTED VARIANT OF CRE SITE-SPECIFIC RECOMBINASE, ALSHG BOUND TO THE ENGINEERED RECOGNITION SITE LOXM7
Authors : Baldwin, E.P.; Martin, S.S.; Abel, J.; Gelato, K.A.; Kim, H.; Schultz, P.G.; Santoro, S.W.
Deposited on : 2003-06-28
Resolution : 2.35 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)	:	Engl & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

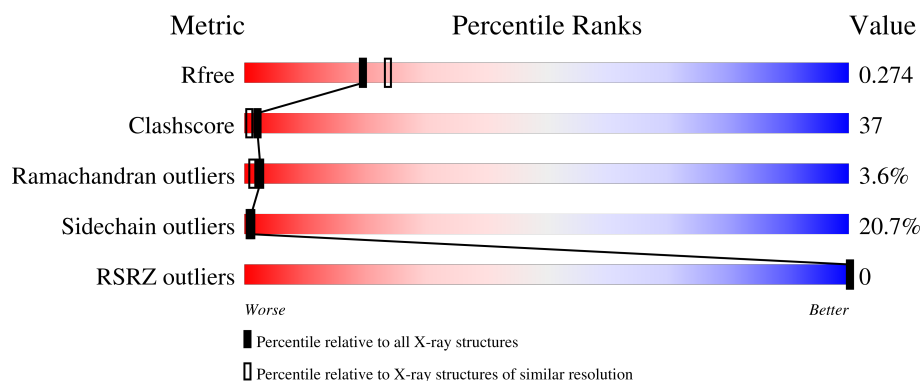
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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	34	32% 65% .
2	D	34	24% 76%
3	A	349	38% 38% 13% . 7%
3	B	349	34% 46% 10% . 9%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6738 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 34-MER.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	33	Total	C	N	O	P	0	0	1
			655	317	115	192	31			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	7	DC	DT	engineered mutation	GB M10145
C	8	DT	DC	engineered mutation	GB M10145
C	9	DA	DG	engineered mutation	GB M10145
C	26	DT	DC	engineered mutation	GB M10145
C	27	DA	DG	engineered mutation	GB M10145
C	28	DG	DA	engineered mutation	GB M10145

- Molecule 2 is a DNA chain called 34-MER.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	34	Total	C	N	O	P	0	4	0
			774	375	138	224	37			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	7	DC	DT	engineered mutation	GB M10494
D	8	DT	DC	engineered mutation	GB M10494
D	9	DA	DG	engineered mutation	GB M10494
D	26	DT	DC	engineered mutation	GB M10494
D	27	DA	DG	engineered mutation	GB M10494
D	28	DG	DA	engineered mutation	GB M10494

- Molecule 3 is a protein called Recombinase cre.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	323	Total 2546	C 1582	N 486	O 463	S 15	34	0	0
3	B	318	Total 2507	C 1560	N 480	O 452	S 15	27	0	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	MET	-	initiating methionine	UNP P06956
A	-4	HIS	-	expression tag	UNP P06956
A	-3	HIS	-	expression tag	UNP P06956
A	-2	HIS	-	expression tag	UNP P06956
A	-1	HIS	-	expression tag	UNP P06956
A	0	HIS	-	expression tag	UNP P06956
A	1	HIS	-	expression tag	UNP P06956
A	174	ALA	ILE	engineered mutation	UNP P06956
A	258	LEU	THR	engineered mutation	UNP P06956
A	259	SER	ARG	engineered mutation	UNP P06956
A	262	HIS	GLU	engineered mutation	UNP P06956
A	266	GLY	GLU	engineered mutation	UNP P06956
B	-5	MET	-	initiating methionine	UNP P06956
B	-4	HIS	-	expression tag	UNP P06956
B	-3	HIS	-	expression tag	UNP P06956
B	-2	HIS	-	expression tag	UNP P06956
B	-1	HIS	-	expression tag	UNP P06956
B	0	HIS	-	expression tag	UNP P06956
B	1	HIS	-	expression tag	UNP P06956
B	174	ALA	ILE	engineered mutation	UNP P06956
B	258	LEU	THR	engineered mutation	UNP P06956
B	259	SER	ARG	engineered mutation	UNP P06956
B	262	HIS	GLU	engineered mutation	UNP P06956
B	266	GLY	GLU	engineered mutation	UNP P06956

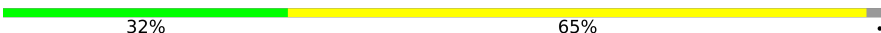
- Molecule 4 is water.

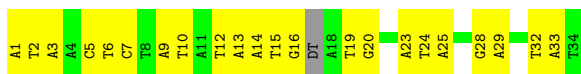
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	31	Total 31	O 31	0	0
4	D	31	Total 31	O 31	0	0
4	A	68	Total 68	O 68	0	0
4	B	126	Total 126	O 126	0	0

3 Residue-property plots

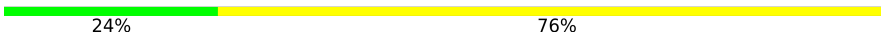
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

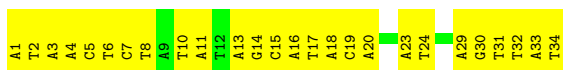
• Molecule 1: 34-MER

Chain C: 

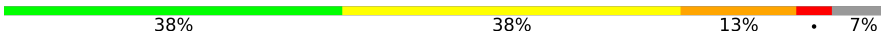


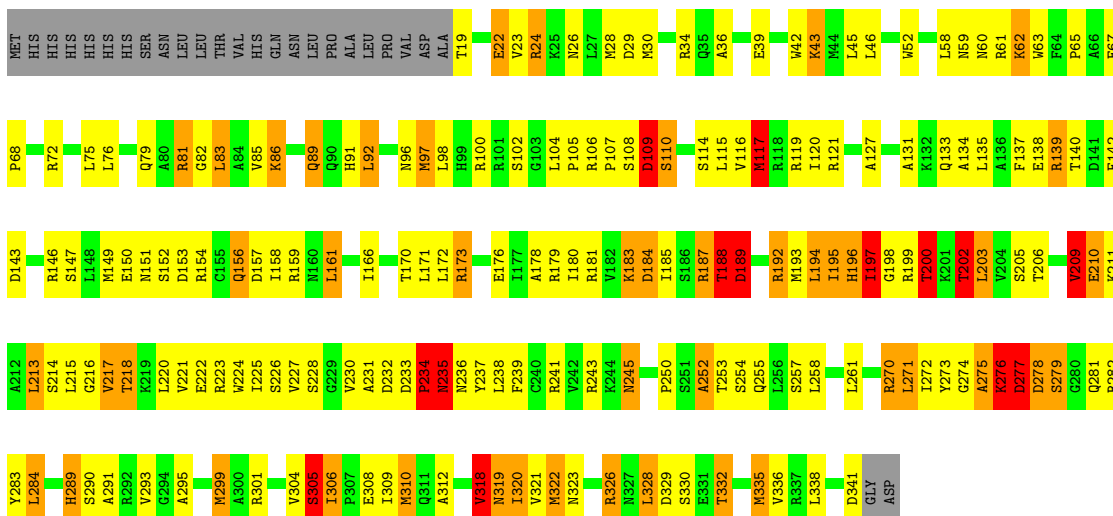
• Molecule 2: 34-MER

Chain D: 

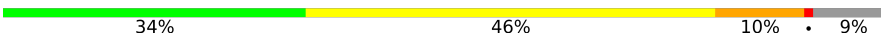


• Molecule 3: Recombinase cre

Chain A: 



• Molecule 3: Recombinase cre

Chain B: 

W286	R292	V217	Q144	E69	MET
S287	V293	T218	V145	E69	HIS
G288	G294	K219	R146	R72	HIS
H289	A295	L220	E150	D73	HIS
	A296	V221	E150	Y74	HIS
	R297	E222	R154	Y77	HIS
	D298	W224	C155	R81	SER
	M299	V230	Q156	R81	ASN
A300	A296	A231	D157	A84	LEU
R301	D298	D232	I158	V85	LEU
	M299	D233	R159	K86	THR
	R301	P234	H160	T87	VAL
		N235	L161	I88	HIS
		N236	I166	Q89	GLN
		Y237	A167	L92	ASN
				L92	LEU
				N96	PRO
				H99	ALA
				R100	LEU
				R101	PRO
				S102	VAL
				G103	ASP
				L104	ASP
				P105	ALA
				R106	T19
				I180	S20
				A252	D21
				V182	E22
				K183	K25
				D184	W26
				I185	L27
				S186	M28
				R187	D29
				T188	M30
				M193	F31
				L194	R32
				I195	D33
				H196	R34
				I197	H40
				G198	T41
				R199	W42
				T200	K43
				K201	K44
				T202	M44
				Y273	L45
				G274	L46
				A275	S47
				K276	V48
				D277	C49
				D278	R50
				S279	R50
				G280	N60
				Q281	R61
				R282	K62
				Y283	W63
				L284	F64
				A285	P65
					P68

4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	107.78Å 121.47Å 180.69Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	5.00 – 2.35 5.00 – 2.35	Depositor EDS
% Data completeness (in resolution range)	95.0 (5.00-2.35) 84.6 (5.00-2.35)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.78 (at 2.34Å)	Xtriage
Refinement program	TNT	Depositor
R, R_{free}	0.232 , 0.294 0.235 , 0.274	Depositor DCC
R_{free} test set	2180 reflections (4.65%)	wwPDB-VP
Wilson B-factor (Å ²)	47.6	Xtriage
Anisotropy	0.301	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 112.0	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	6738	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.73% 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	C	0.25	0/733	1.14	1/1129 (0.1%)
2	D	0.34	0/868	1.01	0/1337
3	A	0.50	0/2588	1.14	22/3490 (0.6%)
3	B	0.54	0/2548	1.15	19/3434 (0.6%)
All	All	0.47	0/6737	1.13	42/9390 (0.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
3	A	1	0

There are no bond length outliers.

All (42) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	322	MET	N-CA-C	11.71	124.05	111.28
3	A	202	THR	N-CA-C	9.96	132.01	110.80
3	A	235	ASN	N-CA-C	-9.88	100.91	113.16
3	A	326	ARG	N-CA-C	9.57	122.92	111.82
3	B	188	THR	N-CA-C	-8.98	97.56	110.59
3	A	127	ALA	N-CA-C	-8.46	101.64	114.16
3	B	279	SER	N-CA-C	8.35	121.31	111.71
3	A	318	VAL	N-CA-C	8.33	126.67	109.34
3	A	81	ARG	N-CA-C	-8.01	103.50	113.20
3	A	232	ASP	N-CA-C	7.90	122.02	112.38
3	A	332	THR	N-CA-C	7.74	121.65	111.75
3	A	188	THR	N-CA-C	7.46	119.91	109.31
3	B	298	ASP	N-CA-C	-7.32	102.48	111.33
3	B	320	ILE	N-CA-C	-6.91	104.03	110.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	203	LEU	N-CA-C	6.59	118.41	108.46
3	B	256	LEU	N-CA-C	-6.28	100.54	109.96
3	B	319	ASN	N-CA-C	6.12	121.26	113.55
3	B	127	ALA	N-CA-C	-6.06	104.31	113.89
3	B	170	THR	N-CA-C	5.99	118.77	111.82
3	A	195	ILE	N-CA-C	5.98	117.53	107.18
1	C	7	DC	P-O3'-C3'	5.98	129.17	120.20
3	A	234	PRO	N-CA-C	5.95	124.73	112.47
3	A	209	VAL	N-CA-C	5.87	121.55	109.34
3	A	277	ASP	N-CA-C	5.69	119.47	109.80
3	B	81	ARG	N-CA-C	-5.66	106.22	113.01
3	A	185	ILE	N-CA-C	5.58	115.92	108.11
3	B	131	ALA	N-CA-C	-5.45	101.58	109.59
3	A	173	ARG	NE-CZ-NH1	-5.44	116.06	121.50
3	B	126	ASP	N-CA-C	-5.42	105.97	112.59
3	B	28	MET	N-CA-C	-5.34	105.46	111.28
3	A	305	SER	CA-C-N	-5.33	112.27	122.13
3	A	305	SER	C-N-CA	-5.33	112.27	122.13
3	A	117	MET	N-CA-C	-5.28	105.42	111.07
3	A	200	THR	N-CA-C	5.25	117.98	108.69
3	A	131	ALA	N-CA-C	-5.23	102.12	109.96
3	B	276	LYS	N-CA-C	5.20	118.17	110.48
3	B	102	SER	N-CA-C	-5.18	106.81	113.23
3	A	243	ARG	N-CA-C	5.17	117.00	110.33
3	A	252	ALA	N-CA-C	-5.11	107.08	113.72
3	B	295	ALA	N-CA-C	-5.06	105.77	111.28
3	B	243	ARG	N-CA-C	5.05	117.04	110.53
3	B	264	ILE	N-CA-C	-5.05	105.47	110.62

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	202	THR	CA

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	655	0	368	28	0
2	D	774	0	434	62	0
3	A	2546	0	2566	205	0
3	B	2507	0	2533	177	0
4	A	68	0	0	13	0
4	B	126	0	0	6	0
4	C	31	0	0	1	0
4	D	31	0	0	3	0
All	All	6738	0	5901	448	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 37.

All (448) 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:D:33:DA:H2''	2:D:34:DT:H5''	1.30	1.11
2:D:15:DC:H2'	2:D:16[B]:DA:C8	1.88	1.07
3:B:306:ILE:HD13	3:B:322:MET:HE1	1.32	1.06
2:D:15:DC:C2'	2:D:16[B]:DA:C8	2.47	0.97
3:B:193:MET:HE2	3:B:213:LEU:HD12	1.43	0.96
3:B:193:MET:HE1	3:B:221:VAL:HG11	1.45	0.96
2:D:1:DA:N7	4:D:63:HOH:O	2.03	0.92
2:D:18[B]:DA:H2''	2:D:19[B]:DC:H5''	1.55	0.88
3:B:310:MET:SD	3:B:318:VAL:HG12	2.13	0.88
3:B:335:MET:HE3	3:B:335:MET:HA	1.56	0.88
1:C:19:DT:H2''	1:C:20:DG:C8	2.07	0.88
3:A:197:ILE:HG22	3:A:198:GLY:H	1.37	0.87
3:A:159:ARG:HB2	3:A:224:TRP:CZ3	2.09	0.87
1:C:16:DG:H5'	3:B:202:THR:HB	1.56	0.85
3:A:58:LEU:HD23	3:A:59:ASN:ND2	1.92	0.84
3:A:86:LYS:H	3:A:86:LYS:HD2	1.42	0.83
3:B:313:GLY:HA3	3:B:315:TRP:CZ3	2.12	0.83
2:D:2:DT:H2''	2:D:3:DA:C8	2.15	0.82
3:A:214:SER:O	3:A:218:THR:HB	1.81	0.81
1:C:15:DT:H2''	1:C:16:DG:C8	2.16	0.81
3:B:306:ILE:CD1	3:B:322:MET:HE1	2.09	0.81
3:B:121:ARG:HG2	3:B:121:ARG:HH11	1.45	0.80
3:A:158:ILE:CD1	3:A:224:TRP:HA	2.12	0.80
3:B:104:LEU:HB3	3:B:105:PRO:HD2	1.63	0.79
3:A:104:LEU:HB3	3:A:105:PRO:HD2	1.65	0.79
4:C:58:HOH:O	3:B:317:ASN:HB2	1.81	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:217:VAL:O	3:B:221:VAL:HG23	1.84	0.77
2:D:6:DT:H2''	2:D:7:DC:C5'	2.14	0.77
3:A:217:VAL:O	3:A:221:VAL:HG23	1.85	0.77
3:A:183:LYS:HG2	3:A:234:PRO:O	1.86	0.76
2:D:5:DC:H2'	2:D:6:DT:C6	2.21	0.76
3:B:146:ARG:O	3:B:150:GLU:HB2	1.84	0.76
3:A:245:ASN:N	3:A:245:ASN:HD22	1.81	0.75
3:B:145:VAL:HG22	3:B:272:ILE:HD11	1.68	0.75
3:A:139:ARG:HD2	3:A:143:ASP:OD2	1.86	0.75
1:C:12:DT:OP2	3:B:87:THR:HG21	1.86	0.74
3:A:188:THR:CG2	3:A:194:LEU:HD12	2.18	0.74
3:A:193:MET:HG3	3:A:218:THR:OG1	1.88	0.74
2:D:14:DG:H2''	2:D:15:DC:H6	1.52	0.73
3:A:310:MET:SD	3:A:318:VAL:HG22	2.29	0.73
2:D:15:DC:H2'	2:D:16[B]:DA:N7	2.04	0.72
3:B:197:ILE:HB	3:B:209:VAL:CG2	2.18	0.72
2:D:15:DC:H2'	2:D:16[B]:DA:H8	1.49	0.72
2:D:15:DC:H2''	2:D:16[B]:DA:C8	2.23	0.72
3:B:197:ILE:HB	3:B:209:VAL:HG22	1.71	0.72
3:A:60:ASN:O	3:A:61:ARG:HD3	1.90	0.71
3:B:279:SER:OG	3:B:281:GLN:HG3	1.89	0.71
1:C:16:DG:C5'	3:B:202:THR:HB	2.20	0.71
3:A:19:THR:HA	4:A:386:HOH:O	1.90	0.70
3:A:86:LYS:NZ	3:A:89:GLN:HE22	1.88	0.70
3:B:317:ASN:HB3	3:B:319:ASN:HD21	1.57	0.70
2:D:18[A]:DA:H2''	2:D:19[A]:DC:H5'	1.73	0.70
2:D:16[A]:DA:H2''	2:D:17[A]:DT:C5	2.26	0.70
3:A:188:THR:OG1	3:A:189:ASP:N	2.24	0.70
3:A:154:ARG:HB2	3:A:157:ASP:HB2	1.72	0.70
3:A:245:ASN:H	3:A:245:ASN:ND2	1.89	0.70
3:A:231:ALA:O	3:A:234:PRO:HD3	1.92	0.69
3:B:85:VAL:O	3:B:89:GLN:HG3	1.91	0.69
3:B:159:ARG:HB2	3:B:224:TRP:CZ3	2.28	0.69
2:D:6:DT:H2''	2:D:7:DC:H5''	1.72	0.69
1:C:28:DG:H2''	1:C:29:DA:H8	1.57	0.69
2:D:15:DC:C2'	2:D:16[B]:DA:H8	1.99	0.69
3:A:277:ASP:CG	3:A:284:LEU:HD13	2.18	0.69
3:A:139:ARG:HH12	3:B:339:LEU:HD23	1.58	0.68
3:B:180:ILE:CD1	3:B:195:ILE:HG21	2.24	0.68
3:A:245:ASN:HD22	3:A:245:ASN:H	1.39	0.68
3:A:188:THR:HG22	3:A:194:LEU:HD12	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:195:ILE:HD11	3:B:213:LEU:HD11	1.75	0.68
2:D:19[B]:DC:H2''	2:D:20:DA:O5'	1.94	0.67
3:A:26:ASN:O	3:A:29:ASP:HB2	1.94	0.67
3:B:99:HIS:O	3:B:102:SER:HB2	1.93	0.67
3:B:268:THR:O	3:B:271:LEU:HB3	1.95	0.67
3:B:106:ARG:O	3:B:109:ASP:HB2	1.93	0.67
2:D:16[A]:DA:H4'	2:D:17[A]:DT:OP1	1.94	0.66
3:A:221:VAL:O	3:A:225:ILE:HG13	1.95	0.66
3:A:341:ASP:HB3	4:A:407:HOH:O	1.96	0.66
3:B:27:LEU:CD1	3:B:102:SER:HA	2.26	0.66
3:A:156:GLN:HG3	3:A:156:GLN:O	1.95	0.66
3:A:228:SER:OG	3:A:230:VAL:HG12	1.96	0.66
2:D:2:DT:H2''	2:D:3:DA:N7	2.10	0.66
3:B:27:LEU:HD13	3:B:102:SER:HA	1.78	0.65
3:B:145:VAL:CG2	3:B:272:ILE:HD11	2.26	0.65
3:A:24:ARG:HG3	3:A:24:ARG:HH11	1.61	0.65
1:C:32:DT:H2''	1:C:33:DA:C8	2.31	0.65
3:A:146:ARG:O	3:A:150:GLU:HG2	1.97	0.65
3:B:317:ASN:HB3	3:B:319:ASN:ND2	2.12	0.65
3:A:134:ALA:HA	3:A:283:TYR:CD1	2.32	0.65
3:A:277:ASP:O	3:A:279:SER:N	2.29	0.65
3:A:181:ARG:HA	3:A:237:TYR:HA	1.78	0.64
3:B:129:GLU:C	3:B:130:ARG:HD2	2.23	0.64
1:C:2:DT:H2''	1:C:3:DA:N7	2.11	0.64
1:C:28:DG:H2''	1:C:29:DA:C8	2.31	0.64
3:A:139:ARG:HB2	4:A:398:HOH:O	1.97	0.64
3:A:238:LEU:HB3	4:A:383:HOH:O	1.96	0.64
3:B:305:SER:O	3:B:308:GLU:N	2.31	0.64
3:B:121:ARG:HG2	3:B:121:ARG:NH1	2.13	0.64
2:D:15:DC:H2''	2:D:16[A]:DA:H5'	1.78	0.63
3:A:230:VAL:HG23	3:A:236:ASN:ND2	2.13	0.63
3:B:161:LEU:HG	3:B:220:LEU:HD22	1.79	0.63
3:A:24:ARG:HG3	3:A:24:ARG:NH1	2.13	0.63
3:A:96:ASN:ND2	3:A:108:SER:OG	2.30	0.63
3:A:149:MET:HE2	3:A:161:LEU:HG	1.80	0.63
3:A:277:ASP:OD1	3:A:277:ASP:N	2.31	0.63
3:B:183:LYS:NZ	3:B:235:ASN:OD1	2.31	0.63
3:B:231:ALA:HB3	4:B:398:HOH:O	1.99	0.63
3:B:178:ALA:HB2	3:B:261:LEU:HD11	1.79	0.63
1:C:10:DT:O4	3:B:43:LYS:HE3	1.98	0.62
3:B:299:MET:O	3:B:304:VAL:HG23	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:65:PRO:HG3	3:A:104:LEU:HD13	1.81	0.62
3:B:245:ASN:OD1	3:B:247:VAL:HG23	1.98	0.62
3:A:200:THR:HG21	3:A:205:SER:HB2	1.81	0.62
3:A:213:LEU:HG	3:A:217:VAL:HG22	1.80	0.62
3:A:39:GLU:O	3:A:43:LYS:HG2	1.99	0.62
3:B:119:ARG:O	3:B:123:GLU:HG3	1.99	0.62
3:B:233:ASP:O	3:B:236:ASN:HB2	1.99	0.62
3:A:181:ARG:HG3	3:A:237:TYR:CD1	2.34	0.62
2:D:15:DC:H4'	2:D:15:DC:OP1	2.00	0.62
3:A:277:ASP:OD2	3:A:284:LEU:HD13	1.99	0.62
3:A:236:ASN:HD21	3:A:250:PRO:HB3	1.65	0.62
3:B:139:ARG:HG2	3:B:139:ARG:HH11	1.65	0.61
1:C:5:DC:C2'	1:C:6:DT:H5'	2.30	0.61
2:D:16[B]:DA:H2''	2:D:17[B]:DT:OP2	2.00	0.61
3:A:26:ASN:HB3	3:A:102:SER:HA	1.82	0.61
2:D:16[A]:DA:H2''	2:D:17[A]:DT:C6	2.36	0.61
3:A:58:LEU:HD23	3:A:59:ASN:HD21	1.65	0.61
3:A:106:ARG:HB2	3:A:109:ASP:OD2	2.01	0.61
3:B:194:LEU:HD13	3:B:210:GLU:HG2	1.81	0.61
3:B:134:ALA:HA	3:B:283:TYR:CD1	2.35	0.61
3:B:193:MET:HE2	3:B:213:LEU:CD1	2.26	0.61
3:B:31:PHE:O	3:B:34:ARG:HG3	2.01	0.60
3:A:97:MET:HG3	3:A:98:LEU:N	2.15	0.60
3:A:139:ARG:NH1	3:B:339:LEU:HD23	2.15	0.60
3:A:159:ARG:HB2	3:A:224:TRP:CE3	2.36	0.60
3:A:197:ILE:HG22	3:A:198:GLY:N	2.14	0.60
3:B:193:MET:CE	3:B:213:LEU:HD12	2.25	0.60
3:A:86:LYS:HD2	3:A:86:LYS:N	2.15	0.60
3:B:218:THR:O	3:B:222:GLU:HG3	2.01	0.60
3:A:100:ARG:HH21	3:A:106:ARG:NH1	2.00	0.60
2:D:16[A]:DA:H2''	2:D:17[A]:DT:C7	2.32	0.60
3:B:25:LYS:HE2	4:B:455:HOH:O	2.02	0.60
3:A:235:ASN:HB3	3:A:252:ALA:HB1	1.84	0.59
3:A:194:LEU:HA	3:A:211:LYS:O	2.01	0.59
3:B:193:MET:HE1	3:B:221:VAL:CG1	2.27	0.59
3:A:109:ASP:HB2	4:A:376:HOH:O	2.02	0.59
2:D:33:DA:C2'	2:D:34:DT:H5''	2.18	0.59
3:B:104:LEU:HB3	3:B:105:PRO:CD	2.31	0.59
2:D:4:DA:H2''	2:D:5:DC:H5''	1.84	0.59
3:A:223:ARG:O	3:A:224:TRP:C	2.46	0.59
1:C:9:DA:H2'	1:C:10:DT:C6	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:75:LEU:HD11	3:A:92:LEU:HD22	1.86	0.58
3:A:289:HIS:ND1	4:A:346:HOH:O	2.30	0.58
3:B:50:ARG:NH2	4:B:369:HOH:O	2.36	0.58
2:D:1:DA:H2'	2:D:2:DT:C6	2.38	0.58
3:A:158:ILE:HD11	3:A:224:TRP:HE3	1.67	0.58
2:D:6:DT:H2''	2:D:7:DC:H5'	1.86	0.58
2:D:18[B]:DA:H2''	2:D:19[B]:DC:C5'	2.33	0.58
3:A:200:THR:OG1	3:A:206:THR:HG22	2.03	0.58
3:A:335:MET:HB2	4:A:396:HOH:O	2.03	0.57
3:B:320:ILE:O	3:B:321:VAL:C	2.46	0.57
3:A:301:ARG:NH1	3:A:328:LEU:HD11	2.20	0.57
3:B:306:ILE:N	3:B:307:PRO:HD2	2.19	0.57
3:A:230:VAL:HG23	3:A:236:ASN:HD22	1.69	0.57
3:B:60:ASN:O	3:B:61:ARG:HD2	2.05	0.57
3:B:44:MET:O	3:B:48:VAL:HG23	2.05	0.57
3:B:182:VAL:HG21	3:B:230:VAL:O	2.05	0.57
3:B:336:VAL:HG12	3:B:340:GLU:OE1	2.04	0.57
2:D:11:DA:N3	3:A:282:ARG:NH2	2.47	0.56
2:D:14:DG:H2''	2:D:15:DC:C6	2.39	0.56
3:A:24:ARG:O	3:A:28:MET:HG3	2.04	0.56
3:B:154:ARG:HD3	3:B:157:ASP:OD2	2.04	0.56
3:A:139:ARG:HH22	3:B:339:LEU:HA	1.71	0.56
3:A:195:ILE:N	3:A:211:LYS:O	2.38	0.56
3:A:309:ILE:O	3:A:310:MET:C	2.48	0.56
3:A:86:LYS:HZ3	3:A:89:GLN:HE22	1.53	0.56
3:A:187:ARG:HD3	3:A:193:MET:HG2	1.87	0.56
3:B:101:ARG:HG2	3:B:101:ARG:HH11	1.71	0.56
3:A:309:ILE:HG22	3:A:310:MET:N	2.22	0.55
3:B:180:ILE:HD13	3:B:195:ILE:HG21	1.87	0.55
3:B:74:TYR:O	3:B:77:TYR:HB3	2.06	0.55
3:A:188:THR:N	3:A:192:ARG:O	2.36	0.55
3:A:213:LEU:HG	3:A:217:VAL:CG2	2.36	0.55
2:D:6:DT:C2'	2:D:7:DC:H5''	2.36	0.55
3:A:42:TRP:CE3	3:A:45:LEU:HD23	2.42	0.55
3:B:173:ARG:NH1	3:B:176:GLU:OE2	2.33	0.55
3:B:306:ILE:HD13	3:B:322:MET:CE	2.23	0.54
3:A:188:THR:HG21	3:A:194:LEU:HD12	1.90	0.54
3:B:323:ASN:O	3:B:326:ARG:HD3	2.08	0.54
3:A:96:ASN:HA	3:A:107:PRO:HD2	1.89	0.54
1:C:16:DG:OP1	3:B:315:TRP:HA	2.08	0.54
3:A:100:ARG:HH21	3:A:106:ARG:HH12	1.56	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:155:CYS:HB3	3:B:242:VAL:HG11	1.90	0.53
3:B:197:ILE:HB	3:B:209:VAL:HG23	1.90	0.53
3:B:96:ASN:ND2	3:B:108:SER:HB2	2.22	0.53
2:D:18[B]:DA:H2''	2:D:19[B]:DC:O4'	2.08	0.53
3:A:187:ARG:HH11	3:A:187:ARG:CG	2.20	0.53
3:A:81:ARG:NH1	3:A:83:LEU:HD21	2.22	0.53
3:B:25:LYS:NZ	3:B:29:ASP:OD2	2.37	0.53
3:B:170:THR:O	3:B:171:LEU:HB2	2.08	0.53
3:B:139:ARG:HG2	3:B:139:ARG:NH1	2.23	0.53
1:C:14:DA:N7	3:B:86:LYS:NZ	2.57	0.53
2:D:15:DC:C2	2:D:16[B]:DA:N7	2.77	0.53
3:A:195:ILE:O	3:A:197:ILE:HG12	2.09	0.53
3:A:89:GLN:OE1	3:A:121:ARG:NH2	2.42	0.53
3:A:85:VAL:HB	3:A:86:LYS:HE2	1.90	0.52
3:A:92:LEU:HD23	3:A:117:MET:HG3	1.91	0.52
2:D:15:DC:C4	2:D:16[B]:DA:N6	2.77	0.52
2:D:16[A]:DA:H2''	2:D:17[A]:DT:H71	1.91	0.52
3:B:313:GLY:HA3	3:B:315:TRP:CE3	2.44	0.52
3:A:86:LYS:HZ3	3:A:89:GLN:NE2	2.07	0.52
3:A:192:ARG:HD2	3:A:215:LEU:CD2	2.40	0.52
3:A:194:LEU:HD22	3:A:210:GLU:CG	2.38	0.52
3:A:310:MET:CE	3:A:318:VAL:HG22	2.39	0.52
2:D:17[A]:DT:H2''	2:D:18[A]:DA:C8	2.44	0.52
3:B:130:ARG:HD2	3:B:130:ARG:N	2.25	0.52
3:B:140:THR:O	3:B:144:GLN:HG3	2.09	0.52
3:A:180:ILE:O	3:A:237:TYR:HD1	1.93	0.52
3:B:69:GLU:HB2	4:B:422:HOH:O	2.09	0.52
3:B:181:ARG:NH1	3:B:252:ALA:O	2.30	0.52
1:C:16:DG:H5'	3:B:202:THR:CB	2.35	0.52
3:A:309:ILE:O	3:A:312:ALA:N	2.42	0.52
3:B:180:ILE:HD13	3:B:195:ILE:CG2	2.40	0.52
3:A:72:ARG:HH11	3:A:72:ARG:HG2	1.75	0.51
3:A:275:ALA:O	3:A:276:LYS:C	2.52	0.51
3:B:128:GLY:O	3:B:129:GLU:O	2.28	0.51
3:B:181:ARG:HD3	3:B:235:ASN:O	2.10	0.51
3:A:158:ILE:HD11	3:A:224:TRP:HA	1.92	0.51
3:A:202:THR:HG23	3:A:206:THR:O	2.10	0.51
3:A:278:ASP:O	3:A:279:SER:C	2.54	0.51
2:D:17[A]:DT:C5'	2:D:17[A]:DT:H6	2.24	0.51
4:D:51:HOH:O	3:B:288:GLY:HA3	2.11	0.51
3:B:181:ARG:O	3:B:184:ASP:HB2	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:192:ARG:HD2	3:A:215:LEU:HD23	1.92	0.51
3:B:181:ARG:HG2	3:B:235:ASN:O	2.11	0.51
3:A:76:LEU:HD23	3:A:120:ILE:HD11	1.93	0.51
3:B:27:LEU:HD11	3:B:102:SER:OG	2.11	0.51
3:A:158:ILE:CD1	3:A:224:TRP:HE3	2.24	0.50
1:C:16:DG:O5'	3:B:316:THR:OG1	2.27	0.50
3:B:84:ALA:O	3:B:87:THR:HG23	2.11	0.50
3:A:291:ALA:HB3	4:A:351:HOH:O	2.11	0.50
3:A:230:VAL:CG2	3:A:236:ASN:HD22	2.23	0.50
3:A:24:ARG:HH11	3:A:24:ARG:CG	2.25	0.50
3:A:270:ARG:O	3:A:274:GLY:N	2.36	0.50
3:B:205:SER:OG	3:B:207:ALA:HB3	2.11	0.50
3:A:187:ARG:HA	3:A:192:ARG:O	2.11	0.50
2:D:10:DT:H2''	2:D:11:DA:C8	2.46	0.50
3:A:166:ILE:HD12	3:A:239:PHE:CE2	2.47	0.50
3:B:277:ASP:OD1	3:B:278:ASP:OD1	2.28	0.50
3:A:216:GLY:HA3	4:A:370:HOH:O	2.11	0.50
3:A:274:GLY:O	3:A:275:ALA:O	2.29	0.50
3:B:96:ASN:HD21	3:B:108:SER:HB2	1.77	0.50
3:B:318:VAL:HG23	3:B:318:VAL:O	2.11	0.50
2:D:15:DC:C2	2:D:16[B]:DA:C5	3.00	0.50
3:A:194:LEU:HD22	3:A:210:GLU:HG2	1.93	0.50
3:B:237:TYR:CE2	3:B:255:GLN:HG3	2.46	0.50
1:C:5:DC:H2''	1:C:6:DT:H5'	1.94	0.49
2:D:16[B]:DA:N3	2:D:17[B]:DT:C6	2.79	0.49
3:A:278:ASP:O	3:A:279:SER:O	2.29	0.49
3:A:34:ARG:C	3:A:36:ALA:H	2.20	0.49
3:A:85:VAL:HG12	3:A:86:LYS:NZ	2.26	0.49
3:B:297:ARG:O	3:B:298:ASP:C	2.54	0.49
3:B:276:LYS:O	3:B:277:ASP:O	2.30	0.49
3:A:139:ARG:HD2	3:A:143:ASP:CG	2.37	0.49
3:A:134:ALA:HB3	3:A:293:VAL:HG21	1.93	0.49
3:A:138:GLU:OE1	3:A:301:ARG:NH2	2.45	0.49
2:D:18[A]:DA:P	3:B:121:ARG:HE	2.35	0.49
3:B:72:ARG:HG2	3:B:72:ARG:HH11	1.78	0.49
3:A:96:ASN:OD1	3:A:107:PRO:HD2	2.11	0.49
3:B:241:ARG:HG3	3:B:249:ALA:HB3	1.94	0.49
3:A:341:ASP:C	4:A:409:HOH:O	2.55	0.49
3:B:335:MET:HA	3:B:335:MET:CE	2.36	0.49
3:A:67:GLU:O	3:A:68:PRO:C	2.56	0.48
3:B:22:GLU:O	3:B:25:LYS:N	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:84:ALA:HB3	3:B:87:THR:CG2	2.42	0.48
3:B:179:ARG:HG2	3:B:255:GLN:HE22	1.78	0.48
3:A:215:LEU:HG	3:B:340:GLU:OE2	2.13	0.48
2:D:16[A]:DA:C2'	2:D:17[A]:DT:C5	2.96	0.48
2:D:17[A]:DT:H6	2:D:17[A]:DT:H5''	1.79	0.48
3:B:194:LEU:HD23	3:B:212:ALA:HA	1.94	0.48
3:B:249:ALA:N	3:B:250:PRO:HD3	2.27	0.48
1:C:13:DA:C2	2:D:23:DA:C2	3.02	0.48
3:A:170:THR:OG1	3:A:172:LEU:HD12	2.14	0.48
3:B:154:ARG:O	3:B:158:ILE:HG13	2.13	0.48
3:B:181:ARG:HA	3:B:237:TYR:HA	1.96	0.48
3:B:27:LEU:HD21	3:B:102:SER:OG	2.14	0.48
3:B:317:ASN:ND2	4:B:432:HOH:O	2.47	0.48
3:A:203:LEU:HD13	3:B:125:VAL:HG12	1.95	0.48
3:A:299:MET:HE3	3:A:309:ILE:HG12	1.96	0.48
3:B:293:VAL:HG22	3:B:324:TYR:CE1	2.49	0.48
2:D:24:DT:H5''	3:B:289:HIS:CE1	2.49	0.48
3:A:227:VAL:O	3:A:228:SER:C	2.56	0.48
3:B:60:ASN:HD22	3:B:60:ASN:HA	1.51	0.47
3:A:104:LEU:CB	3:A:105:PRO:HD2	2.39	0.47
3:B:128:GLY:O	3:B:129:GLU:C	2.58	0.47
2:D:24:DT:H4'	3:B:289:HIS:CE1	2.49	0.47
3:B:173:ARG:HB2	3:B:176:GLU:HG3	1.95	0.47
3:A:85:VAL:CG1	3:A:86:LYS:HE2	2.44	0.47
3:A:183:LYS:HD3	4:A:380:HOH:O	2.14	0.47
3:B:101:ARG:HH11	3:B:101:ARG:CG	2.27	0.47
2:D:17[B]:DT:H2''	2:D:18[B]:DA:O5'	2.14	0.47
3:B:282:ARG:O	3:B:283:TYR:HB2	2.15	0.47
2:D:15:DC:N3	2:D:16[B]:DA:N6	2.62	0.47
3:A:153:ASP:OD1	3:A:153:ASP:N	2.47	0.47
1:C:16:DG:P	3:B:316:THR:H	2.38	0.46
3:B:277:ASP:HB3	3:B:284:LEU:CD1	2.45	0.46
3:A:166:ILE:HD12	3:A:239:PHE:HE2	1.81	0.46
3:A:23:VAL:HG22	3:A:102:SER:O	2.15	0.46
3:A:86:LYS:NZ	3:A:89:GLN:NE2	2.58	0.46
3:A:171:LEU:HD21	3:A:295:ALA:HB3	1.97	0.46
3:A:178:ALA:HB2	3:A:261:LEU:HD11	1.98	0.46
3:A:275:ALA:O	3:A:276:LYS:O	2.33	0.46
3:A:299:MET:HB3	3:A:309:ILE:HD11	1.97	0.46
2:D:10:DT:H2''	2:D:11:DA:H8	1.79	0.46
3:A:19:THR:HB	3:A:22:GLU:OE1	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:149:MET:HG2	4:A:401:HOH:O	2.15	0.46
3:A:30:MET:HG2	3:A:42:TRP:HH2	1.80	0.46
3:B:335:MET:HE3	3:B:335:MET:CA	2.34	0.46
1:C:23:DA:H2''	1:C:24:DT:O5'	2.15	0.46
3:A:224:TRP:NE1	3:A:238:LEU:O	2.37	0.46
3:B:60:ASN:C	3:B:61:ARG:HD2	2.41	0.46
3:B:203:LEU:C	3:B:203:LEU:HD12	2.40	0.46
3:B:211:LYS:HB3	3:B:211:LYS:HE2	1.30	0.46
3:B:279:SER:CB	3:B:281:GLN:HG3	2.45	0.46
3:A:42:TRP:CZ3	3:A:45:LEU:HD23	2.51	0.46
3:A:65:PRO:HB3	3:A:104:LEU:HD13	1.98	0.46
3:A:142:PHE:O	3:A:146:ARG:HB2	2.16	0.46
3:A:306:ILE:HG23	3:A:310:MET:HG3	1.97	0.46
3:B:242:VAL:HG22	3:B:248:ALA:HA	1.98	0.46
3:A:86:LYS:HA	3:A:89:GLN:NE2	2.31	0.46
3:B:113:VAL:O	3:B:116:VAL:HG12	2.15	0.46
3:A:152:SER:OG	3:A:154:ARG:HG3	2.15	0.45
3:B:202:THR:O	3:B:203:LEU:HB3	2.16	0.45
2:D:23:DA:H2'	2:D:24:DT:C7	2.47	0.45
3:A:52:TRP:NE1	3:A:63:TRP:HB2	2.32	0.45
3:A:79:GLN:O	3:A:82:GLY:N	2.45	0.45
3:B:277:ASP:CB	3:B:284:LEU:HD13	2.46	0.45
3:B:301:ARG:HG3	3:B:301:ARG:HH11	1.81	0.45
3:A:187:ARG:CG	3:A:187:ARG:NH1	2.79	0.45
3:A:188:THR:HG21	3:A:194:LEU:CD1	2.47	0.45
3:B:269:HIS:HB2	3:B:286:TRP:CE3	2.50	0.45
3:A:92:LEU:CD2	3:A:117:MET:HG3	2.46	0.45
3:B:92:LEU:HD23	3:B:117:MET:HG2	1.99	0.45
3:B:245:ASN:CG	3:B:247:VAL:HG23	2.40	0.45
3:A:67:GLU:HG2	3:A:68:PRO:HD2	1.97	0.45
3:A:257:SER:O	3:A:258:LEU:C	2.60	0.45
3:A:304:VAL:CG1	3:A:308:GLU:HG2	2.46	0.45
2:D:1:DA:H2''	2:D:2:DT:H5'	1.98	0.45
3:A:91:HIS:O	3:A:92:LEU:C	2.59	0.45
3:A:150:GLU:O	3:A:223:ARG:NH1	2.50	0.45
3:A:224:TRP:CZ2	3:A:228:SER:HB3	2.51	0.45
3:A:233:ASP:O	3:A:236:ASN:N	2.50	0.45
3:A:86:LYS:N	3:A:86:LYS:CD	2.80	0.45
3:A:234:PRO:C	3:A:236:ASN:H	2.15	0.45
3:B:133:GLN:HG3	4:B:427:HOH:O	2.17	0.45
3:B:183:LYS:N	3:B:234:PRO:O	2.43	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:31:DT:H73	4:D:64:HOH:O	2.17	0.44
3:A:230:VAL:O	3:A:236:ASN:ND2	2.50	0.44
3:B:145:VAL:HG22	3:B:272:ILE:CD1	2.42	0.44
3:A:137:PHE:HB2	3:A:290:SER:HB3	1.98	0.44
3:A:179:ARG:HA	3:A:255:GLN:OE1	2.17	0.44
3:B:179:ARG:HG2	3:B:255:GLN:NE2	2.32	0.44
2:D:7:DC:H2''	2:D:8:DT:H5'	1.98	0.44
3:A:82:GLY:HA2	4:A:348:HOH:O	2.18	0.44
3:B:199:ARG:HB2	3:B:204:VAL:HG13	2.00	0.44
3:A:161:LEU:HD23	3:A:161:LEU:HA	1.89	0.44
3:A:137:PHE:HB3	3:A:291:ALA:HA	1.99	0.44
3:A:221:VAL:O	3:A:222:GLU:C	2.60	0.44
3:A:233:ASP:O	3:A:235:ASN:N	2.50	0.44
3:B:293:VAL:O	3:B:296:ALA:HB3	2.17	0.44
3:A:121:ARG:NH1	3:A:121:ARG:HG3	2.33	0.44
3:A:180:ILE:HG22	3:A:181:ARG:N	2.32	0.43
1:C:9:DA:H2''	1:C:10:DT:O4'	2.18	0.43
3:A:184:ASP:O	3:A:195:ILE:HA	2.17	0.43
3:A:310:MET:CG	3:A:318:VAL:HG13	2.48	0.43
3:B:185:ILE:HG22	3:B:186:SER:N	2.32	0.43
3:B:332:THR:OG1	3:B:333:GLY:N	2.51	0.43
3:A:62:LYS:HA	3:A:62:LYS:HD3	1.49	0.43
3:B:251:SER:HG	3:B:254:SER:H	1.62	0.43
3:B:68:PRO:HB3	3:B:110:SER:OG	2.18	0.43
2:D:16[A]:DA:C2'	2:D:17[A]:DT:C7	2.96	0.43
3:B:175:ALA:HA	3:B:258:LEU:HD21	2.00	0.43
3:B:257:SER:O	3:B:260:ALA:HB3	2.18	0.43
3:A:308:GLU:O	3:A:312:ALA:HB2	2.19	0.43
1:C:15:DT:H2''	1:C:16:DG:H8	1.75	0.43
3:B:19:THR:C	3:B:21:ASP:N	2.76	0.43
3:A:108:SER:C	3:A:110:SER:H	2.27	0.43
3:A:224:TRP:CE2	3:A:228:SER:HB3	2.53	0.43
3:B:306:ILE:N	3:B:307:PRO:CD	2.81	0.43
2:D:15:DC:N3	2:D:16[B]:DA:C6	2.87	0.42
3:B:194:LEU:HD13	3:B:210:GLU:CG	2.48	0.42
3:B:324:TYR:HD1	3:B:324:TYR:HA	1.67	0.42
3:A:19:THR:HB	3:A:22:GLU:HB2	2.01	0.42
3:A:65:PRO:CG	3:A:104:LEU:HD13	2.46	0.42
3:B:40:HIS:HD2	3:B:43:LYS:NZ	2.17	0.42
3:B:233:ASP:HB3	3:B:236:ASN:CG	2.43	0.42
3:B:279:SER:CB	3:B:281:GLN:HE21	2.31	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:329:ASP:HA	3:A:332:THR:HG23	2.00	0.42
3:B:159:ARG:HB2	3:B:224:TRP:CE3	2.54	0.42
3:B:233:ASP:HA	3:B:234:PRO:HD2	1.94	0.42
1:C:28:DG:C2'	1:C:29:DA:C8	3.02	0.42
3:A:187:ARG:HH11	3:A:187:ARG:HG2	1.84	0.42
2:D:13:DA:C2	2:D:14:DG:C4	3.08	0.42
3:A:223:ARG:O	3:A:226:SER:N	2.53	0.42
3:A:217:VAL:O	3:A:217:VAL:HG23	2.19	0.42
3:A:320:ILE:HG22	3:A:321:VAL:N	2.33	0.42
3:B:101:ARG:CG	3:B:101:ARG:NH1	2.82	0.42
1:C:1:DA:H2''	1:C:2:DT:O5'	2.17	0.42
3:A:62:LYS:HD3	3:A:63:TRP:N	2.35	0.42
3:A:121:ARG:HH11	3:A:121:ARG:CG	2.32	0.42
3:B:180:ILE:HD12	3:B:195:ILE:HG21	1.97	0.42
1:C:16:DG:H3'	3:B:316:THR:OG1	2.20	0.41
3:A:173:ARG:HH11	3:A:173:ARG:HD3	1.61	0.41
3:B:241:ARG:CG	3:B:249:ALA:HB3	2.50	0.41
1:C:25:DA:C8	1:C:25:DA:H5'	2.55	0.41
3:A:270:ARG:O	3:A:271:LEU:C	2.62	0.41
3:A:319:ASN:HD22	3:A:319:ASN:HA	1.67	0.41
3:A:181:ARG:NH2	3:A:252:ALA:O	2.42	0.41
3:A:209:VAL:O	3:A:210:GLU:O	2.38	0.41
3:A:272:ILE:HG22	3:A:273:TYR:CD1	2.54	0.41
3:A:305:SER:HB3	3:A:308:GLU:HB3	2.02	0.41
3:B:72:ARG:HG2	3:B:72:ARG:NH1	2.35	0.41
3:B:177:ILE:O	3:B:180:ILE:HG13	2.19	0.41
3:B:305:SER:O	3:B:308:GLU:HB2	2.19	0.41
1:C:16:DG:O6	2:D:19[B]:DC:N4	2.34	0.41
2:D:29:DA:H2''	2:D:30:DG:OP2	2.20	0.41
3:B:42:TRP:O	3:B:46:LEU:HD22	2.20	0.41
3:B:194:LEU:HD23	3:B:194:LEU:HA	1.68	0.41
3:A:272:ILE:CG2	3:A:273:TYR:CE1	3.03	0.41
2:D:32:DT:H2'	2:D:32:DT:O5'	2.20	0.41
3:B:301:ARG:HG3	3:B:301:ARG:NH1	2.36	0.41
1:C:14:DA:H1'	3:B:201:LYS:NZ	2.36	0.41
3:A:196:HIS:ND1	3:A:196:HIS:C	2.79	0.41
3:A:233:ASP:N	3:A:234:PRO:CD	2.84	0.41
3:A:193:MET:CE	3:A:222:GLU:HG3	2.51	0.41
3:A:234:PRO:C	3:A:236:ASN:N	2.76	0.41
3:A:277:ASP:HB2	3:A:278:ASP:H	1.63	0.41
3:A:306:ILE:HD13	3:A:322:MET:HE1	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:270:ARG:O	3:B:274:GLY:N	2.48	0.41
3:A:299:MET:O	3:A:304:VAL:HG23	2.21	0.40
2:D:8:DT:H5'	2:D:8:DT:H6	1.86	0.40
3:A:86:LYS:HZ1	3:A:121:ARG:NH2	2.19	0.40
3:A:173:ARG:HG3	3:A:176:GLU:OE2	2.21	0.40
3:B:166:ILE:O	3:B:167:ALA:C	2.63	0.40
3:B:64:PHE:HA	3:B:65:PRO:C	2.46	0.40
3:B:277:ASP:HB2	3:B:284:LEU:HD13	2.03	0.40
2:D:23:DA:H5'	3:B:201:LYS:CB	2.52	0.40
3:A:299:MET:HE2	3:A:299:MET:HB2	1.74	0.40
3:A:308:GLU:OE2	3:B:334:ALA:HB2	2.21	0.40
3:B:22:GLU:O	3:B:25:LYS:HB3	2.21	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	
3	A	321/349 (92%)	269 (84%)	35 (11%)	17 (5%)	1	0
3	B	314/349 (90%)	290 (92%)	18 (6%)	6 (2%)	6	5
All	All	635/698 (91%)	559 (88%)	53 (8%)	23 (4%)	2	1

All (23) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	202	THR
3	A	210	GLU
3	A	234	PRO
3	A	275	ALA
3	A	278	ASP
3	A	279	SER

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Mol	Chain	Res	Type
3	A	305	SER
3	A	318	VAL
3	B	129	GLU
3	B	277	ASP
3	A	276	LYS
3	A	203	LEU
3	A	281	GLN
3	B	314	GLY
3	B	318	VAL
3	A	109	ASP
3	A	189	ASP
3	A	184	ASP
3	A	209	VAL
3	A	319	ASN
3	B	288	GLY
3	A	197	ILE
3	B	198	GLY

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	
3	A	268/291 (92%)	204 (76%)	64 (24%)	1	0
3	B	263/291 (90%)	217 (82%)	46 (18%)	2	1
All	All	531/582 (91%)	421 (79%)	110 (21%)	1	1

All (110) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	22	GLU
3	A	24	ARG
3	A	43	LYS
3	A	46	LEU
3	A	62	LYS
3	A	83	LEU

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Mol	Chain	Res	Type
3	A	86	LYS
3	A	89	GLN
3	A	92	LEU
3	A	97	MET
3	A	109	ASP
3	A	110	SER
3	A	114	SER
3	A	115	LEU
3	A	116	VAL
3	A	117	MET
3	A	119	ARG
3	A	133	GLN
3	A	135	LEU
3	A	139	ARG
3	A	140	THR
3	A	147	SER
3	A	151	ASN
3	A	156	GLN
3	A	161	LEU
3	A	183	LYS
3	A	187	ARG
3	A	188	THR
3	A	189	ASP
3	A	192	ARG
3	A	194	LEU
3	A	196	HIS
3	A	197	ILE
3	A	199	ARG
3	A	200	THR
3	A	202	THR
3	A	213	LEU
3	A	217	VAL
3	A	218	THR
3	A	220	LEU
3	A	235	ASN
3	A	241	ARG
3	A	245	ASN
3	A	253	THR
3	A	254	SER
3	A	270	ARG
3	A	271	LEU
3	A	276	LYS

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Mol	Chain	Res	Type
3	A	277	ASP
3	A	284	LEU
3	A	289	HIS
3	A	299	MET
3	A	306	ILE
3	A	310	MET
3	A	318	VAL
3	A	320	ILE
3	A	322	MET
3	A	323	ASN
3	A	326	ARG
3	A	328	LEU
3	A	330	SER
3	A	335	MET
3	A	336	VAL
3	A	338	LEU
3	B	19	THR
3	B	20	SER
3	B	27	LEU
3	B	28	MET
3	B	32	ARG
3	B	41	THR
3	B	43	LYS
3	B	46	LEU
3	B	60	ASN
3	B	62	LYS
3	B	87	THR
3	B	100	ARG
3	B	101	ARG
3	B	102	SER
3	B	108	SER
3	B	122	LYS
3	B	125	VAL
3	B	132	LYS
3	B	138	GLU
3	B	171	LEU
3	B	180	ILE
3	B	183	LYS
3	B	199	ARG
3	B	200	THR
3	B	203	LEU
3	B	205	SER

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Mol	Chain	Res	Type
3	B	211	LYS
3	B	219	LYS
3	B	244	LYS
3	B	254	SER
3	B	259	SER
3	B	276	LYS
3	B	289	HIS
3	B	292	ARG
3	B	297	ARG
3	B	305	SER
3	B	310	MET
3	B	319	ASN
3	B	320	ILE
3	B	321	VAL
3	B	325	ILE
3	B	326	ARG
3	B	332	THR
3	B	335	MET
3	B	338	LEU
3	B	340	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
3	A	59	ASN
3	A	79	GLN
3	A	89	GLN
3	A	144	GLN
3	A	151	ASN
3	A	236	ASN
3	A	245	ASN
3	A	269	HIS
3	A	281	GLN
3	A	289	HIS
3	A	319	ASN
3	B	35	GLN
3	B	40	HIS
3	B	60	ASN
3	B	156	GLN
3	B	255	GLN
3	B	281	GLN
3	B	289	HIS

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Mol	Chain	Res	Type
3	B	317	ASN
3	B	319	ASN

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	D	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	15:DC	O3'	16[B]:DA	P	1.84
1	D	19[B]:DC	O3'	20:DA	P	1.26

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	C	33/34 (97%)	-1.01	0 100 100	32, 54, 85, 100	0
2	D	34/34 (100%)	-1.08	0 100 100	27, 47, 59, 78	4 (11%)
3	A	322/349 (92%)	-0.41	0 100 100	27, 59, 96, 99	9 (2%)
3	B	318/349 (91%)	-0.74	0 100 100	25, 45, 83, 98	7 (2%)
All	All	707/766 (92%)	-0.62	0 100 100	25, 53, 90, 100	20 (2%)

There are no RSRZ outliers to report.

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.