



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 09:37 PM GMT

PDB ID : 1PVP
Title : BASIS FOR A SWITCH IN SUBSTRATE SPECIFICITY: CRYSTAL
STRUCTURE OF SELECTED VARIANT OF CRE SITE-SPECIFIC RE-
COMBINASE, 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

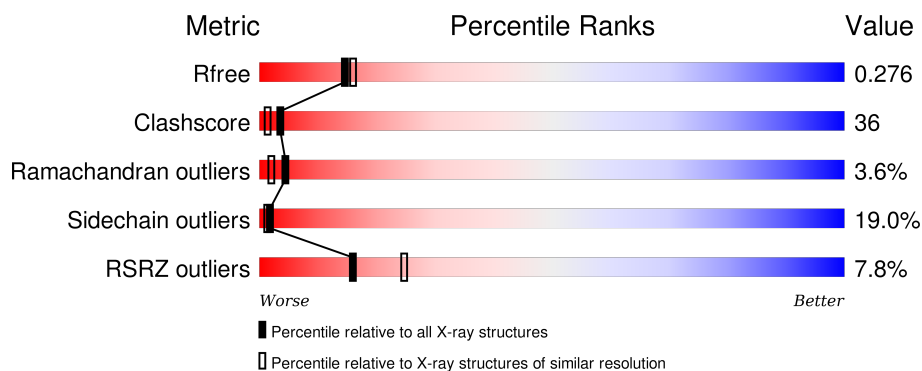
1 Overall quality at a glance

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}	91344	1352 (2.38-2.34)
Clashscore	102246	1456 (2.38-2.34)
Ramachandran outliers	100387	1435 (2.38-2.34)
Sidechain outliers	100360	1436 (2.38-2.34)
RSRZ outliers	91569	1358 (2.38-2.34)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	<div> <div>9%</div> <div>29%</div> <div>59%</div> <div>9%</div> <div>.</div> </div>
2	D	34	<div> <div>6%</div> <div>18%</div> <div>71%</div> <div>12%</div> </div>
3	A	349	<div> <div>12%</div> <div>39%</div> <div>40%</div> <div>11%</div> <div>.</div> <div>7%</div> </div>
3	B	349	<div> <div>3%</div> <div>38%</div> <div>45%</div> <div>9%</div> <div>9%</div> </div>

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	T	ENGINEERED	GB 215623
C	8	DT	C	ENGINEERED	GB 215623
C	9	DA	G	ENGINEERED	GB 215623
C	26	DT	C	ENGINEERED	GB 215623
C	27	DA	G	ENGINEERED	GB 215623
C	28	DG	A	ENGINEERED	GB 215623

- 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	T	ENGINEERED	GB 215626
D	8	DT	C	ENGINEERED	GB 215626
D	9	DA	G	ENGINEERED	GB 215626
D	26	DT	C	ENGINEERED	GB 215626
D	27	DA	G	ENGINEERED	GB 215626
D	28	DG	A	ENGINEERED	GB 215626

- Molecule 3 is a protein called Recombinase CRE.

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

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	UNP P06956
A	258	LEU	THR	ENGINEERED	UNP P06956
A	259	SER	ARG	ENGINEERED	UNP P06956
A	262	HIS	GLU	ENGINEERED	UNP P06956
A	266	GLY	GLU	ENGINEERED	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	UNP P06956
B	258	LEU	THR	ENGINEERED	UNP P06956
B	259	SER	ARG	ENGINEERED	UNP P06956
B	262	HIS	GLU	ENGINEERED	UNP P06956
B	266	GLY	GLU	ENGINEERED	UNP P06956

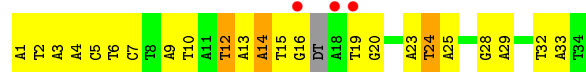
- Molecule 4 is water.

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

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

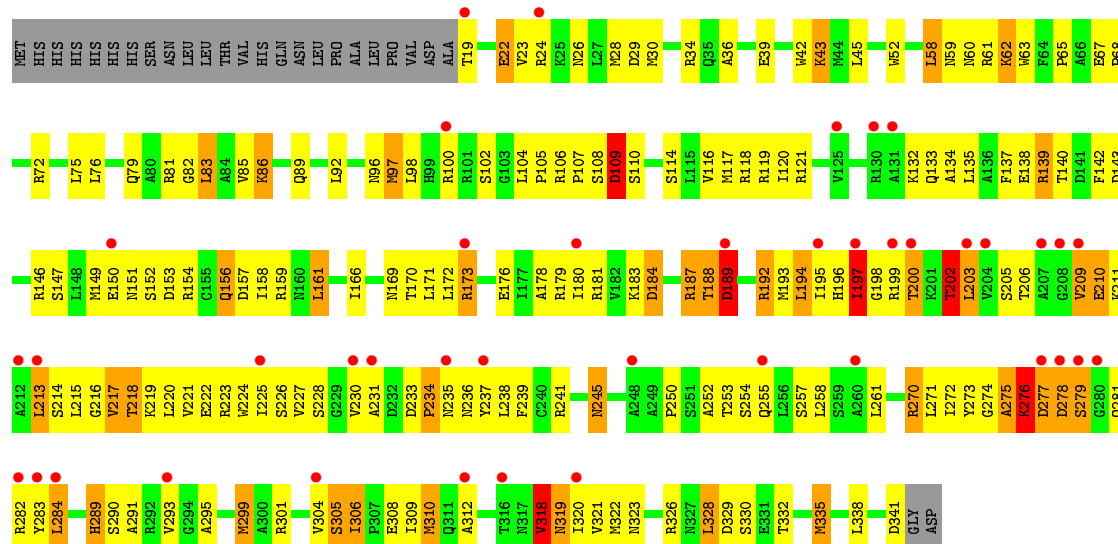
• Molecule 1: 34-MER



• Molecule 2: 34-MER



• Molecule 3: Recombinase CRE



• Molecule 3: Recombinase CRE





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 80.62 – 2.35	Depositor EDS
% Data completeness (in resolution range)	95.0 (5.00-2.35) 94.6 (80.62-2.35)	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 0.224 , 0.276	Depositor DCC
R_{free} test set	1916 reflections (4.79%)	DCC
Wilson B-factor (Å ²)	47.6	Xtriage
Anisotropy	0.301	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 85.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 46893 reflections	Xtriage
F_o, F_c correlation	0.93	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, 0.375 respectively for untwinned datasets, and 0.333, 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	0.60	0/733	1.43	5/1129 (0.4%)
2	D	0.80	1/868 (0.1%)	1.43	11/1337 (0.8%)
3	A	0.37	0/2588	0.72	3/3490 (0.1%)
3	B	0.42	1/2548 (0.0%)	0.71	0/3434
All	All	0.49	2/6737 (0.0%)	0.96	19/9390 (0.2%)

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

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	10	DT	C5-C7	8.08	1.54	1.50
3	B	259	SER	CB-OG	5.91	1.50	1.42

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	4	DA	O4'-C1'-N9	9.59	114.71	108.00
3	A	173	ARG	NE-CZ-NH1	-8.48	116.06	120.30
2	D	3	DA	O4'-C4'-C3'	-7.90	101.26	106.00
1	C	7	DC	P-O3'-C3'	7.89	129.17	119.70
3	A	202	THR	N-CA-C	7.78	132.01	111.00
2	D	10	DT	C6-C5-C7	-6.19	119.19	122.90
1	C	12	DT	P-O3'-C3'	6.10	127.02	119.70
2	D	3	DA	OP1-P-OP2	-5.95	110.68	119.60
2	D	10	DT	C5-C6-N1	-5.92	120.15	123.70
3	A	318	VAL	N-CA-C	5.80	126.67	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	24	DT	P-O3'-C3'	5.80	126.66	119.70
1	C	4	DA	O4'-C1'-N9	5.69	111.98	108.00
2	D	32	DT	C3'-C2'-C1'	-5.68	95.69	102.50
2	D	26	DT	O4'-C1'-N1	5.65	111.95	108.00
1	C	14	DA	P-O3'-C3'	5.57	126.38	119.70
2	D	4	DA	C1'-O4'-C4'	-5.43	104.67	110.10
2	D	10	DT	C6-N1-C2	5.28	123.94	121.30
2	D	12	DT	P-O3'-C3'	5.21	125.95	119.70
2	D	3	DA	C4'-C3'-C2'	5.07	107.67	103.10

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	197	0
3	B	2507	0	2533	173	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	436	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 36.

All (436) 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
2:D:15:DC:C2'	2:D:16[B]:DA:C8	2.47	0.97
2:D:1:DA:N7	4:D:63:HOH:O	2.03	0.92
3:B:193:MET:HE1	3:B:221:VAL:HG11	1.52	0.91
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
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:HD2	3:A:86:LYS:H	1.42	0.83
3:B:313:GLY:HA3	3:B:315:TRP:CZ3	2.12	0.83
3:B:193:MET:HE2	3:B:213:LEU:HD12	1.59	0.82
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:121:ARG:HG2	3:B:121:ARG:HH11	1.45	0.80
3:B:335:MET:HA	3:B:335:MET:HE3	1.63	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
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:C8	2.23	0.72
2:D:15:DC:H2'	2:D:16[B]:DA:H8	1.49	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:197:ILE:HB	3:B:209:VAL:HG22	1.71	0.72
3:B:279:SER:OG	3:B:281:GLN:HG3	1.89	0.71
3:A:60:ASN:O	3:A:61:ARG:HD3	1.90	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:245:ASN:H	3:A:245:ASN:ND2	1.89	0.70
3:A:154:ARG:HB2	3:A:157:ASP:HB2	1.72	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
3:B:306:ILE:HD13	3:B:322:MET:CE	2.23	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: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:H	3:A:245:ASN:HD22	1.39	0.68
3:B:195:ILE:HD11	3:B:213:LEU:HD11	1.75	0.68
3:A:188:THR:HG22	3:A:194:LEU:HD12	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:B:27:LEU:CD1	3:B:102:SER:HA	2.26	0.66
3:A:341:ASP:HB3	4:A:407:HOH:O	1.96	0.66
3:A:228:SER:OG	3:A:230:VAL:HG12	1.96	0.66
3:A:156:GLN:O	3:A:156:GLN:HG3	1.95	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:193:MET:CE	3:B:213:LEU:HD12	2.25	0.65
3:A:289:HIS:ND1	4:A:346:HOH:O	2.30	0.65
3:B:145:VAL:CG2	3:B:272:ILE:HD11	2.26	0.65
3:A:24:ARG:HH11	3:A:24:ARG:HG3	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:245:ASN:N	3:A:245:ASN:ND2	2.45	0.64
3:A:181:ARG:HA	3:A:237:TYR:HA	1.78	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:238:LEU:HB3	4:A:383:HOH:O	1.96	0.64
3:A:139:ARG:HB2	4:A:398:HOH:O	1.97	0.64
3:A:277:ASP:CG	3:A:284:LEU:HD13	2.18	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:277:ASP:N	3:A:277:ASP:OD1	2.31	0.63
3:B:231:ALA:HB3	4:B:398:HOH:O	1.99	0.63
3:B:183:LYS:NZ	3:B:235:ASN:OD1	2.31	0.63
3:B:178:ALA:HB2	3:B:261:LEU:HD11	1.79	0.63
3:B:299:MET:O	3:B:304:VAL:HG23	1.99	0.62
1:C:10:DT:O4	3:B:43:LYS:HE3	1.98	0.62
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:213:LEU:HG	3:A:217:VAL:HG22	1.80	0.62
3:A:200:THR:HG21	3:A:205:SER:HB2	1.81	0.62
3:B:233:ASP:O	3:B:236:ASN:HB2	1.99	0.62
3:B:119:ARG:O	3:B:123:GLU:HG3	1.99	0.62
3:A:39:GLU:O	3:A:43:LYS:HG2	1.99	0.62
3:A:181:ARG:HG3	3:A:237:TYR:CD1	2.34	0.62
2:D:15:DC:OP1	2:D:15:DC:H4'	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
3:B:306:ILE:HD13	3:B:322:MET:HE1	1.82	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:31:PHE:O	3:B:34:ARG:HG3	2.01	0.60
3:A:159:ARG:HB2	3:A:224:TRP:CE3	2.36	0.60
3:A:139:ARG:NH1	3:B:339:LEU:HD23	2.15	0.60
3:A:97:MET:HG3	3:A:98:LEU:N	2.15	0.60
3:A:197:ILE:HG22	3:A:198:GLY:N	2.14	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:129:GLU:C	3:B:130:ARG:HD2	2.23	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:B:193:MET:HE2	3:B:213:LEU:CD1	2.30	0.58
1:C:9:DA:H2'	1:C:10:DT:C6	2.38	0.58
3:A:75:LEU:HD11	3:A:92:LEU:HD22	1.86	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:306:ILE:N	3:B:307:PRO:HD2	2.19	0.57
3:A:301:ARG:NH1	3:A:328:LEU:HD11	2.20	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:336:VAL:HG12	3:B:340:GLU:OE1	2.04	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:11:DA:N3	3:A:282:ARG:NH2	2.47	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: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:HH11	3:B:101:ARG:HG2	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:HE3	1.88	0.54
3:A:188:THR:HG21	3:A:194:LEU:HD12	1.90	0.54
3:A:223:ARG:O	3:A:224:TRP:C	2.46	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
3:B:197:ILE:HB	3:B:209:VAL:HG23	1.90	0.53
3:B:155:CYS:HB3	3:B:242:VAL:HG11	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:B:25:LYS:NZ	3:B:29:ASP:OD2	2.37	0.53
3:A:81:ARG:NH1	3:A:83:LEU:HD21	2.22	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
2:D:15:DC:C2	2:D:16[B]:DA:N7	2.77	0.53
1:C:14:DA:N7	3:B:86:LYS:NZ	2.57	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:B:320:ILE:O	3:B:321:VAL:C	2.46	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:16[A]:DA:H2''	2:D:17[A]:DT:H71	1.91	0.52
2:D:15:DC:C4	2:D:16[B]:DA:N6	2.77	0.52
3:B:313:GLY:HA3	3:B:315:TRP:CE3	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:194:LEU:HD22	3:A:210:GLU:CG	2.38	0.52
3:A:192:ARG:HD2	3:A:215:LEU:CD2	2.40	0.52
3:A:86:LYS:HZ3	3:A:89:GLN:NE2	2.07	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:N	3:B:130:ARG:HD2	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:181:ARG:NH1	3:B:252:ALA:O	2.30	0.52
3:B:69:GLU:HB2	4:B:422:HOH:O	2.09	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:HG2	3:A:72:ARG:HH11	1.75	0.51
3:B:181:ARG:HD3	3:B:235:ASN:O	2.10	0.51
3:B:128:GLY:O	3:B:129:GLU:O	2.28	0.51
3:A:158:ILE:HD11	3:A:224:TRP:HA	1.92	0.51
3:A:309:ILE:O	3:A:310:MET:C	2.48	0.51
3:A:202:THR:HG23	3:A:206:THR:O	2.10	0.51
2:D:17[A]:DT:C5'	2:D:17[A]:DT:H6	2.24	0.51
3:B:181:ARG:O	3:B:184:ASP:HB2	2.10	0.51
4:D:51:HOH:O	3:B:288:GLY:HA3	2.11	0.51
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:B:27:LEU:HD11	3:B:102:SER:OG	2.11	0.51
3:A:76:LEU:HD23	3:A:120:ILE:HD11	1.93	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:B:205:SER:OG	3:B:207:ALA:HB3	2.11	0.50
3:A:270:ARG:O	3:A:274:GLY:N	2.36	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:B:277:ASP:OD1	3:B:278:ASP:OD1	2.28	0.50
3:A:166:ILE:HD12	3:A:239:PHE:CE2	2.47	0.50
3:B:318:VAL:HG23	3:B:318:VAL:O	2.11	0.50
3:B:96:ASN:HD21	3:B:108:SER:HB2	1.77	0.50
3:A:274:GLY:O	3:A:275:ALA:O	2.29	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:216:GLY:HA3	4:A:370:HOH: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
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
1:C:5:DC:H2''	1:C:6:DT:H5'	1.94	0.49
3:A:85:VAL:HG12	3:A:86:LYS:NZ	2.26	0.49
3:B:276:LYS:O	3:B:277:ASP:O	2.30	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:B:335:MET:HA	3:B:335:MET:CE	2.36	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:B:22:GLU:O	3:B:25:LYS:N	2.46	0.48
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:H5''	2:D:17[A]:DT:H6	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
3:B:181:ARG:HA	3:B:237:TYR:HA	1.96	0.48
3:B:154:ARG:O	3:B:158:ILE:HG13	2.13	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:317:ASN:ND2	4:B:432:HOH:O	2.47	0.48
3:B:27:LEU:HD21	3:B:102:SER:OG	2.14	0.48
3:B:293:VAL:HG22	3:B:324:TYR:CE1	2.49	0.48
3:A:203:LEU:HD13	3:B:125:VAL:HG12	1.95	0.48
2:D:24:DT:H5''	3:B:289:HIS:CE1	2.49	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:173:ARG:HB2	3:B:176:GLU:HG3	1.95	0.47
2:D:24:DT:H4'	3:B:289:HIS:CE1	2.49	0.47
3:A:183:LYS:HD3	4:A:380:HOH:O	2.14	0.47
3:A:85:VAL:CG1	3:A:86:LYS:HE2	2.44	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:282:ARG:O	3:B:283:TYR:HB2	2.15	0.47
3:A:275:ALA:O	3:A:276:LYS:C	2.52	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
3:A:278:ASP:O	3:A:279:SER:C	2.54	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:86:LYS:NZ	3:A:89:GLN:NE2	2.58	0.46
3:A:23:VAL:HG22	3:A:102:SER:O	2.15	0.46
3:A:275:ALA:O	3:A:276:LYS:O	2.33	0.46
3:A:178:ALA:HB2	3:A:261:LEU:HD11	1.98	0.46
3:A:171:LEU:HD21	3:A:295:ALA:HB3	1.97	0.46
3:A:299:MET:HB3	3:A:309:ILE:HD11	1.97	0.46
3:A:19:THR:HB	3:A:22:GLU:OE1	2.16	0.46
2:D:10:DT:H2''	2:D:11:DA:H8	1.79	0.46
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:A:224:TRP:NE1	3:A:238:LEU:O	2.37	0.46
3:B:279:SER:CB	3:B:281:GLN:HG3	2.45	0.46
1:C:23:DA:H2''	1:C:24:DT:O5'	2.15	0.46
3:B:211:LYS:HE2	3:B:211:LYS:HB3	1.30	0.46
3:A:142:PHE:O	3:A:146:ARG:HB2	2.16	0.46
3:A:65:PRO:HB3	3:A:104:LEU:HD13	1.98	0.46
3:A:306:ILE:HG23	3:A:310:MET:HG3	1.97	0.46
3:A:42:TRP:CZ3	3:A:45:LEU:HD23	2.51	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:B:202:THR:O	3:B:203:LEU:HB3	2.16	0.45
3:A:234:PRO:C	3:A:236:ASN:H	2.15	0.45
3:A:152:SER:OG	3:A:154:ARG:HG3	2.15	0.45
2:D:23:DA:H2'	2:D:24:DT:C7	2.47	0.45
3:B:277:ASP:CB	3:B:284:LEU:HD13	2.46	0.45
3:B:301:ARG:HH11	3:B:301:ARG:HG3	1.81	0.45
3:A:79:GLN:O	3:A:82:GLY:N	2.45	0.45
3:A:52:TRP:NE1	3:A:63:TRP:HB2	2.32	0.45
3:A:187:ARG:NH1	3:A:187:ARG:CG	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:92:LEU:HD23	3:B:117:MET:HG2	1.99	0.45
3:A:304:VAL:CG1	3:A:308:GLU:HG2	2.46	0.45
3:A:67:GLU:HG2	3:A:68:PRO:HD2	1.97	0.45
3:A:34:ARG:C	3:A:36:ALA:H	2.20	0.45
2:D:1:DA:H2''	2:D:2:DT:H5'	1.98	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:B:297:ARG:O	3:B:298:ASP:C	2.54	0.45
3:A:86:LYS:CD	3:A:86:LYS:N	2.80	0.45
3:B:183:LYS:N	3:B:234:PRO:O	2.43	0.45
3:B:133:GLN:HG3	4:B:427:HOH:O	2.17	0.45
3:A:139:ARG:HD2	3:A:143:ASP:CG	2.37	0.44
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:341:ASP:C	4:A:409:HOH:O	2.55	0.44
3:B:179:ARG:HG2	3:B:255:GLN:NE2	2.32	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
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:227:VAL:O	3:A:228:SER:C	2.56	0.44
3:A:137:PHE:HB3	3:A:291:ALA:HA	1.99	0.44
3:A:67:GLU:O	3:A:68:PRO:C	2.56	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
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
1:C:9:DA:H2''	1:C:10:DT:O4'	2.18	0.43
3:B:332:THR:OG1	3:B:333:GLY:N	2.51	0.43
3:B:185:ILE:HG22	3:B:186:SER:N	2.32	0.43
3:A:62:LYS:HA	3:A:62:LYS:HD3	1.49	0.43
3:B:68:PRO:HB3	3:B:110:SER:OG	2.18	0.43
3:A:320:ILE:HG22	3:A:321:VAL:N	2.33	0.43
2:D:16[A]:DA:C2'	2:D:17[A]:DT:C7	2.96	0.43
3:B:257:SER:O	3:B:260:ALA:HB3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:175:ALA:HA	3:B:258:LEU:HD21	2.00	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:251:SER:HG	3:B:254:SER:H	1.63	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:128:GLY:O	3:B:129:GLU:C	2.58	0.42
3:B:324:TYR:HA	3:B:324:TYR:HD1	1.67	0.42
3:A:65:PRO:CG	3:A:104:LEU:HD13	2.46	0.42
3:B:279:SER:CB	3:B:281:GLN:HE21	2.31	0.42
3:A:19:THR:HB	3:A:22:GLU:HB2	2.01	0.42
3:B:149:MET:HE2	3:B:161:LEU:HB2	2.00	0.42
3:B:40:HIS:HD2	3:B:43:LYS:NZ	2.17	0.42
3:B:159:ARG:HB2	3:B:224:TRP:CE3	2.54	0.42
3:A:329:ASP:HA	3:A:332:THR:HG23	2.00	0.42
3:B:233:ASP:HA	3:B:234:PRO:HD2	1.94	0.42
3:A:187:ARG:HH11	3:A:187:ARG:HG2	1.84	0.42
1:C:28:DG:C2'	1:C:29:DA:C8	3.02	0.42
2:D:13:DA:C2	2:D:14:DG:C4	3.08	0.42
3:B:193:MET:HE3	3:B:193:MET:HB3	1.67	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: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:B:180:ILE:HD12	3:B:195:ILE:HG21	1.97	0.42
3:A:121:ARG:HH11	3:A:121:ARG:CG	2.32	0.42
3:A:62:LYS:HD3	3:A:63:TRP:N	2.35	0.42
1:C:16:DG:H3'	3:B:316:THR:OG1	2.20	0.41
3:B:241:ARG:CG	3:B:249:ALA:HB3	2.50	0.41
3:A:173:ARG:HH11	3:A:173:ARG:HD3	1.61	0.41
3:A:319:ASN:HD22	3:A:319:ASN:HA	1.67	0.41
1:C:25:DA:C8	1:C:25:DA:H5'	2.55	0.41
3:B:177:ILE:O	3:B:180:ILE:HG13	2.19	0.41
3:A:209:VAL:O	3:A:210:GLU:O	2.38	0.41
3:A:181:ARG:NH2	3:A:252:ALA:O	2.42	0.41
3:A:305:SER:HB3	3:A:308:GLU:HB3	2.02	0.41
3:B:305:SER:O	3:B:308:GLU:HB2	2.19	0.41
3:B:60:ASN:C	3:B:61:ARG:HD2	2.41	0.41
3:B:72:ARG:NH1	3:B:72:ARG:HG2	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:272:ILE:HG22	3:A:273:TYR:CD1	2.54	0.41
1:C:16:DG:O6	2:D:19[B]:DC:N4	2.34	0.41
3:B:194:LEU:HD23	3:B:194:LEU:HA	1.68	0.41
3:B:42:TRP:O	3:B:46:LEU:HD22	2.20	0.41
2:D:29:DA:H2''	2:D:30:DG:OP2	2.20	0.41
3:B:203:LEU:C	3:B:203:LEU:HD12	2.40	0.41
3:A:272:ILE:CG2	3:A:273:TYR:CE1	3.03	0.41
3:B:301:ARG:HG3	3:B:301:ARG:NH1	2.36	0.41
2:D:32:DT:H2'	2:D:32:DT:O5'	2.20	0.41
3:A:233:ASP:N	3:A:234:PRO:CD	2.84	0.41
1:C:14:DA:H1'	3:B:201:LYS:NZ	2.36	0.41
3:A:193:MET:CE	3:A:222:GLU:HG3	2.51	0.41
3:A:277:ASP:HB2	3:A:278:ASP:H	1.63	0.41
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
3:A:86:LYS:HZ1	3:A:121:ARG:NH2	2.19	0.40
2:D:8:DT:H5'	2:D:8:DT:H6	1.86	0.40
3:A:299:MET:HE3	3:A:309:ILE:HG12	2.02	0.40
3:B:245:ASN:CG	3:B:247:VAL:HG23	2.40	0.40
3:A:173:ARG:HG3	3:A:176:GLU:OE2	2.21	0.40
3:B:277:ASP:HB2	3:B:284:LEU:HD13	2.03	0.40
3:A:257:SER:O	3:A:258:LEU:C	2.60	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
2:D:23:DA:H5'	3:B:201:LYS:CB	2.52	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%)	2 0

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	B	314/349 (90%)	290 (92%)	18 (6%)	6 (2%)	10	7
All	All	635/698 (91%)	559 (88%)	53 (8%)	23 (4%)	4	2

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
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%)	209 (78%)	59 (22%)	1	1

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	B	263/291 (90%)	221 (84%)	42 (16%)	3	2
All	All	531/582 (91%)	430 (81%)	101 (19%)	2	1

All (101) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	22	GLU
3	A	43	LYS
3	A	58	LEU
3	A	62	LYS
3	A	83	LEU
3	A	86	LYS
3	A	97	MET
3	A	109	ASP
3	A	110	SER
3	A	114	SER
3	A	116	VAL
3	A	118	ARG
3	A	119	ARG
3	A	132	LYS
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	169	ASN
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

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Mol	Chain	Res	Type
3	A	219	LYS
3	A	220	LEU
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
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	322	MET
3	A	323	ASN
3	A	326	ARG
3	A	328	LEU
3	A	330	SER
3	A	335	MET
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	37	PHE
3	B	38	SER
3	B	43	LYS
3	B	46	LEU
3	B	60	ASN
3	B	87	THR
3	B	100	ARG
3	B	101	ARG
3	B	102	SER
3	B	108	SER
3	B	118	ARG
3	B	132	LYS
3	B	138	GLU
3	B	169	ASN

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Mol	Chain	Res	Type
3	B	180	ILE
3	B	181	ARG
3	B	183	LYS
3	B	199	ARG
3	B	200	THR
3	B	203	LEU
3	B	205	SER
3	B	211	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	319	ASN
3	B	320	ILE
3	B	321	VAL
3	B	325	ILE
3	B	326	ARG
3	B	332	THR
3	B	338	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
3	A	59	ASN
3	A	79	GLN
3	A	89	GLN
3	A	133	GLN
3	A	144	GLN
3	A	151	ASN
3	A	236	ASN
3	A	245	ASN
3	A	281	GLN
3	A	319	ASN
3	B	40	HIS
3	B	60	ASN
3	B	90	GLN
3	B	156	GLN
3	B	281	GLN

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Mol	Chain	Res	Type
3	B	289	HIS
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 carbohydrates 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	C	33/34 (97%)	0.34	3 (9%) 11 18	32, 54, 85, 100	0
2	D	34/34 (100%)	0.33	2 (5%) 26 39	35, 48, 76, 78	0
3	A	322/349 (92%)	0.98	41 (12%) 5 9	27, 61, 96, 99	9 (2%)
3	B	318/349 (91%)	0.58	9 (2%) 56 69	25, 45, 87, 98	7 (2%)
All	All	707/766 (92%)	0.74	55 (7%) 16 25	25, 54, 93, 100	16 (2%)

All (55) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	A	204	VAL	6.8
3	A	225	ILE	6.4
3	A	208	GLY	5.6
3	A	197	ILE	5.4
3	A	283	TYR	4.9
3	A	282	ARG	4.8
3	A	278	ASP	4.8
3	A	19	THR	4.1
3	A	231	ALA	4.0
3	A	280	GLY	3.9
3	B	336	VAL	3.9
3	A	207	ALA	3.8
3	A	199	ARG	3.7
3	A	284	LEU	3.6
3	A	277	ASP	3.6
1	C	18	DA	3.6
3	B	324	TYR	3.5
3	B	19	THR	3.5
3	A	230	VAL	3.4
3	A	131	ALA	3.3
2	D	17[A]	DT	3.3

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Mol	Chain	Res	Type	RSRZ
3	A	279	SER	3.1
3	A	189	ASP	2.9
3	A	212	ALA	2.9
3	A	200	THR	2.9
3	B	203	LEU	2.7
3	A	130	ARG	2.7
3	A	209	VAL	2.6
1	C	19	DT	2.6
3	A	150	GLU	2.6
3	A	195	ILE	2.5
3	A	316	THR	2.5
3	B	247	VAL	2.5
3	A	312	ALA	2.5
3	B	339	LEU	2.5
3	A	180	ILE	2.4
1	C	16	DG	2.4
3	A	213	LEU	2.4
3	A	125	VAL	2.3
3	A	304	VAL	2.3
3	A	248	ALA	2.3
3	B	204	VAL	2.2
3	A	203	LEU	2.2
3	A	255	GLN	2.2
3	A	320	ILE	2.2
3	A	237	TYR	2.2
3	A	100	ARG	2.1
3	B	302	ALA	2.1
3	A	235	ASN	2.1
3	A	293	VAL	2.1
3	A	24	ARG	2.1
3	B	316	THR	2.1
2	D	16[A]	DA	2.0
3	A	260	ALA	2.0
3	A	173	ARG	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates 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.