



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:54 PM GMT

PDB ID : 4JUO
Title : A low-resolution three-gate structure of topoisomerase IV from *Streptococcus pneumoniae* in space group H32
Authors : Laponogov, I.; Veselkov, D.A.; Pan, X.-S.; Crevel, I.; Fisher, L.M.; Sanderson, M.R.
Deposited on : 2013-03-25
Resolution : 6.53 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

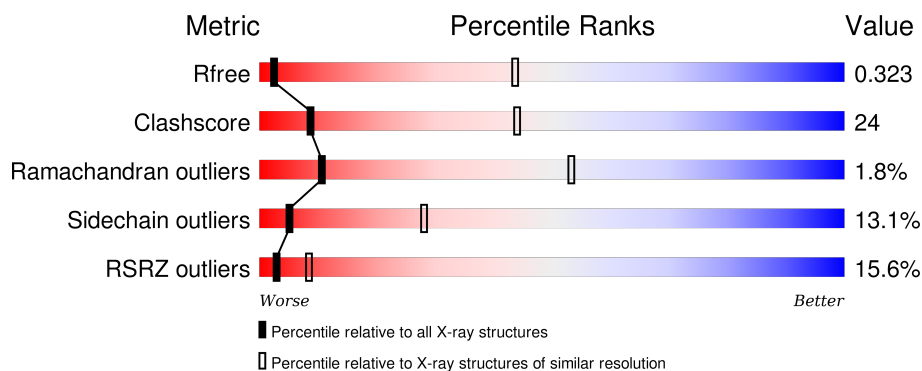
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 6.53 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	1012 (9.00-3.66)
Clashscore	102246	1060 (9.00-3.70)
Ramachandran outliers	100387	1033 (9.00-3.66)
Sidechain outliers	100360	1004 (9.00-3.66)
RSRZ outliers	91569	1011 (9.00-3.66)

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	A	496	
2	C	670	
3	E	11	
4	F	15	
5	G	11	

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Mol	Chain	Length	Quality of chain
6	H	15	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
7	MG	C	701	-	-	-	X

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 8283 atoms, of which 19 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called DNA topoisomerase 4 subunit A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	479	Total	C	N	O	S	0	1	0
			3720	2357	645	705	13			

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	257	THR	ILE	CONFLICT	UNP P72525
A	489	LEU	-	EXPRESSION TAG	UNP P72525
A	490	GLU	-	EXPRESSION TAG	UNP P72525
A	491	HIS	-	EXPRESSION TAG	UNP P72525
A	492	HIS	-	EXPRESSION TAG	UNP P72525
A	493	HIS	-	EXPRESSION TAG	UNP P72525
A	494	HIS	-	EXPRESSION TAG	UNP P72525
A	495	HIS	-	EXPRESSION TAG	UNP P72525
A	496	HIS	-	EXPRESSION TAG	UNP P72525

- Molecule 2 is a protein called DNA topoisomerase 4 subunit B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	546	Total	C	N	O	S	0	0	0
			3786	2407	653	719	7			

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-22	MET	-	EXPRESSION TAG	UNP Q59961
C	-21	GLY	-	EXPRESSION TAG	UNP Q59961
C	-20	HIS	-	EXPRESSION TAG	UNP Q59961
C	-19	HIS	-	EXPRESSION TAG	UNP Q59961
C	-18	HIS	-	EXPRESSION TAG	UNP Q59961
C	-17	HIS	-	EXPRESSION TAG	UNP Q59961
C	-16	HIS	-	EXPRESSION TAG	UNP Q59961

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-15	HIS	-	EXPRESSION TAG	UNP Q59961
C	-14	HIS	-	EXPRESSION TAG	UNP Q59961
C	-13	HIS	-	EXPRESSION TAG	UNP Q59961
C	-12	HIS	-	EXPRESSION TAG	UNP Q59961
C	-11	HIS	-	EXPRESSION TAG	UNP Q59961
C	-10	SER	-	EXPRESSION TAG	UNP Q59961
C	-9	SER	-	EXPRESSION TAG	UNP Q59961
C	-8	GLY	-	EXPRESSION TAG	UNP Q59961
C	-7	HIS	-	EXPRESSION TAG	UNP Q59961
C	-6	ILE	-	EXPRESSION TAG	UNP Q59961
C	-5	ASP	-	EXPRESSION TAG	UNP Q59961
C	-4	ASP	-	EXPRESSION TAG	UNP Q59961
C	-3	ASP	-	EXPRESSION TAG	UNP Q59961
C	-2	ASP	-	EXPRESSION TAG	UNP Q59961
C	-1	LYS	-	EXPRESSION TAG	UNP Q59961
C	0	HIS	-	EXPRESSION TAG	UNP Q59961
C	217	ASP	ASN	CONFLICT	UNP Q59961
C	460	ILE	VAL	CONFLICT	UNP Q59961
C	644	ALA	THR	CONFLICT	UNP Q59961

- Molecule 3 is a DNA chain called E-site DNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	7	Total	C	N	O	P	0	7	0
			140	69	27	38	6			

- Molecule 4 is a DNA chain called E-site DNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	F	11	Total	C	N	O	P	0	11	0
			225	108	39	67	11			

- Molecule 5 is a DNA chain called E-site DNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	G	7	Total	C	N	O	P	0	7	0
			139	68	25	40	6			

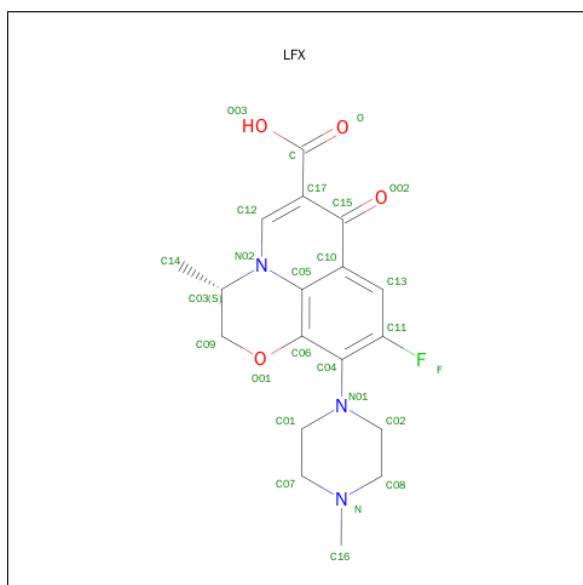
- Molecule 6 is a DNA chain called E-site DNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	H	11	Total	C	N	O	P	0	11	0
			226	107	43	65	11			

- Molecule 7 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	Mg	0	0
			1	1		
7	C	1	Total	Mg	0	0
			1	1		

- Molecule 8 is (3S)-9-FLUORO-3-METHYL-10-(4-METHYLPYPERAZIN-1-YL)-7-OXO-2,3-DIHYDRO-7H-[1,4]OXAZINO[2,3,4-IJ]QUINOLINE-6-CARBOXYLIC ACID (three-letter code: LFX) (formula: C₁₈H₂₀FN₃O₄).

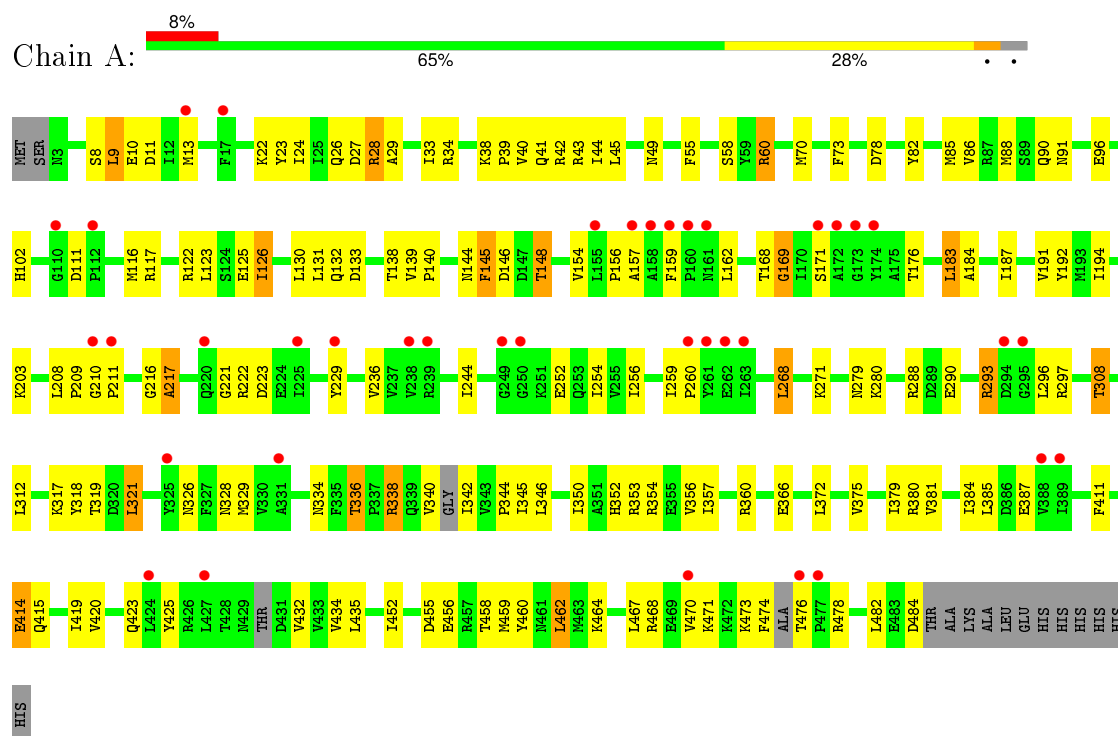


Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
8	F	1	Total	C	F	H	N	O	0	0
			45	18	1	19	3	4		

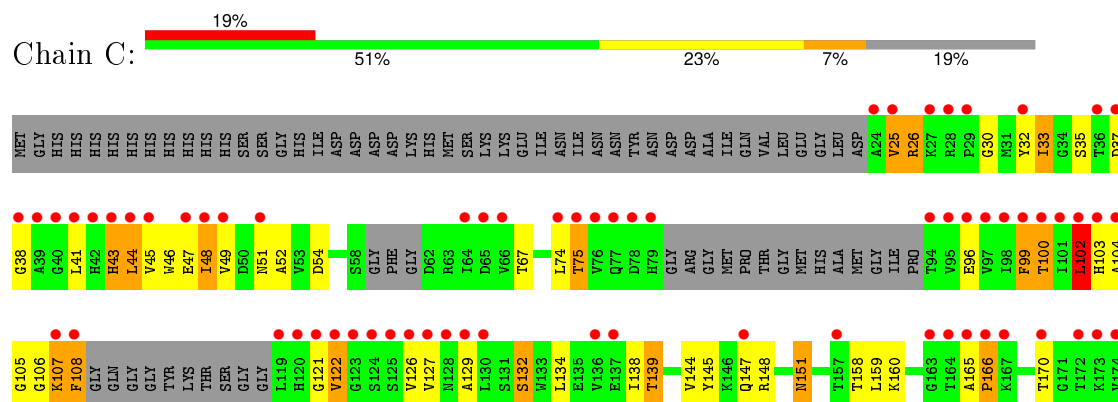
3 Residue-property plots

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: DNA topoisomerase 4 subunit A



• Molecule 2: DNA topoisomerase 4 subunit B





4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	213.58Å 213.58Å 211.83Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.44 – 6.53 53.40 – 6.53	Depositor EDS
% Data completeness (in resolution range)	99.1 (46.44-6.53) 99.3 (53.40-6.53)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.83 (at 6.69Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, R_{free}	0.247 , 0.298 0.316 , 0.323	Depositor DCC
R_{free} test set	170 reflections (4.81%)	DCC
Wilson B-factor (Å ²)	378.8	Xtriage
Anisotropy	0.474	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 304.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 3708 reflections	Xtriage
F_o, F_c correlation	0.82	EDS
Total number of atoms	8283	wwPDB-VP
Average B, all atoms (Å ²)	183.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.55% 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

Bond lengths and bond angles in the following residue types are not validated in this section: MG, LFX

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.45	0/3779	0.63	1/5109 (0.0%)
2	C	0.39	0/3845	0.63	2/5251 (0.0%)
3	E	0.88	0/157	1.64	3/241 (1.2%)
4	F	0.83	0/251	1.80	12/385 (3.1%)
5	G	0.76	0/155	1.42	1/238 (0.4%)
6	H	0.75	0/253	1.67	3/388 (0.8%)
All	All	0.47	0/8440	0.81	22/11612 (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
2	C	0	1

There are no bond length outliers.

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	H	10[B]	DC	O4'-C4'-C3'	-11.97	98.82	106.00
4	F	1[A]	DA	O4'-C1'-N9	10.86	115.60	108.00
3	E	10[A]	DA	O4'-C1'-N9	8.04	113.63	108.00
6	H	1[B]	DG	O4'-C1'-N9	7.95	113.56	108.00
4	F	3[A]	DT	O4'-C4'-C3'	-7.89	101.26	106.00
4	F	6[A]	DT	O4'-C4'-C3'	-6.75	101.80	104.50
4	F	5[A]	DA	O4'-C1'-N9	6.61	112.63	108.00
2	C	102	LEU	CA-CB-CG	6.54	130.34	115.30
3	E	11[A]	DT	C4-C5-C7	6.09	122.65	119.00
4	F	3[A]	DT	O4'-C1'-N1	5.96	112.17	108.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	183	LEU	CA-CB-CG	5.92	128.92	115.30
5	G	12[B]	DG	O4'-C1'-N9	-5.91	103.86	108.00
4	F	6[A]	DT	C4'-C3'-C2'	-5.80	97.88	103.10
4	F	6[A]	DT	C1'-O4'-C4'	-5.73	104.37	110.10
4	F	8[A]	DC	C1'-O4'-C4'	-5.65	104.45	110.10
4	F	3[A]	DT	C5-C4-O4	-5.51	121.04	124.90
4	F	1[A]	DA	C3'-C2'-C1'	-5.43	95.98	102.50
2	C	364	LEU	CA-CB-CG	5.35	127.61	115.30
3	E	11[A]	DT	C6-C5-C7	-5.13	119.82	122.90
4	F	1[A]	DA	C1'-O4'-C4'	-5.12	104.98	110.10
6	H	10[B]	DC	C1'-O4'-C4'	-5.11	104.99	110.10
4	F	1[A]	DA	O4'-C1'-C2'	-5.11	101.82	105.90

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	102	LEU	Peptide

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3720	0	3629	179	0
2	C	3786	0	3303	181	0
3	E	140	0	71	3	0
4	F	225	0	116	5	0
5	G	139	0	71	1	0
6	H	226	0	115	8	0
7	A	1	0	0	0	0
7	C	1	0	0	0	0
8	F	26	19	19	1	0
All	All	8264	19	7324	368	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 24.

All (368) 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:C:583:LEU:HB3	2:C:586:MET:CE	1.24	1.67
2:C:583:LEU:CB	2:C:586:MET:CE	1.75	1.56
2:C:583:LEU:CB	2:C:586:MET:HE3	1.28	1.53
2:C:583:LEU:HD22	2:C:586:MET:CE	1.56	1.35
2:C:583:LEU:CD2	2:C:586:MET:CE	2.06	1.32
2:C:583:LEU:CG	2:C:586:MET:CE	2.06	1.31
2:C:583:LEU:CD2	2:C:586:MET:HE2	1.65	1.24
1:A:338:ARG:HH12	1:A:344:PRO:CG	1.30	1.20
1:A:354:ARG:NE	1:A:456:GLU:OE1	1.76	1.18
1:A:60:ARG:HB2	1:A:60:ARG:HH11	1.07	1.15
1:A:28:ARG:HG3	1:A:28:ARG:HH11	1.05	1.14
1:A:354:ARG:CD	1:A:456:GLU:OE1	1.96	1.13
1:A:455:ASP:O	1:A:456:GLU:N	1.82	1.12
1:A:184:ALA:HB1	1:A:471:LYS:HE3	1.28	1.12
2:C:583:LEU:HD22	2:C:586:MET:HE1	1.18	1.12
1:A:338:ARG:NH1	1:A:344:PRO:HG2	1.56	1.11
2:C:583:LEU:CB	2:C:586:MET:HE2	1.65	1.11
1:A:357:ILE:CG2	1:A:459:MET:HG2	1.79	1.11
1:A:33:ILE:HD11	1:A:345:ILE:HA	1.37	1.06
1:A:33:ILE:HD11	1:A:345:ILE:CG1	1.84	1.06
1:A:70:MET:HE1	1:A:78:ASP:HB3	1.37	1.06
1:A:354:ARG:HD2	1:A:456:GLU:OE1	1.54	1.06
1:A:33:ILE:HD11	1:A:345:ILE:HG12	1.38	1.05
1:A:455:ASP:C	1:A:456:GLU:N	2.09	1.05
2:C:583:LEU:CA	2:C:586:MET:HE2	1.87	1.05
1:A:354:ARG:HE	1:A:456:GLU:CD	1.62	1.04
2:C:524:ARG:HH11	2:C:524:ARG:HG3	1.13	1.04
2:C:583:LEU:CD2	2:C:586:MET:HE1	1.74	1.03
1:A:357:ILE:HG21	1:A:459:MET:CG	1.89	1.02
2:C:108:PHE:CD1	2:C:276:ASN:HB3	1.94	1.02
1:A:474:PHE:O	1:A:476:THR:HG23	1.61	1.00
1:A:33:ILE:CD1	1:A:345:ILE:HG12	1.95	0.96
1:A:357:ILE:HG21	1:A:459:MET:HG2	0.98	0.96
1:A:338:ARG:HH12	1:A:344:PRO:HG3	1.28	0.96
1:A:144:ASN:HD21	1:A:148:THR:HG23	1.31	0.95
1:A:60:ARG:HH11	1:A:60:ARG:CB	1.80	0.95
2:C:108:PHE:CE1	2:C:276:ASN:HA	1.99	0.95
1:A:33:ILE:CD1	1:A:345:ILE:HA	1.97	0.93
2:C:108:PHE:CE1	2:C:276:ASN:CA	2.46	0.93
1:A:10:GLU:O	2:C:617:ARG:HD2	1.68	0.93
2:C:583:LEU:CG	2:C:586:MET:HE1	1.87	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:583:LEU:CA	2:C:586:MET:CE	2.47	0.91
2:C:524:ARG:HH11	2:C:524:ARG:CG	1.81	0.91
1:A:33:ILE:HD11	1:A:345:ILE:CA	2.01	0.91
1:A:338:ARG:NH1	1:A:344:PRO:CG	1.96	0.91
2:C:583:LEU:HA	2:C:586:MET:HE2	1.53	0.90
1:A:60:ARG:HB2	1:A:60:ARG:NH1	1.86	0.89
1:A:293:ARG:HB3	1:A:293:ARG:HH11	1.36	0.89
1:A:357:ILE:CG2	1:A:459:MET:CG	2.50	0.88
2:C:583:LEU:CD1	2:C:586:MET:HE1	2.05	0.86
1:A:384:ILE:O	1:A:387:GLU:HG2	1.74	0.86
2:C:524:ARG:NH1	2:C:524:ARG:HG3	1.87	0.86
1:A:28:ARG:HG3	1:A:28:ARG:NH1	1.86	0.86
1:A:256:ILE:HD13	1:A:321:LEU:HD21	1.56	0.85
2:C:583:LEU:CG	2:C:586:MET:HE2	1.92	0.84
2:C:516:THR:O	2:C:520:THR:HG23	1.78	0.83
6:H:10[B]:DC:H2"	6:H:11[B]:DG:H5"	1.62	0.81
1:A:44:ILE:HD12	1:A:88:MET:CE	2.10	0.81
2:C:108:PHE:HE1	2:C:276:ASN:HA	1.43	0.81
2:C:583:LEU:HD13	2:C:586:MET:HE1	1.62	0.81
1:A:125:GLU:OE2	1:A:473:LYS:NZ	2.13	0.80
1:A:34:ARG:HD2	1:A:352:HIS:CG	2.17	0.80
2:C:520:THR:HG21	2:C:622:MET:HG3	1.62	0.80
1:A:139:VAL:HG11	1:A:154:VAL:O	1.82	0.79
2:C:203:LEU:HD21	2:C:274:PHE:CD2	2.18	0.79
1:A:38:LYS:H	1:A:41:GLN:NE2	1.83	0.76
1:A:384:ILE:C	1:A:385:LEU:N	2.39	0.76
1:A:33:ILE:HD11	1:A:345:ILE:CB	2.15	0.75
1:A:24:ILE:HG22	1:A:171:SER:HB2	1.70	0.74
1:A:28:ARG:CG	1:A:28:ARG:HH11	1.94	0.74
1:A:357:ILE:HD12	1:A:459:MET:SD	2.27	0.74
1:A:187:ILE:HD13	1:A:467:LEU:O	1.86	0.74
2:C:51:ASN:ND2	2:C:99:PHE:O	2.21	0.74
1:A:169:GLY:HA2	1:A:176:THR:HG22	1.69	0.73
2:C:304:LYS:O	2:C:306:GLY:N	2.21	0.73
1:A:146:ASP:HB3	1:A:148:THR:HG22	1.70	0.73
2:C:301:TYR:HD2	2:C:379:ILE:HD11	1.54	0.73
2:C:583:LEU:CD1	2:C:586:MET:CE	2.64	0.73
3:E:9[A]:DC:H2"	3:E:10[A]:DA:H5"	1.71	0.72
1:A:183:LEU:CD1	1:A:471:LYS:HA	2.19	0.72
2:C:256:GLN:HB3	2:C:331:LEU:HB2	1.71	0.72
2:C:611:LEU:HD13	2:C:611:LEU:C	2.10	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:139:VAL:HG13	1:A:140:PRO:HD2	1.71	0.72
2:C:203:LEU:CD2	2:C:274:PHE:CD2	2.73	0.72
2:C:584:GLY:CA	2:C:586:MET:N	2.50	0.71
1:A:317:LYS:HE3	1:A:318:TYR:CE2	2.25	0.71
2:C:259:VAL:HG22	2:C:328:LEU:HD23	1.70	0.71
1:A:8:SER:HB3	1:A:11:ASP:OD1	1.90	0.71
2:C:242:LEU:HD22	2:C:423:ASN:ND2	2.05	0.71
2:C:583:LEU:HD23	2:C:586:MET:HE2	1.70	0.71
1:A:184:ALA:HB1	1:A:471:LYS:CE	2.15	0.70
2:C:108:PHE:CG	2:C:276:ASN:HB3	2.27	0.69
1:A:138:THR:HG22	1:A:360:ARG:HB2	1.73	0.69
2:C:75:THR:HB	2:C:175:THR:HB	1.74	0.69
2:C:431:LEU:HD22	2:C:479:MET:HE3	1.73	0.69
2:C:332:VAL:HG12	2:C:334:GLU:H	1.56	0.69
1:A:40:VAL:O	1:A:44:ILE:HG13	1.93	0.69
1:A:244:ILE:HD12	1:A:244:ILE:N	2.08	0.69
2:C:201:ALA:HB2	2:C:209:LEU:HD11	1.75	0.68
2:C:511:GLY:O	2:C:515:GLN:HG3	1.94	0.68
1:A:138:THR:O	1:A:356:VAL:HG22	1.94	0.67
2:C:67:THR:HB	2:C:75:THR:HG23	1.74	0.67
1:A:156:PRO:O	1:A:353:ARG:NH1	2.27	0.67
1:A:138:THR:HB	1:A:356:VAL:HG13	1.75	0.67
2:C:203:LEU:HD21	2:C:274:PHE:CE2	2.29	0.67
1:A:10:GLU:O	2:C:617:ARG:CD	2.43	0.67
1:A:271:LYS:HE3	1:A:319:THR:HB	1.75	0.67
1:A:252:GLU:OE1	1:A:308:THR:HG21	1.95	0.67
1:A:70:MET:CE	1:A:78:ASP:HB3	2.19	0.67
2:C:33:ILE:HD11	2:C:44:LEU:HB3	1.76	0.67
2:C:474:GLU:O	2:C:478:THR:HG23	1.93	0.66
2:C:265:ASP:O	2:C:421:SER:CB	2.44	0.66
1:A:146:ASP:CB	1:A:148:THR:HG22	2.25	0.66
1:A:146:ASP:CG	1:A:148:THR:HG22	2.16	0.66
1:A:38:LYS:H	1:A:41:GLN:HE21	1.42	0.66
8:F:101:LFX:H01	6:H:4[B]:DT:O2	1.95	0.66
6:H:5[B]:DA:H2"	6:H:6[B]:DT:O5'	1.96	0.66
1:A:146:ASP:OD2	1:A:148:THR:HG22	1.96	0.65
2:C:102:LEU:HD21	2:C:127:VAL:HG22	1.79	0.65
2:C:294:ILE:HA	2:C:297:VAL:HG12	1.78	0.65
2:C:203:LEU:CD2	2:C:274:PHE:CE2	2.80	0.65
2:C:104:ALA:O	2:C:106:GLY:N	2.30	0.64
2:C:491:PHE:CE1	2:C:528:PRO:HG2	2.32	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:126:ILE:HG13	1:A:474:PHE:CD2	2.32	0.64
1:A:222:ARG:HD3	1:A:484:ASP:HA	1.78	0.64
1:A:70:MET:HE1	1:A:78:ASP:CB	2.20	0.64
1:A:209:PRO:HB2	1:A:482:LEU:CD1	2.26	0.64
1:A:169:GLY:CA	1:A:176:THR:HG22	2.27	0.64
1:A:60:ARG:HH11	1:A:60:ARG:CG	2.11	0.64
2:C:583:LEU:HB3	2:C:586:MET:HB2	1.80	0.63
2:C:527:ARG:N	2:C:528:PRO:HD2	2.13	0.63
2:C:441:ALA:HB1	2:C:452:ILE:HD12	1.80	0.63
2:C:473:ASN:O	2:C:477:ASN:HB2	1.98	0.63
1:A:288:ARG:HD2	1:A:290:GLU:OE2	1.99	0.63
4:F:3[A]:DT:H4'	4:F:4[A]:DC:OP1	1.99	0.62
2:C:583:LEU:HA	2:C:586:MET:CE	2.21	0.62
2:C:102:LEU:HD23	2:C:126:VAL:HG22	1.81	0.62
1:A:211:PRO:O	1:A:478:ARG:NH2	2.30	0.62
1:A:259:ILE:HB	1:A:260:PRO:CD	2.30	0.62
2:C:583:LEU:HD13	2:C:586:MET:CE	2.30	0.62
2:C:132:SER:O	2:C:151:ASN:N	2.25	0.61
1:A:381:VAL:HG23	1:A:411:PHE:CZ	2.36	0.61
1:A:194:ILE:CD1	1:A:464:LYS:HG3	2.31	0.61
2:C:301:TYR:CD2	2:C:379:ILE:HD11	2.37	0.60
1:A:338:ARG:HH12	1:A:344:PRO:HG2	1.19	0.60
1:A:22:LYS:O	1:A:26:GLN:HG3	2.01	0.60
1:A:23:TYR:HD1	1:A:24:ILE:HD13	1.66	0.60
6:H:3[B]:DC:H2'	6:H:4[B]:DT:C6	2.37	0.60
2:C:431:LEU:HD22	2:C:479:MET:CE	2.32	0.60
1:A:381:VAL:CG2	1:A:411:PHE:CZ	2.85	0.59
2:C:139:THR:HG23	2:C:144:VAL:HB	1.84	0.59
1:A:145:PHE:CE1	1:A:146:ASP:HB2	2.38	0.59
1:A:354:ARG:NE	1:A:456:GLU:CD	2.37	0.59
1:A:146:ASP:OD2	1:A:148:THR:CG2	2.50	0.59
1:A:381:VAL:HG23	1:A:411:PHE:CE1	2.37	0.59
2:C:583:LEU:CB	2:C:586:MET:HB2	2.32	0.59
1:A:33:ILE:CD1	1:A:345:ILE:CG1	2.64	0.58
2:C:271:ILE:HD11	2:C:324:LEU:HD13	1.85	0.58
1:A:184:ALA:CB	1:A:471:LYS:HE3	2.19	0.58
1:A:183:LEU:HD11	1:A:470:VAL:HG12	1.86	0.58
2:C:134:LEU:HD12	2:C:176:PHE:HB3	1.86	0.58
1:A:317:LYS:HE3	1:A:318:TYR:CZ	2.38	0.57
2:C:446:ASP:OD1	2:C:449:PHE:CE1	2.58	0.57
2:C:51:ASN:HD21	2:C:99:PHE:HA	1.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:192:TYR:CZ	1:A:203:LYS:HE2	2.39	0.57
2:C:616:ARG:O	2:C:620:VAL:HG23	2.04	0.57
2:C:583:LEU:CA	2:C:586:MET:HB2	2.32	0.57
2:C:416:LEU:HG	2:C:417:THR:N	2.20	0.57
2:C:48:ILE:HD11	2:C:127:VAL:HG11	1.85	0.57
1:A:259:ILE:HB	1:A:260:PRO:HD2	1.86	0.56
1:A:288:ARG:NH1	1:A:290:GLU:OE2	2.30	0.56
2:C:584:GLY:HA2	2:C:586:MET:N	2.21	0.55
2:C:584:GLY:C	2:C:586:MET:N	2.59	0.55
2:C:190:TYR:CD2	2:C:213:ASP:HB2	2.42	0.55
2:C:48:ILE:HD11	2:C:127:VAL:HG21	1.87	0.55
6:H:11[B]:DG:H5'	6:H:11[B]:DG:C8	2.42	0.55
1:A:210:GLY:HA2	1:A:229:TYR:OH	2.07	0.55
1:A:139:VAL:HG13	1:A:140:PRO:CD	2.36	0.55
2:C:257:VAL:HB	2:C:330:ILE:HG22	1.88	0.54
2:C:197:LEU:HD22	2:C:209:LEU:HD22	1.90	0.54
1:A:184:ALA:HA	1:A:471:LYS:HD2	1.90	0.54
2:C:253:ASN:ND2	2:C:253:ASN:O	2.36	0.54
2:C:491:PHE:HE1	2:C:528:PRO:HG2	1.71	0.54
2:C:380:ARG:HD3	2:C:495:ASP:HA	1.89	0.54
1:A:13:MET:O	2:C:621:LEU:CD1	2.56	0.54
2:C:431:LEU:HD11	2:C:501:ILE:CG2	2.39	0.53
1:A:117[A]:ARG:HH22	4:F:1[A]:DA:H8	1.56	0.53
2:C:442:LYS:O	2:C:445:ARG:HD3	2.08	0.53
2:C:479:MET:HE1	2:C:522:PHE:CZ	2.44	0.53
1:A:290:GLU:HB2	1:A:297:ARG:HG2	1.90	0.53
2:C:285:THR:HG23	2:C:347:LEU:O	2.09	0.53
1:A:293:ARG:NH1	1:A:293:ARG:HB3	2.15	0.53
1:A:326:ASN:ND2	4:F:11[A]:DG:H4'	2.24	0.53
2:C:52:ALA:HB2	2:C:99:PHE:CE1	2.44	0.53
1:A:146:ASP:CG	1:A:148:THR:CG2	2.78	0.52
2:C:373:GLU:C	2:C:375:ALA:H	2.11	0.52
1:A:192:TYR:OH	1:A:203:LYS:HE2	2.09	0.52
1:A:194:ILE:HD13	1:A:464:LYS:HG3	1.91	0.52
2:C:591:LEU:HD22	2:C:596:MET:HG3	1.91	0.52
1:A:216:GLY:O	1:A:217:ALA:HB3	2.08	0.52
1:A:452:ILE:HG12	1:A:458:THR:CG2	2.40	0.52
1:A:357:ILE:CD1	1:A:459:MET:SD	2.97	0.52
1:A:33:ILE:HD13	1:A:345:ILE:HA	1.89	0.51
1:A:126:ILE:HG13	1:A:474:PHE:CE2	2.44	0.51
2:C:139:THR:O	2:C:170:THR:HA	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:96:GLU:HG2	2:C:138:ILE:HD11	1.91	0.51
2:C:373:GLU:O	2:C:375:ALA:N	2.43	0.51
1:A:434:VAL:HG13	1:A:435:LEU:N	2.25	0.51
1:A:256:ILE:CD1	1:A:321:LEU:HD21	2.33	0.51
2:C:590:GLN:O	2:C:594:THR:HG23	2.11	0.51
2:C:54:ASP:OD1	2:C:107:LYS:HA	2.11	0.50
2:C:479:MET:CE	2:C:522:PHE:CZ	2.94	0.50
2:C:611:LEU:HD13	2:C:611:LEU:O	2.10	0.50
2:C:132:SER:N	2:C:177:MET:O	2.42	0.50
2:C:321:ARG:HG2	2:C:324:LEU:HD12	1.92	0.50
2:C:43:HIS:O	2:C:47:GLU:HG2	2.12	0.49
2:C:464:LYS:HD2	6:H:8[B]:DC:OP2	2.12	0.49
1:A:350:ILE:HG23	1:A:460:TYR:CE1	2.48	0.49
1:A:159:PHE:HB3	1:A:470:VAL:HG11	1.94	0.49
1:A:194:ILE:HG21	1:A:464:LYS:CD	2.42	0.49
6:H:3[B]:DC:H4'	6:H:4[B]:DT:OP1	2.12	0.49
1:A:357:ILE:CG2	1:A:459:MET:HG3	2.40	0.49
2:C:360:VAL:O	2:C:364:LEU:HD12	2.13	0.49
1:A:354:ARG:NE	1:A:456:GLU:OE2	2.40	0.48
1:A:38:LYS:N	1:A:41:GLN:HE21	2.07	0.48
2:C:263:TYR:CE2	2:C:378:LEU:HD21	2.47	0.48
2:C:592:TRP:CE2	2:C:597:ASN:HB2	2.47	0.48
1:A:452:ILE:HG12	1:A:458:THR:HG22	1.96	0.48
2:C:351:LEU:HD22	2:C:355:VAL:HG13	1.95	0.48
2:C:516:THR:O	2:C:520:THR:CG2	2.57	0.48
2:C:203:LEU:HD23	2:C:274:PHE:CD2	2.46	0.48
1:A:194:ILE:HD12	1:A:464:LYS:CG	2.43	0.48
1:A:360:ARG:HH12	1:A:462:LEU:HD13	1.79	0.47
1:A:381:VAL:HG22	1:A:411:PHE:CZ	2.49	0.47
2:C:246:LEU:O	2:C:260:ALA:HA	2.15	0.47
2:C:242:LEU:CD2	2:C:423:ASN:ND2	2.76	0.47
2:C:361:ALA:O	2:C:365:THR:OG1	2.32	0.47
2:C:179:ASP:OD1	2:C:182:ILE:HG23	2.15	0.47
2:C:190:TYR:HD2	2:C:213:ASP:HB2	1.79	0.47
1:A:96:GLU:HG2	1:A:126:ILE:HD12	1.95	0.47
1:A:268:LEU:HD11	1:A:321:LEU:HD23	1.97	0.47
1:A:130:LEU:HD23	1:A:157:ALA:HA	1.96	0.47
1:A:334:ASN:O	1:A:336:THR:HG23	2.15	0.47
2:C:524:ARG:NH1	2:C:524:ARG:CG	2.54	0.47
1:A:44:ILE:HD13	1:A:85:MET:HB2	1.96	0.47
1:A:360:ARG:HH12	1:A:462:LEU:CD1	2.28	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:44:ILE:HD12	1:A:88:MET:HE1	1.96	0.46
2:C:303:ARG:NH1	2:C:310:GLU:HA	2.30	0.46
1:A:146:ASP:OD2	1:A:146:ASP:O	2.33	0.46
2:C:255:PHE:CE2	2:C:332:VAL:HG22	2.50	0.46
2:C:304:LYS:C	2:C:306:GLY:H	2.18	0.46
2:C:41:LEU:HD11	2:C:178:PRO:HG3	1.98	0.46
1:A:194:ILE:HD12	1:A:464:LYS:HG3	1.97	0.46
2:C:374:LEU:O	2:C:378:LEU:HB2	2.16	0.46
1:A:49:ASN:HB2	1:A:131:LEU:HD13	1.97	0.46
1:A:338:ARG:HB3	1:A:340:VAL:HG13	1.98	0.46
1:A:229:TYR:O	1:A:342:ILE:HB	2.15	0.46
2:C:263:TYR:CZ	2:C:378:LEU:HD21	2.50	0.46
2:C:455:LEU:CD1	2:C:518:LEU:HD11	2.46	0.46
1:A:24:ILE:HD13	1:A:24:ILE:N	2.29	0.45
2:C:611:LEU:C	2:C:611:LEU:CD1	2.81	0.45
1:A:33:ILE:CG1	1:A:345:ILE:HG12	2.44	0.45
2:C:526:MET:C	2:C:528:PRO:HD2	2.36	0.45
2:C:623:GLY:O	2:C:629:ARG:NH2	2.38	0.45
1:A:86:VAL:O	1:A:90:GLN:HG3	2.16	0.45
2:C:75:THR:HB	2:C:175:THR:CB	2.43	0.45
2:C:242:LEU:CD2	2:C:423:ASN:HD22	2.30	0.45
2:C:25:VAL:HB	2:C:32:TYR:CZ	2.51	0.45
2:C:523:TYR:OH	2:C:615:GLU:HB2	2.16	0.45
2:C:265:ASP:HB2	2:C:421:SER:CB	2.47	0.45
2:C:100:THR:O	2:C:102:LEU:HD13	2.17	0.45
1:A:187:ILE:HG12	1:A:467:LEU:HD22	1.99	0.45
2:C:334:GLU:HA	2:C:337:LEU:HB2	1.98	0.45
1:A:44:ILE:HG21	1:A:88:MET:HE3	1.99	0.45
1:A:82:TYR:CD1	1:A:116:MET:HB3	2.51	0.45
2:C:307:LEU:N	2:C:307:LEU:HD13	2.32	0.45
2:C:509:THR:O	2:C:512:ALA:HB3	2.16	0.44
1:A:296:LEU:C	1:A:296:LEU:HD23	2.38	0.44
1:A:42:ARG:NE	1:A:154:VAL:HA	2.32	0.44
1:A:194:ILE:HG21	1:A:464:LYS:HD2	2.00	0.44
1:A:45:LEU:HD22	1:A:123:LEU:HD22	1.98	0.44
1:A:415:GLN:O	1:A:419:ILE:HG13	2.18	0.44
1:A:169:GLY:HA3	1:A:176:THR:O	2.18	0.44
3:E:13[A]:DA:H2''	3:E:14[A]:DA:O5'	2.17	0.44
2:C:108:PHE:CD1	2:C:276:ASN:CB	2.69	0.44
2:C:30:GLY:HA2	2:C:35:SER:H	1.83	0.44
1:A:132:GLN:O	1:A:133:ASP:HB2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:144:ASN:HD21	1:A:148:THR:CG2	2.14	0.43
2:C:26:ARG:HD2	2:C:129:ALA:O	2.18	0.43
2:C:352:ALA:HA	2:C:355:VAL:HG22	2.00	0.43
1:A:326:ASN:CG	4:F:11[A]:DG:H4'	2.39	0.43
1:A:43:ARG:HG2	1:A:73:PHE:HB3	2.01	0.43
2:C:203:LEU:HD21	2:C:274:PHE:CG	2.53	0.43
1:A:29:ALA:O	1:A:38:LYS:HE2	2.19	0.43
2:C:388:ALA:HA	2:C:391:ALA:HB3	2.00	0.43
2:C:285:THR:OG1	2:C:352:ALA:HB3	2.18	0.43
2:C:298:MET:SD	2:C:368:LEU:HD21	2.58	0.43
2:C:431:LEU:CD2	2:C:479:MET:CE	2.96	0.43
1:A:55:PHE:HA	1:A:122:ARG:HD2	2.00	0.43
2:C:524:ARG:CB	2:C:524:ARG:HH11	2.32	0.43
2:C:341:GLY:O	2:C:343:THR:N	2.44	0.43
6:H:10[B]:DC:H2''	6:H:11[B]:DG:C5'	2.40	0.43
1:A:169:GLY:CA	1:A:176:THR:CG2	2.95	0.43
2:C:283:GLY:HA2	2:C:287:GLU:OE1	2.19	0.42
2:C:328:LEU:HD22	2:C:329:SER:N	2.34	0.42
1:A:423:GLN:NE2	1:A:425:TYR:HE1	2.17	0.42
5:G:13[B]:DC:H2''	5:G:14[B]:DA:O5'	2.19	0.42
1:A:191:VAL:HG22	1:A:464:LYS:HG2	2.00	0.42
1:A:194:ILE:CG2	1:A:464:LYS:HD2	2.49	0.42
2:C:639:PHE:O	2:C:640:THR:CB	2.67	0.42
1:A:312:LEU:HD12	1:A:312:LEU:HA	1.80	0.42
1:A:375:VAL:O	1:A:379:ILE:HG13	2.19	0.42
1:A:184:ALA:HB2	1:A:471:LYS:HG3	2.00	0.42
2:C:197:LEU:HA	2:C:197:LEU:HD23	1.87	0.42
2:C:37:ASP:HA	2:C:38:GLY:HA2	1.71	0.42
1:A:414:GLU:CD	1:A:414:GLU:H	2.22	0.42
2:C:536:TYR:N	2:C:536:TYR:CD2	2.87	0.42
1:A:191:VAL:HG11	1:A:468:ARG:NH2	2.35	0.42
1:A:346:LEU:HD23	1:A:346:LEU:HA	1.84	0.42
2:C:431:LEU:HD11	2:C:501:ILE:HG22	2.02	0.42
2:C:297:VAL:HG11	2:C:364:LEU:HD11	2.01	0.42
4:F:6[A]:DT:H2''	4:F:7[A]:DT:H5'	2.02	0.42
1:A:146:ASP:OD2	1:A:148:THR:HB	2.20	0.42
2:C:380:ARG:CD	2:C:495:ASP:HA	2.49	0.42
1:A:184:ALA:CB	1:A:471:LYS:HG3	2.50	0.42
2:C:297:VAL:HG11	2:C:364:LEU:CD1	2.50	0.42
2:C:441:ALA:O	2:C:445:ARG:HB3	2.20	0.42
1:A:13:MET:CE	2:C:618:VAL:HA	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:280:LYS:HB3	1:A:280:LYS:HE3	1.79	0.42
1:A:385:LEU:HA	1:A:385:LEU:HD23	1.86	0.41
2:C:102:LEU:HB2	2:C:103:HIS:H	1.71	0.41
2:C:601:ARG:CZ	2:C:603:LEU:HD11	2.50	0.41
1:A:23:TYR:CD1	1:A:24:ILE:HD13	2.52	0.41
2:C:99:PHE:CD1	2:C:99:PHE:C	2.93	0.41
2:C:96:GLU:O	2:C:99:PHE:HB3	2.19	0.41
2:C:485:ALA:HB3	2:C:491:PHE:CE2	2.56	0.41
1:A:334:ASN:O	1:A:336:THR:CG2	2.69	0.41
2:C:145:TYR:HA	2:C:160:LYS:O	2.19	0.41
1:A:357:ILE:CB	1:A:459:MET:CG	2.99	0.41
1:A:169:GLY:HA2	1:A:176:THR:CG2	2.46	0.41
2:C:165:ALA:HA	2:C:166:PRO:HD3	1.90	0.41
1:A:244:ILE:CD1	1:A:244:ILE:N	2.79	0.41
2:C:446:ASP:OD1	2:C:449:PHE:HE1	2.00	0.41
2:C:74:LEU:HB2	2:C:188:PHE:CE2	2.55	0.41
1:A:184:ALA:HA	1:A:471:LYS:CD	2.50	0.41
2:C:523:TYR:HH	2:C:615:GLU:HB2	1.86	0.41
1:A:321:LEU:HD23	1:A:321:LEU:HA	1.89	0.41
2:C:220:ILE:HG22	2:C:221:GLU:H	1.86	0.41
1:A:44:ILE:HD12	1:A:88:MET:HE3	1.99	0.41
2:C:337:LEU:HD23	2:C:337:LEU:HA	1.81	0.41
1:A:27:ASP:HA	1:A:39:PRO:HG2	2.03	0.41
2:C:627:GLU:N	2:C:628:PRO:CD	2.84	0.41
1:A:340:VAL:HB	1:A:345:ILE:HG13	1.85	0.41
2:C:147:GLN:HB2	2:C:159:LEU:HA	2.03	0.41
1:A:29:ALA:HB3	1:A:171:SER:HB3	2.02	0.40
3:E:9[A]:DC:C2'	3:E:10[A]:DA:H5''	2.48	0.40
1:A:28:ARG:CG	1:A:28:ARG:NH1	2.64	0.40
2:C:383:ILE:HG13	2:C:383:ILE:H	1.62	0.40
2:C:520:THR:CG2	2:C:622:MET:HG3	2.44	0.40
2:C:41:LEU:O	2:C:44:LEU:HD12	2.21	0.40
2:C:340:GLU:HB3	2:C:341:GLY:H	1.50	0.40
1:A:254:ILE:HD13	1:A:312:LEU:HD13	2.04	0.40
2:C:235:LEU:HA	2:C:235:LEU:HD12	1.88	0.40
1:A:13:MET:O	2:C:621:LEU:HD13	2.21	0.40
2:C:236:ASN:ND2	2:C:264:ASN:HD22	2.20	0.40
2:C:283:GLY:O	2:C:286:HIS:HE1	2.04	0.40
2:C:236:ASN:HD21	2:C:264:ASN:HD22	1.69	0.40
1:A:9:LEU:O	1:A:9:LEU:CD2	2.69	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	468/496 (94%)	443 (95%)	20 (4%)	5 (1%)	17	63
2	C	524/670 (78%)	455 (87%)	56 (11%)	13 (2%)	7	46
All	All	992/1166 (85%)	898 (90%)	76 (8%)	18 (2%)	11	53

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	305	THR
2	C	373	GLU
1	A	145	PHE
1	A	329	MET
2	C	105	GLY
2	C	122	VAL
2	C	304	LYS
2	C	340	GLU
2	C	496	ALA
2	C	107	LYS
2	C	151	ASN
2	C	374	LEU
1	A	169	GLY
2	C	132	SER
1	A	217	ALA
1	A	221	GLY
2	C	121	GLY
2	C	166	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	
1	A	377/431 (88%)	348 (92%)	29 (8%)	16	52
2	C	313/558 (56%)	252 (80%)	61 (20%)	2	12
All	All	690/989 (70%)	600 (87%)	90 (13%)	5	28

All (90) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	LEU
1	A	28	ARG
1	A	58	SER
1	A	60	ARG
1	A	91	ASN
1	A	102	HIS
1	A	111	ASP
1	A	126	ILE
1	A	148	THR
1	A	162	LEU
1	A	168	THR
1	A	208	LEU
1	A	223	ASP
1	A	236	VAL
1	A	268	LEU
1	A	279	ASN
1	A	293	ARG
1	A	308	THR
1	A	321	LEU
1	A	328	ASN
1	A	336	THR
1	A	338	ARG
1	A	366	GLU
1	A	372	LEU
1	A	380	ARG
1	A	414	GLU
1	A	420	VAL
1	A	432	VAL
1	A	462	LEU
2	C	25	VAL
2	C	26	ARG
2	C	33	ILE
2	C	43	HIS

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Mol	Chain	Res	Type
2	C	44	LEU
2	C	45	VAL
2	C	46	TRP
2	C	48	ILE
2	C	49	VAL
2	C	75	THR
2	C	99	PHE
2	C	100	THR
2	C	102	LEU
2	C	108	PHE
2	C	122	VAL
2	C	139	THR
2	C	148	ARG
2	C	158	THR
2	C	182	ILE
2	C	203	LEU
2	C	204	LEU
2	C	208	THR
2	C	209	LEU
2	C	211	LEU
2	C	220	ILE
2	C	231	PHE
2	C	235	LEU
2	C	242	LEU
2	C	245	VAL
2	C	253	ASN
2	C	259	VAL
2	C	275	VAL
2	C	278	VAL
2	C	286	HIS
2	C	288	THR
2	C	298	MET
2	C	299	ASN
2	C	307	LEU
2	C	324	LEU
2	C	328	LEU
2	C	331	LEU
2	C	337	LEU
2	C	340	GLU
2	C	351	LEU
2	C	363	LYS
2	C	364	LEU

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Mol	Chain	Res	Type
2	C	365	THR
2	C	368	LEU
2	C	378	LEU
2	C	429	LEU
2	C	431	LEU
2	C	445	ARG
2	C	453	LEU
2	C	477	ASN
2	C	509	THR
2	C	516	THR
2	C	520	THR
2	C	524	ARG
2	C	536	TYR
2	C	591	LEU
2	C	595	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	41	GLN
1	A	91	ASN
1	A	267	ASN
1	A	328	ASN
1	A	423	GLN
2	C	51	ASN
2	C	264	ASN
2	C	477	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
8	LFX	F	101	7	21,29,29	1.57	2 (9%)	28,44,44	1.82	9 (32%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	LFX	F	101	7	-	0/4/27/27	0/3/4/4

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	F	101	LFX	C13-C11	2.21	1.37	1.35
8	F	101	LFX	C15-C10	6.60	1.50	1.41

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	F	101	LFX	C17-C15-C10	-5.44	112.63	121.87
8	F	101	LFX	O01-C06-C04	-2.43	115.37	118.03
8	F	101	LFX	F-C11-C04	-2.41	114.99	118.32
8	F	101	LFX	C06-C04-C11	-2.02	113.89	115.92
8	F	101	LFX	C14-C03-C09	-2.00	105.16	113.04
8	F	101	LFX	C06-C05-C10	2.39	122.73	118.46
8	F	101	LFX	C02-N01-C01	2.39	116.62	111.59
8	F	101	LFX	C13-C11-C04	2.40	126.67	123.29
8	F	101	LFX	C15-C10-C05	3.16	122.53	119.76

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	F	101	LFX	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	479/496 (96%)	0.40	38 (7%) 15 19	37, 120, 215, 273	0
2	C	546/670 (81%)	1.05	124 (22%) 1 6	62, 212, 491, 533	0
3	E	7/11 (63%)	0.81	0 100 100	54, 61, 129, 144	7 (100%)
4	F	11/15 (73%)	1.02	1 (9%) 11 16	55, 92, 113, 136	11 (100%)
5	G	7/11 (63%)	0.78	0 100 100	53, 59, 129, 144	7 (100%)
6	H	11/15 (73%)	1.00	2 (18%) 2 7	56, 95, 113, 134	11 (100%)
All	All	1061/1218 (87%)	0.75	165 (15%) 3 8	37, 161, 464, 533	36 (3%)

All (165) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	100	THR	17.6
2	C	101	ILE	13.2
2	C	99	PHE	11.3
2	C	164	THR	9.3
1	A	249	GLY	8.5
2	C	125	SER	8.4
2	C	102	LEU	7.7
2	C	124	SER	7.6
2	C	181	THR	7.4
2	C	76	VAL	6.9
2	C	180	ALA	6.5
2	C	276	ASN	6.1
2	C	103	HIS	6.0
2	C	157	THR	6.0
2	C	45	VAL	5.7
2	C	166	PRO	5.7
2	C	123	GLY	5.5
1	A	158	ALA	5.5
2	C	272	LEU	5.5

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Mol	Chain	Res	Type	RSRZ
2	C	163	GLY	5.4
2	C	126	VAL	5.4
2	C	96	GLU	5.3
2	C	66	VAL	5.1
2	C	48	ILE	5.1
2	C	39	ALA	5.1
2	C	38	GLY	5.0
2	C	165	ALA	4.8
2	C	173	LYS	4.7
2	C	42	HIS	4.6
2	C	107	LYS	4.6
2	C	174	VAL	4.5
2	C	271	ILE	4.5
2	C	185	THR	4.5
2	C	556	ALA	4.3
2	C	184	SER	4.2
1	A	159	PHE	4.2
2	C	40	GLY	4.2
2	C	172	THR	4.2
1	A	294	ASP	4.2
2	C	187	ASP	4.1
2	C	183	PHE	4.0
2	C	179	ASP	4.0
2	C	94	THR	4.0
2	C	28	ARG	3.9
2	C	209	LEU	3.9
2	C	78	ASP	3.8
2	C	41	LEU	3.8
2	C	127	VAL	3.8
2	C	64	ILE	3.8
2	C	44	LEU	3.8
2	C	326	ALA	3.8
2	C	147	GLN	3.6
2	C	182	ILE	3.6
2	C	137	GLU	3.6
2	C	27	LYS	3.6
1	A	476	THR	3.5
2	C	121	GLY	3.5
1	A	172	ALA	3.5
2	C	37	ASP	3.4
1	A	17	PHE	3.4
2	C	505	THR	3.4

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Mol	Chain	Res	Type	RSRZ
2	C	210	SER	3.4
2	C	206	ASN	3.3
2	C	458	LYS	3.3
2	C	459	VAL	3.3
1	A	160	PRO	3.3
2	C	246	LEU	3.3
2	C	65	ASP	3.2
2	C	327	VAL	3.2
1	A	427	LEU	3.2
2	C	108	PHE	3.2
2	C	43	HIS	3.1
1	A	211	PRO	3.1
2	C	261	LEU	3.1
2	C	98	ILE	3.1
2	C	49	VAL	3.1
2	C	74	LEU	3.0
2	C	25	VAL	3.0
2	C	24	ALA	3.0
2	C	618	VAL	3.0
2	C	186	THR	3.0
2	C	342	GLN	3.0
2	C	136	VAL	3.0
2	C	77	GLN	3.0
2	C	503	ILE	3.0
1	A	225	ILE	2.9
2	C	577	LEU	2.9
2	C	267	PHE	2.9
2	C	225	GLU	2.9
1	A	261	TYR	2.9
2	C	51	ASN	2.9
2	C	290	LEU	2.9
1	A	13	MET	2.8
1	A	229	TYR	2.8
2	C	122	VAL	2.8
2	C	188	PHE	2.8
2	C	268	SER	2.8
1	A	250	GLY	2.8
2	C	270	ASN	2.8
1	A	174	TYR	2.7
1	A	295	GLY	2.7
1	A	260	PRO	2.7
1	A	325	TYR	2.7

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Mol	Chain	Res	Type	RSRZ
2	C	266	GLY	2.7
2	C	441	ALA	2.7
2	C	178	PRO	2.7
2	C	97	VAL	2.7
2	C	544	LYS	2.6
1	A	171	SER	2.6
1	A	239	ARG	2.6
1	A	155	LEU	2.6
2	C	538	ALA	2.6
1	A	470	VAL	2.5
2	C	504	MET	2.5
2	C	32	TYR	2.5
4	F	1[A]	DA	2.5
2	C	75	THR	2.5
1	A	477	PRO	2.5
2	C	621	LEU	2.5
2	C	282	ASP	2.5
2	C	192	THR	2.5
2	C	130	LEU	2.4
2	C	95	VAL	2.4
2	C	120	HIS	2.4
2	C	167	LYS	2.4
2	C	585	GLU	2.4
1	A	220	GLN	2.4
1	A	157	ALA	2.3
2	C	170	THR	2.3
1	A	238	VAL	2.3
1	A	331	ALA	2.3
1	A	173	GLY	2.3
2	C	433	GLU	2.3
2	C	47	GLU	2.3
2	C	36	THR	2.3
2	C	221	GLU	2.3
6	H	3[B]	DC	2.3
6	H	2[B]	DA	2.3
2	C	265	ASP	2.2
2	C	582	GLY	2.2
2	C	287	GLU	2.2
2	C	457	GLY	2.2
2	C	244	PRO	2.2
2	C	364	LEU	2.2
2	C	79	HIS	2.2

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Mol	Chain	Res	Type	RSRZ
2	C	129	ALA	2.2
1	A	112	PRO	2.1
2	C	128	ASN	2.1
1	A	262	GLU	2.1
2	C	540	PRO	2.1
2	C	29	PRO	2.1
2	C	537	ILE	2.1
2	C	104	ALA	2.1
1	A	110	GLY	2.1
2	C	277	ASN	2.1
2	C	119	LEU	2.1
1	A	424	LEU	2.1
2	C	294	ILE	2.1
2	C	275	VAL	2.0
1	A	161	ASN	2.0
2	C	431	LEU	2.0
1	A	263	ILE	2.0
1	A	389	ILE	2.0
1	A	210	GLY	2.0
1	A	388	VAL	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 carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
7	MG	C	701	1/1	0.85	0.75	1.98	71,71,71,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
8	LFX	F	101	26/26	0.94	0.35	-0.84	63,89,142,148	0
7	MG	A	501	1/1	0.95	0.29	-1.30	64,64,64,64	0

6.5 Other polymers [i](#)

There are no such residues in this entry.