



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 11:54 AM UTC

PDB ID : 2Y7W / pdb_00002y7w
Title : DntR Inducer Binding Domain
Authors : Devesse, L.; Smirnova, I.; Lonneborg, R.; Kapp, U.; Brzezinski, P.; Leonard, G.A.; Dian, C.
Deposited on : 2011-02-02
Resolution : 2.89 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
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

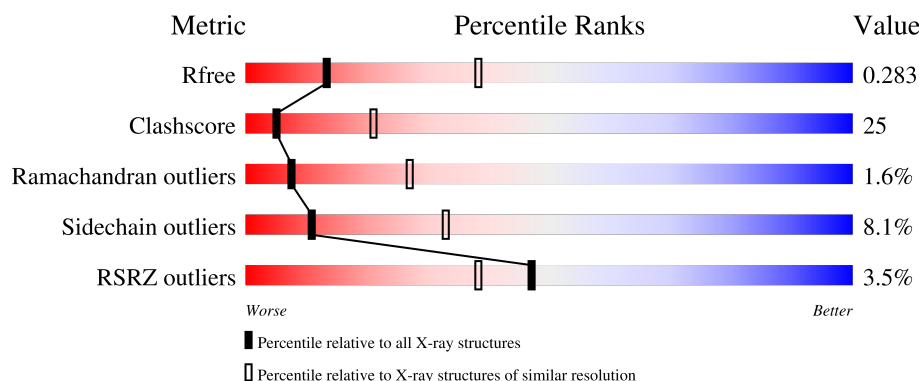
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.89 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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	228	3% 61% 25% 5% 9%
1	B	228	4% 52% 33% 5% 9%
1	C	228	% 52% 35% 9%
1	D	228	5% 53% 32% 7% 8%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6502 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called LYSR-TYPE REGULATORY PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	207	Total	C	N	O	S	0	0	0
			1585	1032	271	271	11			
1	B	207	Total	C	N	O	S	0	0	0
			1596	1036	280	269	11			
1	C	207	Total	C	N	O	S	0	0	0
			1601	1042	280	268	11			
1	D	210	Total	C	N	O	S	0	0	0
			1598	1036	276	275	11			

There are 28 discrepancies between the modelled and reference sequences:

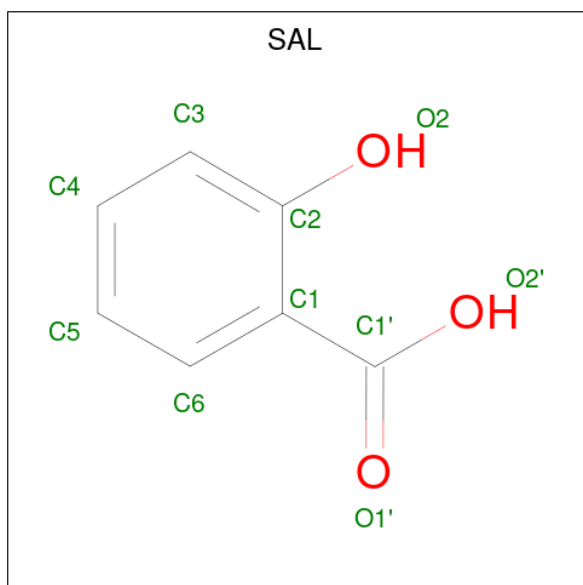
Chain	Residue	Modelled	Actual	Comment	Reference
A	80	MET	LEU	engineered mutation	UNP Q7WT50
A	302	HIS	-	expression tag	UNP Q7WT50
A	303	HIS	-	expression tag	UNP Q7WT50
A	304	HIS	-	expression tag	UNP Q7WT50
A	305	HIS	-	expression tag	UNP Q7WT50
A	306	HIS	-	expression tag	UNP Q7WT50
A	307	HIS	-	expression tag	UNP Q7WT50
B	80	MET	LEU	engineered mutation	UNP Q7WT50
B	302	HIS	-	expression tag	UNP Q7WT50
B	303	HIS	-	expression tag	UNP Q7WT50
B	304	HIS	-	expression tag	UNP Q7WT50
B	305	HIS	-	expression tag	UNP Q7WT50
B	306	HIS	-	expression tag	UNP Q7WT50
B	307	HIS	-	expression tag	UNP Q7WT50
C	80	MET	LEU	engineered mutation	UNP Q7WT50
C	302	HIS	-	expression tag	UNP Q7WT50
C	303	HIS	-	expression tag	UNP Q7WT50
C	304	HIS	-	expression tag	UNP Q7WT50
C	305	HIS	-	expression tag	UNP Q7WT50
C	306	HIS	-	expression tag	UNP Q7WT50
C	307	HIS	-	expression tag	UNP Q7WT50

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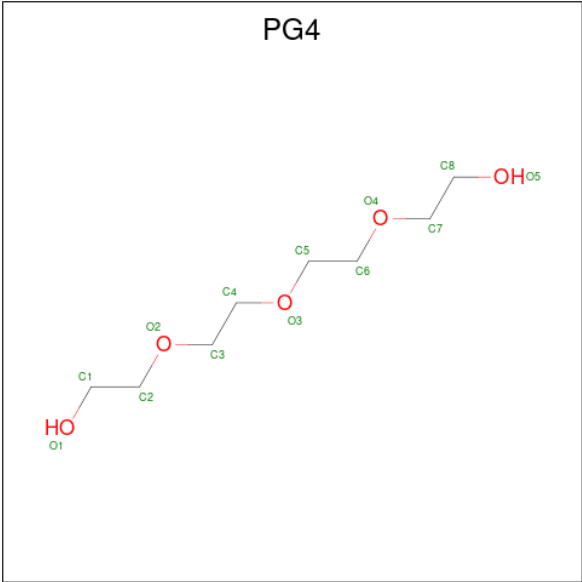
Chain	Residue	Modelled	Actual	Comment	Reference
D	80	MET	LEU	engineered mutation	UNP Q7WT50
D	302	HIS	-	expression tag	UNP Q7WT50
D	303	HIS	-	expression tag	UNP Q7WT50
D	304	HIS	-	expression tag	UNP Q7WT50
D	305	HIS	-	expression tag	UNP Q7WT50
D	306	HIS	-	expression tag	UNP Q7WT50
D	307	HIS	-	expression tag	UNP Q7WT50

- Molecule 2 is 2-HYDROXYBENZOIC ACID (CCD ID: SAL) (formula: $C_7H_6O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			10	7	3		
2	B	1	Total	C	O	0	0
			10	7	3		
2	C	1	Total	C	O	0	0
			10	7	3		

- Molecule 3 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: $C_8H_{18}O_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			13	8	5		
3	A	1	Total	C	O	0	0
			13	8	5		
3	B	1	Total	C	O	0	0
			13	8	5		

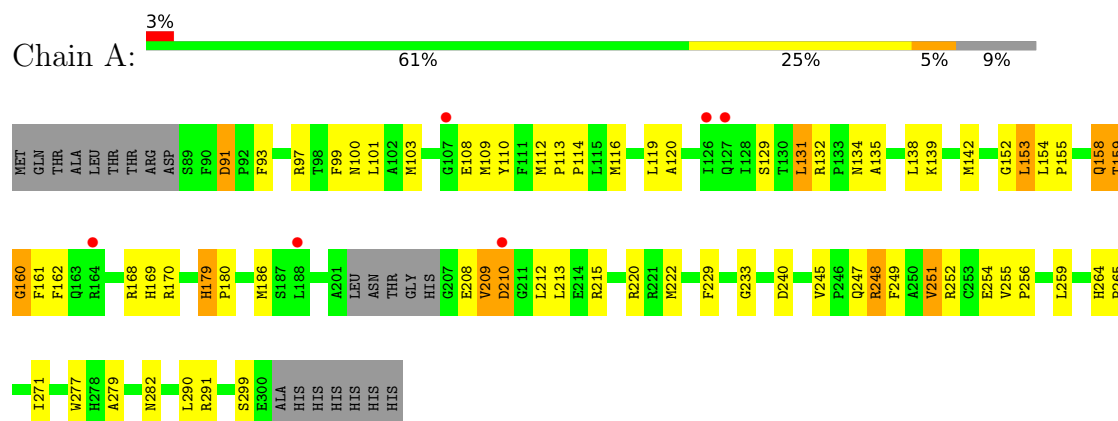
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	12	Total	O	0	0
			12	12		
4	B	14	Total	O	0	0
			14	14		
4	C	13	Total	O	0	0
			13	13		
4	D	14	Total	O	0	0
			14	14		

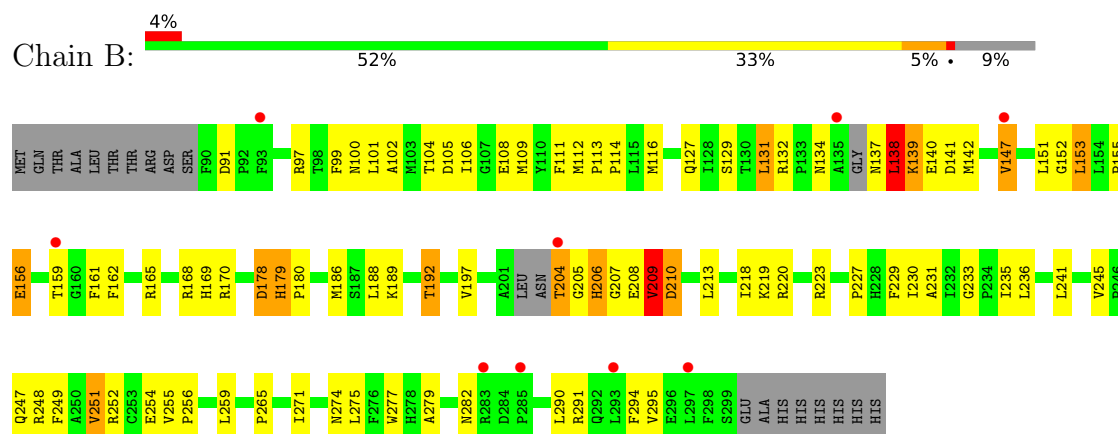
3 Residue-property plots [i](#)

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

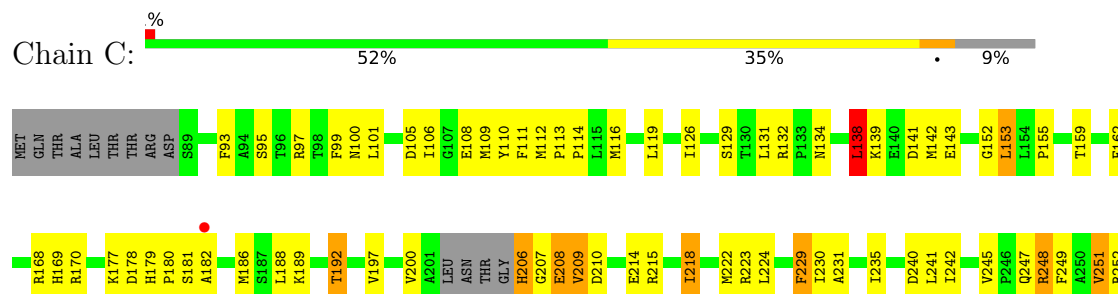
• Molecule 1: LYSR-TYPE REGULATORY PROTEIN



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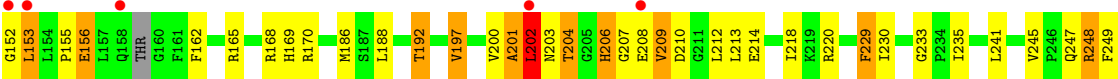
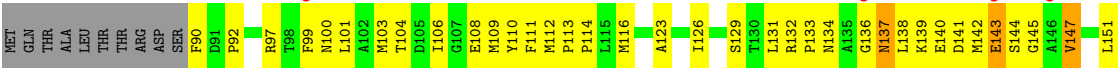


• Molecule 1: LYSR-TYPE REGULATORY PROTEIN





● Molecule 1: LYSR-TYPE REGULATORY PROTEIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	54.19Å 118.96Å 80.56Å 90.00° 108.63° 90.00°	Depositor
Resolution (Å)	47.14 – 2.89 47.14 – 2.89	Depositor EDS
% Data completeness (in resolution range)	93.7 (47.14-2.89) 94.0 (47.14-2.89)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.84 (at 2.91Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE: 1.4_94)	Depositor
R, R_{free}	0.242 , 0.287 0.238 , 0.283	Depositor DCC
R_{free} test set	1057 reflections (5.17%)	wwPDB-VP
Wilson B-factor (Å ²)	41.8	Xtriage
Anisotropy	0.282	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 64.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.037 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	6502	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 13.03% 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 ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: SAL, PG4

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	0.63	0/1629	1.05	9/2215 (0.4%)
1	B	0.63	0/1639	1.03	8/2227 (0.4%)
1	C	0.64	0/1646	0.98	4/2237 (0.2%)
1	D	0.61	0/1642	1.00	6/2238 (0.3%)
All	All	0.63	0/6556	1.02	27/8917 (0.3%)

There are no bond length outliers.

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	179	HIS	CA-C-N	8.08	128.84	119.47
1	B	179	HIS	C-N-CA	8.08	128.84	119.47
1	A	91	ASP	CA-C-N	7.82	127.37	118.85
1	A	91	ASP	C-N-CA	7.82	127.37	118.85
1	D	143	GLU	N-CA-C	-6.97	101.34	110.33
1	B	233	GLY	CA-C-N	6.95	126.20	118.97
1	B	233	GLY	C-N-CA	6.95	126.20	118.97
1	A	229	PHE	N-CA-C	6.24	120.90	113.16
1	C	229	PHE	N-CA-C	6.00	120.60	113.16
1	D	152	GLY	N-CA-C	5.79	117.98	110.45
1	C	152	GLY	N-CA-C	5.71	118.29	110.58
1	D	233	GLY	CA-C-N	5.67	125.14	119.24
1	D	233	GLY	C-N-CA	5.67	125.14	119.24
1	B	208	GLU	N-CA-C	-5.62	106.00	112.86
1	A	233	GLY	CA-C-N	5.62	125.08	119.24
1	A	233	GLY	C-N-CA	5.62	125.08	119.24
1	C	218	ILE	CB-CA-C	-5.62	105.84	111.80
1	B	152	GLY	N-CA-C	5.56	117.68	110.45
1	A	152	GLY	N-CA-C	5.50	118.01	110.58
1	D	229	PHE	N-CA-C	5.42	119.90	113.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	179	HIS	CA-C-N	5.35	126.53	119.84
1	A	179	HIS	C-N-CA	5.35	126.53	119.84
1	A	158	GLN	N-CA-C	-5.21	101.78	109.18
1	D	218	ILE	CB-CA-C	-5.14	106.36	111.80
1	C	138	LEU	N-CA-C	5.07	118.24	111.75
1	B	91	ASP	CA-C-N	5.03	125.06	119.32
1	B	91	ASP	C-N-CA	5.03	125.06	119.32

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1585	0	1542	70	0
1	B	1596	0	1561	78	0
1	C	1601	0	1572	92	0
1	D	1598	0	1538	77	0
2	A	10	0	4	0	0
2	B	10	0	4	0	0
2	C	10	0	4	3	0
3	A	26	0	36	9	0
3	B	13	0	18	3	0
4	A	12	0	0	0	0
4	B	14	0	0	0	0
4	C	13	0	0	1	0
4	D	14	0	0	2	0
All	All	6502	0	6279	316	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 25.

All (316) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:206:HIS:CB	1:C:207:GLY:HA3	1.72	1.20
1:C:206:HIS:HB2	1:C:207:GLY:CA	1.77	1.13
1:A:210:ASP:HB3	3:A:1301:PG4:H32	1.25	1.11
1:A:159:THR:HG23	1:A:160:GLY:H	1.11	1.07
1:C:179:HIS:HE1	1:C:240:ASP:O	1.43	1.01
1:C:223:ARG:HG3	1:C:223:ARG:HH11	1.26	0.98
1:D:201:ALA:HA	1:D:202:LEU:C	1.90	0.95
1:A:159:THR:HG23	1:A:160:GLY:N	1.80	0.93
1:D:206:HIS:ND1	1:D:207:GLY:HA3	1.83	0.93
1:D:104:THR:HG21	1:D:204:THR:HG21	1.52	0.91
1:A:251:VAL:HG12	1:A:252:ARG:HD3	1.51	0.90
1:D:251:VAL:HG12	1:D:252:ARG:HD3	1.52	0.90
1:C:251:VAL:HG12	1:C:252:ARG:HD3	1.52	0.90
1:A:113:PRO:HB2	1:A:114:PRO:HD3	1.54	0.89
1:B:206:HIS:HB3	1:B:207:GLY:HA3	1.52	0.89
1:C:138:LEU:HA	1:C:141:ASP:HB2	1.53	0.89
1:B:204:THR:HB	1:B:206:HIS:HD2	1.38	0.89
1:B:251:VAL:HG12	1:B:252:ARG:HD3	1.56	0.88
3:B:1301:PG4:H12	3:B:1301:PG4:H42	1.57	0.85
1:C:189:LYS:O	1:C:192:THR:HG23	1.78	0.83
1:C:113:PRO:HB2	1:C:114:PRO:HD3	1.60	0.83
1:C:111:PHE:CE2	2:C:1300:SAL:H5	2.14	0.83
1:B:206:HIS:CB	1:B:207:GLY:HA3	2.07	0.82
1:C:138:LEU:O	1:C:142:MET:HG3	1.80	0.82
1:B:189:LYS:O	1:B:192:THR:HG23	1.80	0.81
1:A:131:LEU:HD23	1:A:135:ALA:HB3	1.61	0.81
1:D:113:PRO:HB2	1:D:114:PRO:HD3	1.63	0.80
1:D:104:THR:CG2	1:D:204:THR:HG21	2.12	0.79
1:A:159:THR:CG2	1:A:160:GLY:H	1.95	0.79
1:D:206:HIS:CG	1:D:207:GLY:HA3	2.18	0.79
1:C:179:HIS:CE1	1:C:240:ASP:O	2.35	0.77
1:C:223:ARG:HG3	1:C:223:ARG:NH1	2.00	0.77
1:C:206:HIS:HB2	1:C:207:GLY:HA3	0.85	0.76
1:C:111:PHE:HE2	2:C:1300:SAL:H5	1.51	0.74
1:A:159:THR:O	1:A:161:PHE:N	2.19	0.74
1:A:208:GLU:O	1:A:212:LEU:HD12	1.88	0.73
1:A:277:TRP:CE3	1:A:291:ARG:HD3	2.24	0.72
1:C:109:MET:HE2	1:C:249:PHE:HD1	1.54	0.72
1:B:204:THR:HB	1:B:206:HIS:CD2	2.21	0.72
1:D:108:GLU:CD	1:D:132:ARG:HH12	1.97	0.72
1:A:159:THR:CG2	1:A:160:GLY:N	2.52	0.71
1:B:108:GLU:CD	1:B:132:ARG:HH12	1.99	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:109:MET:HE2	1:A:249:PHE:HD1	1.56	0.70
1:C:200:VAL:O	1:C:206:HIS:HB3	1.92	0.70
1:B:113:PRO:HB2	1:B:114:PRO:HD3	1.74	0.69
1:B:277:TRP:CE3	1:B:291:ARG:HD3	2.27	0.69
1:D:162:PHE:HE1	1:D:279:ALA:HA	1.56	0.69
1:A:158:GLN:O	1:A:159:THR:HG22	1.91	0.69
1:D:162:PHE:CE1	1:D:279:ALA:HA	2.26	0.69
1:A:162:PHE:CE2	1:A:279:ALA:HA	2.27	0.69
1:B:206:HIS:HB3	1:B:207:GLY:CA	2.22	0.68
1:B:165:ARG:HD3	1:B:274:ASN:OD1	1.94	0.68
1:C:138:LEU:HD13	1:C:139:LYS:H	1.57	0.68
1:C:162:PHE:CE1	1:C:279:ALA:HA	2.28	0.68
1:D:109:MET:HE2	1:D:249:PHE:HD1	1.59	0.68
1:C:197:VAL:HG12	1:C:224:LEU:HB3	1.77	0.67
1:A:162:PHE:HE2	1:A:279:ALA:HA	1.57	0.67
1:B:204:THR:O	1:B:206:HIS:HA	1.93	0.67
1:C:162:PHE:HE1	1:C:279:ALA:HA	1.59	0.67
1:B:138:LEU:O	1:B:140:GLU:N	2.27	0.67
1:B:162:PHE:HE1	1:B:279:ALA:HA	1.60	0.67
1:A:255:VAL:HB	1:A:256:PRO:HD3	1.77	0.66
1:A:97:ARG:HD3	1:A:99:PHE:CZ	2.31	0.66
1:D:201:ALA:HA	1:D:202:LEU:O	1.93	0.66
1:C:223:ARG:NH1	1:D:126:ILE:O	2.30	0.65
1:B:162:PHE:CE1	1:B:279:ALA:HA	2.31	0.65
1:C:188:LEU:O	1:C:192:THR:HG22	1.97	0.65
1:B:97:ARG:HD3	1:B:99:PHE:CZ	2.31	0.65
1:D:206:HIS:ND1	1:D:206:HIS:N	2.44	0.65
1:C:223:ARG:NH2	1:D:123:ALA:O	2.30	0.64
1:D:97:ARG:HD3	1:D:99:PHE:CZ	2.32	0.64
1:C:255:VAL:HB	1:C:256:PRO:HD3	1.80	0.64
1:B:109:MET:HE2	1:B:249:PHE:HD1	1.62	0.64
1:A:277:TRP:CZ3	1:A:291:ARG:HD3	2.33	0.63
1:C:277:TRP:CE3	1:C:291:ARG:HD3	2.33	0.63
1:A:108:GLU:CD	1:A:132:ARG:HH12	2.06	0.63
1:C:97:ARG:HD3	1:C:99:PHE:CZ	2.34	0.63
1:A:222:MET:O	1:B:127:GLN:HG3	1.99	0.62
1:D:144:SER:O	1:D:281:TYR:CE1	2.52	0.62
1:C:223:ARG:HH11	1:C:223:ARG:CG	2.07	0.62
1:C:108:GLU:CD	1:C:132:ARG:HH12	2.09	0.61
1:B:277:TRP:CZ3	1:B:291:ARG:HD3	2.35	0.61
1:D:155:PRO:HD2	1:D:156:GLU:OE2	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:255:VAL:HB	1:D:256:PRO:HD3	1.83	0.60
1:B:210:ASP:HB2	1:B:220:ARG:NH2	2.16	0.60
1:D:206:HIS:H	1:D:207:GLY:HA3	1.67	0.60
1:A:139:LYS:HG2	1:C:215:ARG:CZ	2.31	0.59
1:A:210:ASP:HB2	1:A:220:ARG:NH2	2.16	0.59
1:B:255:VAL:HB	1:B:256:PRO:HD3	1.85	0.59
1:A:179:HIS:NE2	1:A:240:ASP:O	2.31	0.59
1:C:116:MET:HA	1:C:116:MET:HE2	1.85	0.59
1:D:100:ASN:O	1:D:101:LEU:HD23	2.02	0.59
1:A:251:VAL:CG1	1:A:252:ARG:HD3	2.29	0.58
1:C:277:TRP:CZ3	1:C:291:ARG:HD3	2.39	0.58
1:C:138:LEU:HD13	1:C:139:LYS:N	2.19	0.58
3:A:1301:PG4:H62	3:A:1301:PG4:O2	2.02	0.58
1:D:116:MET:HE2	1:D:116:MET:HA	1.84	0.58
1:D:201:ALA:CA	1:D:202:LEU:C	2.73	0.57
1:A:113:PRO:HB2	1:A:114:PRO:CD	2.31	0.57
1:B:132:ARG:HB3	1:B:134:ASN:OD1	2.04	0.57
1:A:209:VAL:HG12	1:A:210:ASP:N	2.20	0.57
1:D:251:VAL:CG1	1:D:252:ARG:HD3	2.33	0.56
3:A:1301:PG4:H62	3:A:1301:PG4:C3	2.34	0.56
1:D:153:LEU:O	1:D:155:PRO:HD3	2.05	0.56
1:B:178:ASP:O	1:B:179:HIS:C	2.48	0.56
1:D:136:GLY:C	1:D:138:LEU:H	2.14	0.56
1:A:153:LEU:O	1:A:155:PRO:HD3	2.05	0.56
1:A:168:ARG:HA	1:A:271:ILE:O	2.06	0.56
3:A:1302:PG4:H72	3:A:1302:PG4:H21	1.88	0.56
1:A:116:MET:HE2	1:A:116:MET:HA	1.86	0.56
1:B:142:MET:HE3	1:B:147:VAL:HG22	1.87	0.56
1:B:188:LEU:O	1:B:192:THR:HG22	2.06	0.56
1:D:209:VAL:HG12	1:D:210:ASP:N	2.19	0.56
1:C:111:PHE:O	1:C:114:PRO:HD2	2.07	0.55
1:C:177:LYS:HE3	1:C:258:GLY:HA2	1.87	0.55
1:C:206:HIS:N	1:C:206:HIS:CD2	2.74	0.55
1:D:200:VAL:O	1:D:202:LEU:HD12	2.07	0.55
1:B:179:HIS:CG	1:B:180:PRO:HD2	2.42	0.55
3:B:1301:PG4:H42	3:B:1301:PG4:C1	2.34	0.55
1:D:144:SER:O	1:D:281:TYR:OH	2.21	0.55
1:D:144:SER:O	1:D:281:TYR:HE1	1.88	0.55
1:C:179:HIS:HB3	1:C:182:ALA:HB3	1.87	0.55
1:B:213:LEU:HD12	1:B:220:ARG:CZ	2.37	0.55
1:D:197:VAL:HG12	1:D:241:LEU:HD13	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:116:MET:HE2	1:B:116:MET:HA	1.90	0.54
1:C:179:HIS:CD2	1:C:182:ALA:H	2.26	0.54
1:C:223:ARG:NH1	1:C:223:ARG:CG	2.66	0.54
1:A:120:ALA:HB2	1:B:223:ARG:HH22	1.72	0.54
1:C:251:VAL:CG1	1:C:252:ARG:HD3	2.32	0.54
1:B:205:GLY:HA3	1:B:206:HIS:O	2.07	0.54
1:B:168:ARG:HA	1:B:271:ILE:O	2.08	0.53
1:C:100:ASN:O	1:C:101:LEU:HD23	2.08	0.53
1:D:206:HIS:N	1:D:207:GLY:HA3	2.22	0.53
1:C:179:HIS:HD2	1:C:181:SER:H	1.56	0.53
1:A:220:ARG:HH12	3:A:1301:PG4:H11	1.74	0.53
1:C:153:LEU:O	1:C:155:PRO:HD3	2.08	0.53
1:D:168:ARG:HA	1:D:271:ILE:O	2.09	0.53
1:A:110:TYR:CE1	1:A:248:ARG:HG2	2.44	0.53
1:A:138:LEU:O	1:A:142:MET:HG3	2.09	0.53
1:B:100:ASN:O	1:B:101:LEU:HD23	2.08	0.53
1:B:138:LEU:HD23	1:B:139:LYS:N	2.24	0.52
1:A:120:ALA:HB2	1:B:223:ARG:NH2	2.24	0.52
1:C:110:TYR:CE1	1:C:248:ARG:HG2	2.44	0.52
1:C:111:PHE:CE2	2:C:1300:SAL:C5	2.90	0.52
1:C:168:ARG:HA	1:C:271:ILE:O	2.10	0.52
1:D:138:LEU:O	1:D:141:ASP:N	2.37	0.52
1:A:215:ARG:CZ	1:C:139:LYS:HG2	2.39	0.52
1:A:254:GLU:HG2	1:A:259:LEU:O	2.09	0.52
1:B:169:HIS:CD2	1:B:271:ILE:HB	2.45	0.52
1:A:100:ASN:OD1	1:A:129:SER:HB3	2.10	0.52
1:B:251:VAL:CG1	1:B:252:ARG:HD3	2.36	0.52
1:D:100:ASN:C	1:D:101:LEU:HD23	2.35	0.52
1:A:208:GLU:O	1:A:212:LEU:CD1	2.56	0.51
1:B:100:ASN:C	1:B:101:LEU:HD23	2.36	0.51
1:D:169:HIS:CD2	1:D:271:ILE:HB	2.46	0.51
1:A:100:ASN:C	1:A:101:LEU:HD23	2.36	0.51
1:C:200:VAL:O	1:C:206:HIS:CB	2.59	0.51
1:D:207:GLY:C	1:D:209:VAL:N	2.63	0.51
1:D:136:GLY:O	1:D:138:LEU:N	2.43	0.50
1:B:111:PHE:O	1:B:114:PRO:HD2	2.11	0.50
1:C:177:LYS:O	1:C:177:LYS:HG3	2.11	0.50
1:D:113:PRO:HB2	1:D:114:PRO:CD	2.39	0.50
1:B:134:ASN:OD1	1:B:134:ASN:N	2.39	0.50
1:D:213:LEU:HD12	1:D:220:ARG:CZ	2.42	0.50
1:B:209:VAL:HG12	1:B:210:ASP:N	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:100:ASN:C	1:C:101:LEU:HD23	2.37	0.50
1:A:213:LEU:HD12	1:A:220:ARG:CZ	2.41	0.50
1:A:112:MET:HB2	1:A:113:PRO:HD3	1.95	0.49
1:C:177:LYS:HB3	1:C:260:THR:HG23	1.94	0.49
1:D:100:ASN:OD1	1:D:129:SER:HB3	2.12	0.49
1:C:112:MET:HB2	1:C:113:PRO:HD3	1.93	0.49
1:C:179:HIS:CE1	1:C:240:ASP:HB3	2.46	0.49
1:C:254:GLU:HG2	1:C:259:LEU:O	2.12	0.49
1:D:200:VAL:HG12	1:D:202:LEU:O	2.12	0.49
1:A:220:ARG:HH22	3:A:1301:PG4:H22	1.77	0.49
1:C:105:ASP:HB2	1:D:230:ILE:HG21	1.94	0.49
1:A:100:ASN:O	1:A:101:LEU:HD23	2.12	0.49
1:D:111:PHE:O	1:D:114:PRO:HD2	2.12	0.49
1:C:153:LEU:HD21	4:C:2013:HOH:O	2.13	0.49
1:B:205:GLY:HA3	1:B:206:HIS:C	2.37	0.48
1:D:151:LEU:HD21	1:D:275:LEU:HD13	1.95	0.48
1:A:277:TRP:CD2	1:A:291:ARG:HD3	2.48	0.48
1:B:197:VAL:HG21	1:B:235:ILE:HG21	1.94	0.48
1:A:169:HIS:CD2	1:A:271:ILE:HB	2.49	0.48
1:C:109:MET:HE2	1:C:249:PHE:CD1	2.43	0.48
1:C:197:VAL:HG11	1:C:235:ILE:HG21	1.94	0.48
1:C:282:ASN:O	1:C:291:ARG:NH2	2.44	0.48
1:B:153:LEU:O	1:B:155:PRO:HD3	2.14	0.47
1:B:104:THR:HG21	1:B:204:THR:HG21	1.97	0.47
1:B:165:ARG:HG2	1:B:165:ARG:HH11	1.78	0.47
1:C:169:HIS:CD2	1:C:271:ILE:HB	2.49	0.47
1:C:179:HIS:CB	1:C:182:ALA:HB3	2.43	0.47
1:B:108:GLU:OE2	1:B:132:ARG:NH1	2.48	0.47
1:D:112:MET:HB2	1:D:113:PRO:HD3	1.97	0.47
1:D:155:PRO:CD	1:D:156:GLU:OE2	2.63	0.47
1:D:188:LEU:O	1:D:192:THR:HG23	2.15	0.47
1:D:142:MET:C	1:D:143:GLU:O	2.52	0.47
3:A:1302:PG4:H21	3:A:1302:PG4:H42	1.38	0.47
1:C:179:HIS:CD2	1:C:181:SER:H	2.32	0.47
1:C:209:VAL:HG12	1:C:210:ASP:N	2.29	0.47
1:D:142:MET:HE3	1:D:147:VAL:HG22	1.96	0.47
1:A:93:PHE:CD1	1:A:93:PHE:O	2.68	0.46
1:B:277:TRP:CD2	1:B:291:ARG:HD3	2.49	0.46
1:A:210:ASP:HB3	3:A:1301:PG4:C3	2.19	0.46
1:C:93:PHE:O	1:C:93:PHE:CD1	2.69	0.46
1:C:106:ILE:HD11	1:C:229:PHE:CE1	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:230:ILE:HG23	1:C:231:ALA:N	2.30	0.46
1:A:282:ASN:O	1:A:291:ARG:NH2	2.45	0.46
1:B:112:MET:HB2	1:B:113:PRO:HD3	1.96	0.46
1:C:298:PHE:O	1:C:299:SER:CB	2.64	0.46
1:D:162:PHE:HE1	1:D:279:ALA:CA	2.26	0.46
1:C:186:MET:O	1:C:265:PRO:HG3	2.15	0.46
1:C:188:LEU:HD21	1:C:218:ILE:HD11	1.98	0.46
1:D:208:GLU:O	1:D:212:LEU:HD12	2.15	0.46
3:B:1301:PG4:H52	3:B:1301:PG4:H71	1.59	0.46
1:C:138:LEU:CD1	1:C:138:LEU:N	2.78	0.46
1:C:179:HIS:HD2	1:C:182:ALA:H	1.63	0.46
1:C:197:VAL:HG13	1:C:241:LEU:HD13	1.98	0.45
1:A:112:MET:HE2	1:A:112:MET:HA	1.99	0.45
1:D:108:GLU:OE2	1:D:132:ARG:NH1	2.48	0.45
1:C:162:PHE:HE1	1:C:279:ALA:CA	2.27	0.45
1:D:109:MET:HE2	1:D:249:PHE:CD1	2.46	0.45
1:B:159:THR:H	1:B:161:PHE:HD2	1.65	0.45
1:C:138:LEU:HD12	1:C:138:LEU:H	1.81	0.45
1:A:170:ARG:O	1:A:247:GLN:HB2	2.17	0.45
1:D:186:MET:O	1:D:265:PRO:HG3	2.17	0.45
1:A:251:VAL:HG12	1:A:252:ARG:N	2.31	0.45
1:D:299:SER:O	1:D:300:GLU:HG2	2.17	0.45
1:D:197:VAL:HG11	1:D:235:ILE:HG21	1.98	0.45
1:D:202:LEU:HA	1:D:203:ASN:HA	1.41	0.45
1:D:201:ALA:CA	1:D:202:LEU:O	2.65	0.44
1:A:186:MET:O	1:A:265:PRO:HG3	2.17	0.44
1:B:100:ASN:OD1	1:B:129:SER:HB3	2.17	0.44
1:B:179:HIS:HA	1:B:180:PRO:HD3	1.79	0.44
1:C:170:ARG:O	1:C:247:GLN:HB2	2.17	0.44
1:C:179:HIS:CG	1:C:180:PRO:HD2	2.52	0.44
1:B:179:HIS:CD2	1:B:180:PRO:HD2	2.52	0.44
1:C:138:LEU:HA	1:C:141:ASP:CB	2.37	0.44
1:B:170:ARG:O	1:B:247:GLN:HB2	2.18	0.44
1:D:110:TYR:CE1	1:D:248:ARG:HG2	2.53	0.44
1:D:113:PRO:CB	1:D:114:PRO:HD3	2.41	0.44
1:C:100:ASN:OD1	1:C:129:SER:HB3	2.18	0.43
1:C:116:MET:HE1	1:C:119:LEU:HD12	2.00	0.43
1:B:165:ARG:HG2	1:B:165:ARG:NH1	2.33	0.43
1:C:210:ASP:O	1:C:214:GLU:HG3	2.18	0.43
1:B:290:LEU:HD12	1:B:290:LEU:HA	1.46	0.43
1:D:144:SER:O	1:D:281:TYR:CZ	2.71	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:290:LEU:HA	1:D:290:LEU:HD12	1.48	0.43
1:D:200:VAL:O	1:D:202:LEU:HB2	2.18	0.43
1:A:131:LEU:HA	1:B:227:PRO:HG3	2.01	0.43
1:C:177:LYS:HA	1:C:178:ASP:HA	1.55	0.43
3:A:1302:PG4:H42	3:A:1302:PG4:H62	1.30	0.43
1:D:265:PRO:HA	4:D:2006:HOH:O	2.18	0.43
1:A:179:HIS:HA	1:A:180:PRO:HD3	1.90	0.43
1:B:155:PRO:HD2	1:B:156:GLU:H	1.84	0.42
1:B:282:ASN:O	1:B:291:ARG:NH2	2.45	0.42
1:D:138:LEU:O	1:D:140:GLU:N	2.51	0.42
1:A:179:HIS:CG	1:A:180:PRO:HD2	2.53	0.42
1:B:138:LEU:HD23	1:B:139:LYS:H	1.84	0.42
1:B:151:LEU:HD21	1:B:275:LEU:HD13	2.02	0.42
1:B:230:ILE:HG23	1:B:231:ALA:N	2.33	0.42
1:C:207:GLY:O	1:C:208:GLU:CB	2.66	0.42
1:D:103:MET:HE1	1:D:112:MET:HE3	2.01	0.42
1:B:254:GLU:HG2	1:B:259:LEU:O	2.19	0.42
1:C:294:PHE:O	1:C:295:VAL:C	2.61	0.42
1:B:236:LEU:HD22	1:B:241:LEU:O	2.20	0.42
1:D:133:PRO:HD2	4:D:2003:HOH:O	2.19	0.42
1:A:108:GLU:OE2	1:A:132:ARG:NH1	2.53	0.42
1:C:113:PRO:HB2	1:C:114:PRO:CD	2.37	0.42
1:D:90:PHE:HE1	1:D:92:PRO:HG3	1.85	0.42
1:A:179:HIS:NE2	1:A:240:ASP:HB3	2.35	0.42
1:A:255:VAL:O	1:A:256:PRO:C	2.63	0.42
1:B:106:ILE:HD11	1:B:229:PHE:CE1	2.55	0.42
1:B:113:PRO:HB2	1:B:114:PRO:CD	2.48	0.42
1:B:138:LEU:O	1:B:141:ASP:N	2.40	0.42
1:A:264:HIS:HA	1:A:265:PRO:HD3	1.82	0.42
1:B:102:ALA:HA	1:B:131:LEU:O	2.20	0.42
1:C:206:HIS:CB	1:C:207:GLY:CA	2.58	0.42
1:D:255:VAL:O	1:D:256:PRO:C	2.62	0.42
1:B:186:MET:HE3	1:B:186:MET:HB2	1.87	0.41
1:A:109:MET:CE	1:A:249:PHE:HD1	2.30	0.41
1:A:154:LEU:HA	1:A:155:PRO:HD3	1.86	0.41
1:C:95:SER:HB3	1:C:126:ILE:HD11	2.03	0.41
1:C:222:MET:HE2	1:C:222:MET:HB2	1.89	0.41
1:D:170:ARG:O	1:D:247:GLN:HB2	2.21	0.41
1:C:255:VAL:O	1:C:256:PRO:C	2.62	0.41
1:D:294:PHE:O	1:D:295:VAL:C	2.64	0.41
1:A:116:MET:HE2	1:A:116:MET:CA	2.49	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:162:PHE:HE2	1:A:279:ALA:CA	2.28	0.41
1:B:116:MET:HE2	1:B:116:MET:CA	2.51	0.41
1:B:186:MET:O	1:B:265:PRO:HG3	2.21	0.41
1:A:251:VAL:HG12	1:A:252:ARG:CD	2.37	0.41
1:C:179:HIS:CD2	1:C:180:PRO:HD2	2.56	0.41
1:A:113:PRO:CB	1:A:114:PRO:HD3	2.36	0.41
1:A:116:MET:HE1	1:A:119:LEU:HD12	2.03	0.41
1:A:210:ASP:HB2	1:A:220:ARG:HH22	1.86	0.41
1:B:109:MET:HE2	1:B:249:PHE:CD1	2.50	0.41
1:B:294:PHE:O	1:B:295:VAL:C	2.63	0.41
1:C:277:TRP:CD2	1:C:291:ARG:HD3	2.55	0.41
1:D:106:ILE:HD11	1:D:229:PHE:CE1	2.56	0.41
1:A:103:MET:HE1	1:A:112:MET:HE3	2.03	0.41
1:B:112:MET:HE2	1:B:112:MET:HA	2.03	0.40
1:B:131:LEU:N	1:B:131:LEU:CD1	2.84	0.40
1:D:208:GLU:O	1:D:209:VAL:C	2.64	0.40
1:D:210:ASP:O	1:D:214:GLU:HG3	2.21	0.40
1:A:290:LEU:HA	1:A:290:LEU:HD12	1.55	0.40
1:B:142:MET:HE3	1:B:147:VAL:CG2	2.49	0.40
1:C:113:PRO:CB	1:C:114:PRO:HD3	2.40	0.40
1:C:143:GLU:CD	1:C:278:HIS:HE2	2.29	0.40
1:C:290:LEU:HA	1:C:290:LEU:HD12	1.47	0.40
1:D:165:ARG:HA	1:D:274:ASN:OD1	2.22	0.40
1:B:105:ASP:HB3	1:B:132:ARG:NH2	2.37	0.40
1:B:138:LEU:O	1:B:139:LYS:C	2.64	0.40
1:A:264:HIS:ND1	1:A:265:PRO:HD2	2.37	0.40
1:B:188:LEU:HD21	1:B:218:ILE:HD11	2.03	0.40
1:D:254:GLU:HG2	1:D:259:LEU:O	2.20	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	203/228 (89%)	188 (93%)	12 (6%)	3 (2%)	8	28
1	B	201/228 (88%)	189 (94%)	9 (4%)	3 (2%)	8	28
1	C	203/228 (89%)	190 (94%)	12 (6%)	1 (0%)	24	54
1	D	206/228 (90%)	184 (89%)	16 (8%)	6 (3%)	3	15
All	All	813/912 (89%)	751 (92%)	49 (6%)	13 (2%)	7	27

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	299	SER
1	B	139	LYS
1	D	139	LYS
1	D	201	ALA
1	D	202	LEU
1	A	160	GLY
1	C	208	GLU
1	D	137	ASN
1	D	299	SER
1	D	145	GLY
1	A	91	ASP
1	B	138	LEU
1	B	209	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	160/196 (82%)	151 (94%)	9 (6%)	19	50
1	B	161/196 (82%)	145 (90%)	16 (10%)	7	24
1	C	162/196 (83%)	150 (93%)	12 (7%)	13	38
1	D	160/196 (82%)	145 (91%)	15 (9%)	8	26
All	All	643/784 (82%)	591 (92%)	52 (8%)	11	33

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	131	LEU
1	A	134	ASN
1	A	153	LEU
1	A	159	THR
1	A	209	VAL
1	A	210	ASP
1	A	245	VAL
1	A	248	ARG
1	A	251	VAL
1	B	131	LEU
1	B	137	ASN
1	B	138	LEU
1	B	147	VAL
1	B	153	LEU
1	B	156	GLU
1	B	178	ASP
1	B	192	THR
1	B	204	THR
1	B	206	HIS
1	B	209	VAL
1	B	210	ASP
1	B	219	LYS
1	B	245	VAL
1	B	248	ARG
1	B	251	VAL
1	C	131	LEU
1	C	134	ASN
1	C	138	LEU
1	C	153	LEU
1	C	159	THR
1	C	192	THR
1	C	206	HIS
1	C	209	VAL
1	C	242	ILE
1	C	245	VAL
1	C	248	ARG
1	C	251	VAL
1	D	131	LEU
1	D	134	ASN
1	D	137	ASN
1	D	147	VAL
1	D	153	LEU
1	D	156	GLU

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Mol	Chain	Res	Type
1	D	192	THR
1	D	197	VAL
1	D	202	LEU
1	D	204	THR
1	D	206	HIS
1	D	209	VAL
1	D	245	VAL
1	D	248	ARG
1	D	251	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	190	GLN
1	C	179	HIS
1	C	190	GLN
1	C	206	HIS
1	C	292	GLN

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](#)

6 ligands are modelled in this entry.

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
2	SAL	C	1300	-	10,10,10	0.82	0	13,13,13	1.01	1 (7%)
3	PG4	A	1301	-	12,12,12	1.20	0	11,11,11	2.44	4 (36%)
2	SAL	A	1300	-	10,10,10	1.01	0	13,13,13	0.86	1 (7%)
3	PG4	B	1301	-	12,12,12	0.79	0	11,11,11	1.21	1 (9%)
3	PG4	A	1302	-	12,12,12	0.80	0	11,11,11	1.96	5 (45%)
2	SAL	B	1300	-	10,10,10	1.27	1 (10%)	13,13,13	0.93	1 (7%)

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
2	SAL	C	1300	-	-	0/4/4/4	0/1/1/1
3	PG4	A	1301	-	-	2/10/10/10	-
2	SAL	A	1300	-	-	0/4/4/4	0/1/1/1
3	PG4	B	1301	-	-	5/10/10/10	-
3	PG4	A	1302	-	-	3/10/10/10	-
2	SAL	B	1300	-	-	0/4/4/4	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1300	SAL	C1-C1'	3.32	1.56	1.49

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1301	PG4	O3-C4-C3	4.36	130.25	110.35
3	A	1301	PG4	O2-C3-C4	4.31	129.98	110.35
3	A	1301	PG4	C7-O4-C6	-3.46	98.11	113.26
3	A	1301	PG4	O4-C7-C8	3.15	123.99	110.11
3	A	1302	PG4	O2-C2-C1	3.13	123.89	110.11
3	A	1302	PG4	O4-C6-C5	2.84	123.31	110.35
3	A	1302	PG4	C3-O2-C2	-2.44	102.56	113.26
3	A	1302	PG4	C7-O4-C6	-2.38	102.83	113.26

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1300	SAL	C2-C1-C1'	2.27	122.33	120.00
3	B	1301	PG4	O2-C2-C1	2.15	119.58	110.11
3	A	1302	PG4	O3-C5-C6	-2.13	100.66	110.35
2	C	1300	SAL	C2-C1-C1'	2.04	122.09	120.00
2	A	1300	SAL	O1'-C1'-C1	-2.00	117.19	121.97

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1302	PG4	C6-C5-O3-C4
3	A	1301	PG4	C6-C5-O3-C4
3	A	1302	PG4	C4-C3-O2-C2
3	B	1301	PG4	C5-C6-O4-C7
3	B	1301	PG4	C4-C3-O2-C2
3	B	1301	PG4	C1-C2-O2-C3
3	B	1301	PG4	O3-C5-C6-O4
3	B	1301	PG4	O2-C3-C4-O3
3	A	1301	PG4	O3-C5-C6-O4
3	A	1302	PG4	O2-C3-C4-O3

There are no ring outliers.

4 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1300	SAL	3	0
3	A	1301	PG4	6	0
3	B	1301	PG4	3	0
3	A	1302	PG4	3	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	207/228 (90%)	0.37	6 (2%) 53 45	14, 29, 48, 65	0
1	B	207/228 (90%)	0.42	9 (4%) 40 31	14, 30, 56, 76	0
1	C	207/228 (90%)	0.44	3 (1%) 73 65	15, 30, 47, 71	0
1	D	210/228 (92%)	0.58	11 (5%) 33 26	15, 31, 66, 110	0
All	All	831/912 (91%)	0.45	29 (3%) 47 38	14, 30, 56, 110	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	202	LEU	3.8
1	D	152	GLY	3.7
1	D	146	ALA	3.6
1	D	136	GLY	3.5
1	B	135	ALA	3.2
1	A	164	ARG	3.1
1	A	107	GLY	3.0
1	D	158	GLN	3.0
1	A	126	ILE	2.9
1	C	260	THR	2.9
1	D	208	GLU	2.7
1	B	204	THR	2.6
1	B	159	THR	2.6
1	D	278	HIS	2.5
1	D	153	LEU	2.5
1	B	285	PRO	2.4
1	B	147	VAL	2.3
1	C	182	ALA	2.3
1	B	93	PHE	2.3
1	D	99	PHE	2.2
1	B	297	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	143	GLU	2.2
1	C	299	SER	2.1
1	A	127	GLN	2.1
1	A	210	ASP	2.1
1	B	293	LEU	2.1
1	D	253	CYS	2.0
1	A	188	LEU	2.0
1	B	283	ARG	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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. 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	B-factors(Å ²)	Q<0.9
3	PG4	A	1302	13/13	0.70	0.18	39,64,80,82	0
3	PG4	B	1301	13/13	0.77	0.18	30,48,75,83	0
3	PG4	A	1301	13/13	0.87	0.12	12,28,43,45	0
2	SAL	C	1300	10/10	0.93	0.09	26,32,39,47	0
2	SAL	A	1300	10/10	0.95	0.10	17,23,43,53	0
2	SAL	B	1300	10/10	0.95	0.08	14,21,37,44	0

6.5 Other polymers [i](#)

There are no such residues in this entry.