



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 03:53 PM UTC

PDB ID : 2GRL / pdb_00002grl
Title : Crystal structure of dCT/iCF10 complex
Authors : Shi, K.; Kozlowski, B.K.; Gu, Z.Y.; Ohlendorf, D.H.; Earhart, C.A.; Dunny, G.M.
Deposited on : 2006-04-24
Resolution : 3.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

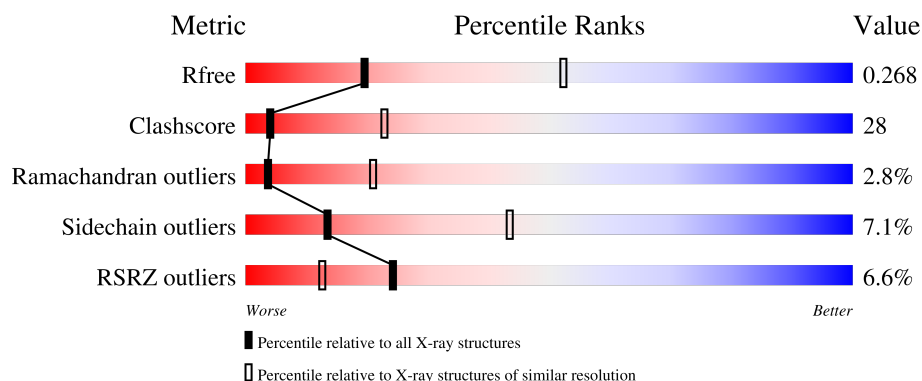
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	317	7% 50% 34% 7% 9%
1	B	317	5% 53% 31% 7% 10%
1	C	317	4% 55% 29% 7% 9%
1	D	317	8% 54% 29% 7% 10%
2	E	7	14% 57% 29% 14%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 9556 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 PrgX.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	287	Total	C	N	O	S	0	0	0
			2368	1536	384	443	5			
1	B	286	Total	C	N	O	S	0	0	0
			2359	1531	383	440	5			
1	C	287	Total	C	N	O	S	0	0	0
			2368	1536	384	443	5			
1	D	286	Total	C	N	O	S	0	0	0
			2359	1531	383	440	5			

- Molecule 2 is a protein called peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	7	Total	C	N	O	0	0	0
			56	40	7	9			

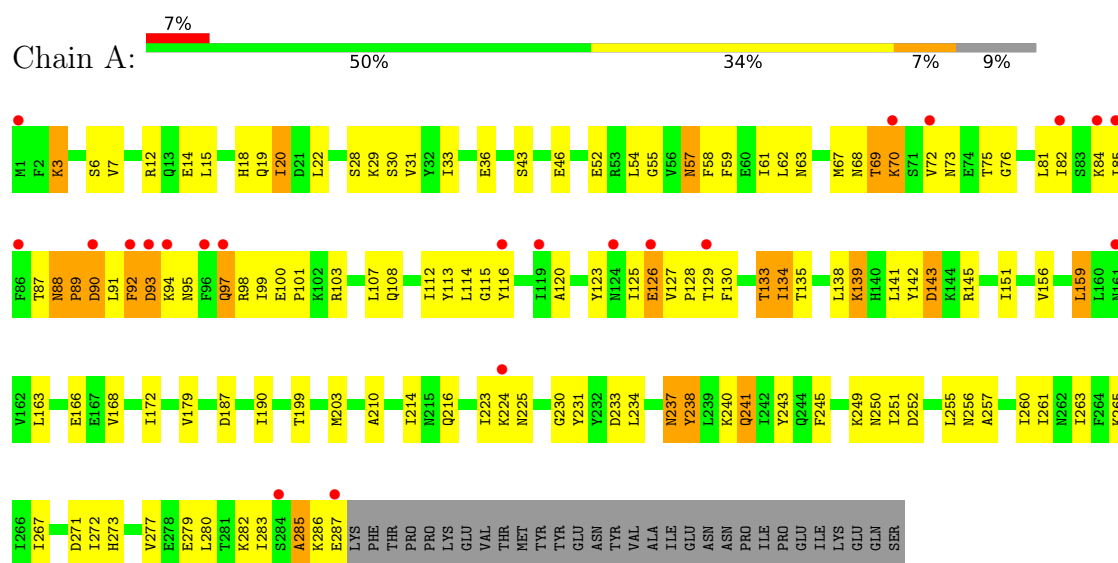
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	11	Total	O	0	0
			11	11		
3	B	16	Total	O	0	0
			16	16		
3	C	11	Total	O	0	0
			11	11		
3	D	8	Total	O	0	0
			8	8		

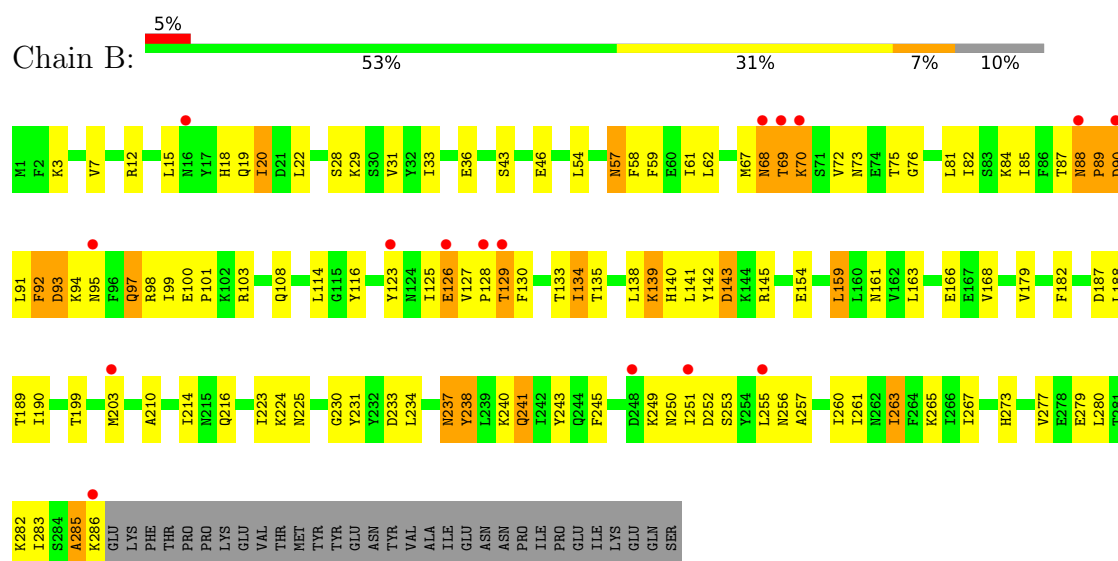
3 Residue-property plots [i](#)

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.

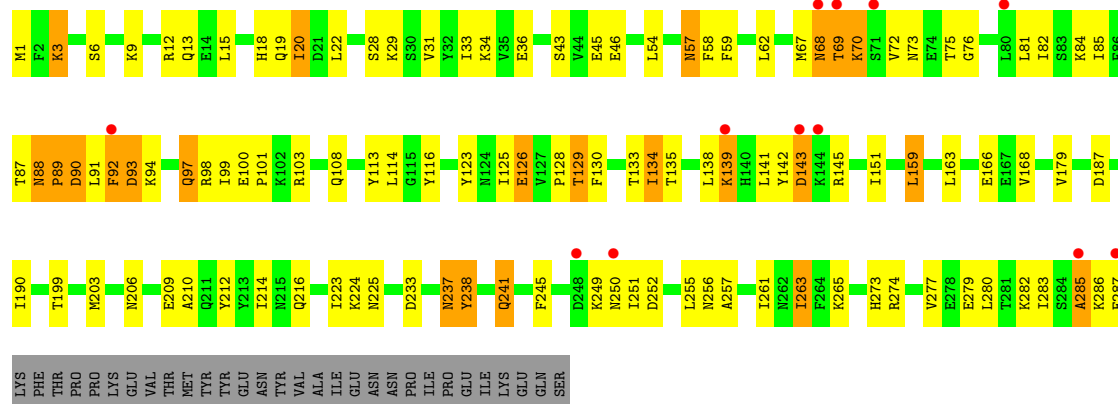
• Molecule 1: PrgX



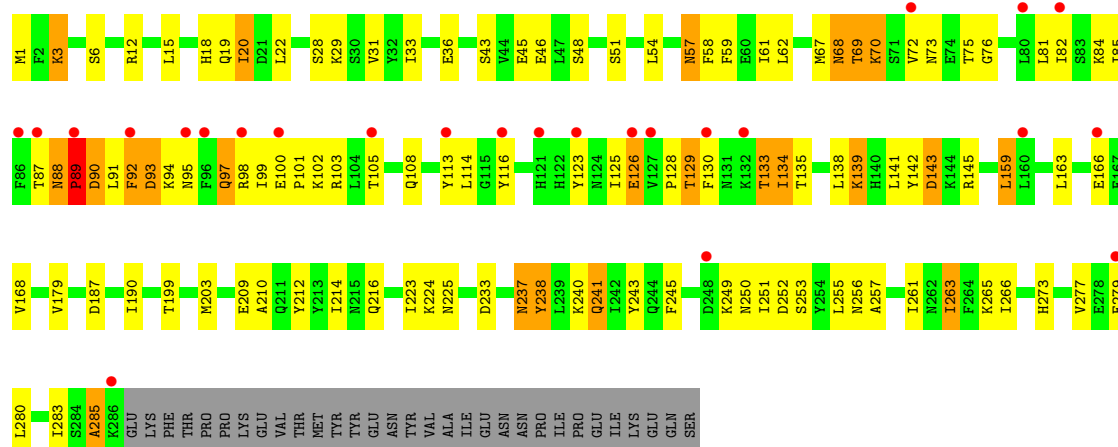
• Molecule 1: PrgX



• Molecule 1: PrgX



• Molecule 1: PrgX



• Molecule 2: peptide



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	83.75Å 110.12Å 188.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 3.00 40.00 – 3.00	Depositor EDS
% Data completeness (in resolution range)	(Not available) (40.00-3.00) 99.6 (40.00-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.98 (at 2.81Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.238 , 0.271 0.238 , 0.268	Depositor DCC
R_{free} test set	2149 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	58.5	Xtriage
Anisotropy	0.355	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 84.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	9556	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 13.80% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.47	0/2414	0.88	4/3258 (0.1%)
1	B	0.46	0/2405	0.88	4/3246 (0.1%)
1	C	0.44	0/2414	0.87	3/3258 (0.1%)
1	D	0.42	0/2405	0.87	4/3246 (0.1%)
2	E	0.64	0/56	1.06	0/74
All	All	0.45	0/9694	0.88	15/13082 (0.1%)

There are no bond length outliers.

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	C	133	THR	N-CA-C	6.84	122.42	114.62
1	A	133	THR	N-CA-C	6.74	122.30	114.62
1	B	133	THR	N-CA-C	6.53	122.07	114.62
1	B	141	LEU	N-CA-C	6.10	118.01	111.36
1	C	141	LEU	N-CA-C	6.05	117.95	111.36
1	B	223	ILE	N-CA-C	5.92	117.10	108.58
1	D	141	LEU	N-CA-C	5.79	117.67	111.36
1	A	141	LEU	N-CA-C	5.78	117.66	111.36
1	B	7	VAL	N-CA-C	-5.68	104.98	110.72
1	D	223	ILE	N-CA-C	5.63	116.69	108.58
1	A	7	VAL	N-CA-C	-5.57	104.94	110.62
1	A	223	ILE	N-CA-C	5.47	116.45	108.58
1	C	223	ILE	N-CA-C	5.18	116.03	108.58
1	D	133	THR	N-CA-C	5.16	121.79	110.80
1	D	266	ILE	N-CA-C	5.14	115.36	110.42

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	2368	0	2410	154	0
1	B	2359	0	2404	149	0
1	C	2368	0	2410	130	0
1	D	2359	0	2404	127	0
2	E	56	0	67	7	0
3	A	11	0	0	15	0
3	B	16	0	0	18	0
3	C	11	0	0	10	0
3	D	8	0	0	11	0
All	All	9556	0	9695	531	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 28.

All (531) 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:ASN:HB2	3:C:323:HOH:O	1.29	1.26
1:A:263:ILE:HG13	1:B:263:ILE:HG13	1.24	1.15
1:C:20:ILE:H	1:C:20:ILE:HD12	1.17	1.09
1:D:255:LEU:HB3	3:D:318:HOH:O	1.51	1.09
1:C:274:ARG:HG3	3:C:322:HOH:O	1.52	1.08
1:C:251:ILE:HB	3:C:324:HOH:O	1.55	1.06
1:A:20:ILE:HD12	1:A:20:ILE:H	1.19	1.03
1:D:20:ILE:HD12	1:D:20:ILE:H	1.18	1.02
1:D:57:ASN:HD22	1:D:58:PHE:N	1.58	1.02
1:A:127:VAL:HA	3:A:328:HOH:O	1.58	1.01
1:B:20:ILE:HD12	1:B:20:ILE:H	1.20	1.01
1:B:57:ASN:HD22	1:B:58:PHE:N	1.59	0.99
1:C:57:ASN:HD22	1:C:58:PHE:N	1.61	0.97
1:C:203:MET:HE3	1:C:287:GLU:HG3	1.47	0.96
1:C:250:ASN:HA	3:C:327:HOH:O	1.67	0.95
1:A:57:ASN:HD22	1:A:58:PHE:N	1.64	0.93
1:A:267:ILE:HG21	1:B:234:LEU:HD23	1.49	0.93
1:A:263:ILE:HG13	1:B:263:ILE:CG1	2.03	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:127:VAL:CG1	3:A:320:HOH:O	2.21	0.88
1:D:88:ASN:O	1:D:91:LEU:HG	1.74	0.87
1:A:88:ASN:O	1:A:91:LEU:HG	1.75	0.86
1:C:88:ASN:O	1:C:91:LEU:HG	1.75	0.86
1:D:20:ILE:H	1:D:20:ILE:CD1	1.89	0.85
1:A:94:LYS:HD3	1:C:13:GLN:OE1	1.76	0.85
1:A:20:ILE:H	1:A:20:ILE:CD1	1.89	0.84
1:A:263:ILE:CG1	1:B:263:ILE:HG13	2.05	0.84
1:C:20:ILE:H	1:C:20:ILE:CD1	1.89	0.83
1:B:57:ASN:HD22	1:B:57:ASN:C	1.84	0.83
1:C:57:ASN:HD22	1:C:57:ASN:C	1.87	0.83
1:D:57:ASN:HD22	1:D:57:ASN:C	1.87	0.83
1:B:126:GLU:HA	3:B:322:HOH:O	1.76	0.82
1:D:250:ASN:HD21	1:D:252:ASP:HB2	1.44	0.82
1:B:20:ILE:H	1:B:20:ILE:CD1	1.91	0.82
1:C:250:ASN:HD21	1:C:252:ASP:HB2	1.44	0.82
1:A:234:LEU:HD23	1:B:267:ILE:HG21	1.60	0.82
1:D:70:LYS:H	1:D:70:LYS:HD2	1.45	0.82
1:B:88:ASN:O	1:B:91:LEU:HG	1.79	0.81
1:A:63:ASN:HB2	3:A:325:HOH:O	1.80	0.81
1:A:250:ASN:HD21	1:A:252:ASP:HB2	1.45	0.81
1:B:70:LYS:HD2	1:B:70:LYS:H	1.45	0.81
1:D:255:LEU:HD12	3:D:318:HOH:O	1.78	0.81
1:A:70:LYS:H	1:A:70:LYS:HD2	1.46	0.81
1:D:20:ILE:HD12	1:D:20:ILE:N	1.97	0.80
1:A:57:ASN:HD22	1:A:57:ASN:C	1.87	0.80
1:B:251:ILE:O	1:B:255:LEU:HD23	1.82	0.80
1:C:70:LYS:H	1:C:70:LYS:HD2	1.46	0.80
1:B:255:LEU:HB3	3:B:318:HOH:O	1.81	0.79
1:D:203:MET:SD	3:D:323:HOH:O	2.40	0.79
1:A:159:LEU:HD12	1:A:168:VAL:HG22	1.65	0.78
1:C:20:ILE:HD12	1:C:20:ILE:N	1.97	0.77
1:A:120:ALA:HB2	3:A:320:HOH:O	1.85	0.77
1:C:159:LEU:HD12	1:C:168:VAL:HG22	1.66	0.77
1:B:250:ASN:HD21	1:B:252:ASP:HB2	1.47	0.77
1:D:251:ILE:O	1:D:255:LEU:HD23	1.85	0.77
1:B:75:THR:HG21	1:B:108:GLN:HB3	1.67	0.76
1:D:159:LEU:HD12	1:D:168:VAL:HG22	1.68	0.76
1:A:234:LEU:HD11	1:B:234:LEU:HD11	1.68	0.75
1:A:20:ILE:HD12	1:A:20:ILE:N	1.99	0.75
1:D:75:THR:HG21	1:D:108:GLN:HB3	1.68	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:75:THR:HG21	1:A:108:GLN:HB3	1.68	0.75
1:C:75:THR:HG21	1:C:108:GLN:HB3	1.68	0.75
1:A:87:THR:C	1:A:88:ASN:HD22	1.95	0.74
1:C:87:THR:C	1:C:88:ASN:HD22	1.95	0.73
1:A:127:VAL:HG11	3:A:320:HOH:O	1.85	0.73
1:D:87:THR:C	1:D:88:ASN:HD22	1.95	0.73
1:A:251:ILE:O	1:A:255:LEU:HD23	1.89	0.73
1:B:159:LEU:HD12	1:B:168:VAL:HG22	1.71	0.73
1:A:159:LEU:CD1	1:A:163:LEU:HD12	2.19	0.72
1:A:92:PHE:HZ	3:A:320:HOH:O	1.72	0.72
1:C:159:LEU:CD1	1:C:163:LEU:HD12	2.19	0.72
1:D:57:ASN:ND2	1:D:59:PHE:H	1.88	0.71
1:B:87:THR:C	1:B:88:ASN:HD22	1.97	0.71
1:B:154:GLU:HG3	2:E:5:ILE:HG22	1.71	0.71
1:B:159:LEU:CD1	1:B:163:LEU:HD12	2.21	0.71
1:B:20:ILE:HD12	1:B:20:ILE:N	2.00	0.71
1:B:255:LEU:HD12	3:B:318:HOH:O	1.90	0.71
1:D:279:GLU:O	1:D:283:ILE:HG13	1.90	0.71
1:C:57:ASN:ND2	1:C:59:PHE:H	1.89	0.70
1:A:70:LYS:O	1:A:76:GLY:HA3	1.91	0.70
1:B:57:ASN:ND2	1:B:59:PHE:H	1.91	0.69
1:B:70:LYS:HD2	1:B:70:LYS:N	2.08	0.69
1:B:89:PRO:C	3:B:326:HOH:O	2.35	0.69
1:A:28:SER:OG	1:A:31:VAL:HG23	1.93	0.68
1:A:279:GLU:O	1:A:283:ILE:HG13	1.93	0.68
1:A:97:GLN:NE2	1:C:13:GLN:HE22	1.91	0.68
1:D:159:LEU:CD1	1:D:163:LEU:HD12	2.23	0.68
1:A:57:ASN:ND2	1:A:59:PHE:H	1.91	0.68
1:D:166:GLU:O	3:D:322:HOH:O	2.10	0.68
1:D:70:LYS:HD2	1:D:70:LYS:N	2.08	0.68
1:D:70:LYS:O	1:D:76:GLY:HA3	1.94	0.68
1:C:43:SER:OG	1:C:46:GLU:HG3	1.93	0.68
1:B:70:LYS:O	1:B:76:GLY:HA3	1.94	0.68
1:A:70:LYS:HD2	1:A:70:LYS:N	2.09	0.67
1:B:88:ASN:HB3	3:B:320:HOH:O	1.95	0.67
1:C:28:SER:OG	1:C:31:VAL:HG23	1.95	0.67
1:B:279:GLU:O	1:B:283:ILE:HG13	1.94	0.66
1:C:70:LYS:HD2	1:C:70:LYS:N	2.09	0.66
1:C:250:ASN:ND2	1:C:252:ASP:HB2	2.10	0.66
1:B:28:SER:OG	1:B:31:VAL:HG23	1.95	0.66
1:C:70:LYS:O	1:C:76:GLY:HA3	1.95	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:251:ILE:O	1:C:255:LEU:HD23	1.96	0.66
1:B:89:PRO:O	3:B:326:HOH:O	2.14	0.66
1:C:279:GLU:O	1:C:283:ILE:HG13	1.94	0.65
1:D:85:ILE:HG13	3:D:320:HOH:O	1.94	0.65
1:B:127:VAL:N	3:B:322:HOH:O	2.29	0.65
1:D:28:SER:OG	1:D:31:VAL:HG23	1.97	0.65
1:D:250:ASN:ND2	1:D:252:ASP:HB2	2.11	0.64
1:B:43:SER:OG	1:B:46:GLU:HG3	1.97	0.64
1:D:88:ASN:HB2	1:D:91:LEU:CD1	2.28	0.64
1:D:43:SER:OG	1:D:46:GLU:HG3	1.99	0.63
1:A:128:PRO:HD2	3:A:328:HOH:O	1.97	0.63
1:B:250:ASN:ND2	1:B:252:ASP:HB2	2.13	0.63
1:C:91:LEU:O	1:C:94:LYS:HE2	1.99	0.63
1:D:99:ILE:HG13	1:D:116:TYR:CE2	2.34	0.63
1:C:251:ILE:HD13	3:C:324:HOH:O	1.99	0.63
1:D:91:LEU:O	1:D:94:LYS:HE2	1.99	0.63
1:D:103:ARG:HH11	1:D:103:ARG:HG2	1.63	0.62
1:B:249:LYS:HA	1:B:249:LYS:HE2	1.81	0.62
1:D:84:LYS:HB3	3:D:320:HOH:O	1.99	0.62
1:A:250:ASN:ND2	1:A:252:ASP:HB2	2.13	0.62
1:C:139:LYS:HG3	1:C:143:ASP:OD2	2.00	0.62
1:C:103:ARG:HG2	1:C:103:ARG:HH11	1.63	0.62
1:C:85:ILE:HA	1:C:91:LEU:HD12	1.81	0.61
1:A:103:ARG:HG2	1:A:103:ARG:HH11	1.65	0.61
1:A:286:LYS:HD3	1:A:286:LYS:C	2.25	0.61
1:A:92:PHE:CZ	3:A:320:HOH:O	2.51	0.61
1:B:62:LEU:HB3	1:B:67:MET:HG3	1.81	0.61
1:C:286:LYS:HG2	1:C:287:GLU:N	2.14	0.61
1:A:271:ASP:HB2	3:A:322:HOH:O	2.01	0.61
1:C:69:THR:O	1:C:72:VAL:HG13	2.00	0.61
1:C:249:LYS:HE2	1:C:249:LYS:HA	1.82	0.61
1:D:249:LYS:HE2	1:D:249:LYS:HA	1.81	0.61
1:A:97:GLN:HE22	1:C:13:GLN:HE22	1.46	0.61
1:A:139:LYS:HG3	1:A:143:ASP:OD2	2.00	0.61
1:B:139:LYS:HG3	1:B:143:ASP:OD2	2.01	0.61
1:C:88:ASN:HB2	1:C:91:LEU:CD1	2.31	0.61
1:A:249:LYS:HE2	1:A:249:LYS:HA	1.81	0.61
1:B:88:ASN:HB2	1:B:91:LEU:CD1	2.31	0.61
1:C:57:ASN:C	1:C:57:ASN:ND2	2.59	0.61
1:A:14:GLU:OE1	1:B:145:ARG:NE	2.32	0.60
1:B:57:ASN:ND2	1:B:59:PHE:N	2.49	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:99:ILE:HG13	1:C:116:TYR:CE2	2.35	0.60
1:D:139:LYS:O	1:D:143:ASP:HB2	2.02	0.60
1:D:69:THR:O	1:D:72:VAL:HG13	2.01	0.60
1:A:69:THR:O	1:A:72:VAL:HG13	2.02	0.60
1:D:139:LYS:HG3	1:D:143:ASP:OD2	2.02	0.60
1:B:85:ILE:HA	1:B:91:LEU:HD12	1.82	0.60
1:C:62:LEU:HB3	1:C:67:MET:HG3	1.83	0.60
1:B:103:ARG:HG2	1:B:103:ARG:HH11	1.66	0.59
1:C:57:ASN:ND2	1:C:59:PHE:N	2.51	0.59
1:B:69:THR:O	1:B:72:VAL:HG13	2.02	0.59
1:D:57:ASN:ND2	1:D:59:PHE:N	2.50	0.59
1:A:93:ASP:OD2	1:C:9:LYS:NZ	2.35	0.59
1:D:85:ILE:HA	1:D:91:LEU:HD12	1.83	0.59
1:C:89:PRO:HG3	1:C:123:TYR:CE2	2.38	0.59
1:A:55:GLY:O	1:B:108:GLN:HG2	2.02	0.59
1:A:57:ASN:C	1:A:57:ASN:ND2	2.60	0.59
1:A:63:ASN:OD1	1:B:182:PHE:HA	2.02	0.59
1:A:91:LEU:O	1:A:94:LYS:HE2	2.02	0.59
1:A:139:LYS:O	1:A:143:ASP:HB2	2.03	0.59
1:D:62:LEU:HB3	1:D:67:MET:HG3	1.84	0.59
1:A:99:ILE:HG13	1:A:116:TYR:CE2	2.37	0.58
1:D:283:ILE:HG12	3:D:323:HOH:O	2.03	0.58
1:A:125:ILE:CD1	3:A:327:HOH:O	2.50	0.58
1:A:286:LYS:O	1:A:287:GLU:HB2	2.02	0.58
1:A:43:SER:OG	1:A:46:GLU:HG3	2.02	0.58
1:B:89:PRO:HG3	1:B:123:TYR:CE2	2.39	0.58
1:A:57:ASN:ND2	1:A:59:PHE:N	2.51	0.58
1:A:88:ASN:HB2	1:A:91:LEU:CD1	2.33	0.58
1:B:91:LEU:O	1:B:94:LYS:HE2	2.04	0.58
1:D:89:PRO:HG3	1:D:123:TYR:CE2	2.38	0.58
1:B:75:THR:CG2	1:B:108:GLN:HB3	2.32	0.57
1:B:99:ILE:HG13	1:B:116:TYR:CE2	2.39	0.57
1:B:139:LYS:O	1:B:143:ASP:HB2	2.05	0.57
1:C:238:TYR:CE2	1:C:261:ILE:HD11	2.38	0.57
1:D:57:ASN:HD21	1:D:59:PHE:H	1.52	0.57
1:A:89:PRO:HG3	1:A:123:TYR:CE2	2.39	0.57
1:B:282:LYS:HG2	1:B:286:LYS:HG2	1.86	0.57
1:A:125:ILE:HG12	3:A:327:HOH:O	2.04	0.57
1:B:100:GLU:HB3	1:B:101:PRO:HD3	1.87	0.57
1:A:62:LEU:HB3	1:A:67:MET:HG3	1.87	0.56
1:B:57:ASN:HD21	1:B:59:PHE:H	1.52	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:120:ALA:CB	3:A:320:HOH:O	2.45	0.56
1:C:88:ASN:HD22	1:C:88:ASN:N	2.02	0.56
1:D:75:THR:CG2	1:D:108:GLN:HB3	2.34	0.56
1:A:75:THR:CG2	1:A:108:GLN:HB3	2.35	0.56
1:C:75:THR:CG2	1:C:108:GLN:HB3	2.34	0.56
1:C:159:LEU:HD13	1:C:163:LEU:HD12	1.88	0.56
1:C:123:TYR:HB2	1:C:125:ILE:HD13	1.89	0.55
1:C:142:TYR:HA	1:C:145:ARG:HG2	1.88	0.55
1:A:29:LYS:O	1:A:33:ILE:HG13	2.06	0.55
1:C:273:HIS:O	1:C:277:VAL:HG23	2.06	0.55
1:A:85:ILE:HA	1:A:91:LEU:HD12	1.87	0.55
1:A:231:TYR:CZ	1:B:230:GLY:HA2	2.41	0.55
1:C:126:GLU:HA	1:C:126:GLU:OE1	2.06	0.55
1:D:123:TYR:HB2	1:D:125:ILE:HD13	1.88	0.55
1:A:57:ASN:HD21	1:A:59:PHE:H	1.54	0.55
1:B:89:PRO:O	1:B:91:LEU:N	2.40	0.55
1:D:88:ASN:HB2	1:D:91:LEU:HD11	1.88	0.55
1:D:29:LYS:O	1:D:33:ILE:HG13	2.07	0.55
1:B:126:GLU:HA	1:B:126:GLU:OE1	2.06	0.55
1:B:238:TYR:CE2	1:B:261:ILE:HD11	2.42	0.55
1:D:238:TYR:CE2	1:D:261:ILE:HD11	2.42	0.55
1:B:134:ILE:HD12	1:B:135:THR:H	1.72	0.54
1:C:57:ASN:HD21	1:C:59:PHE:H	1.53	0.54
1:D:88:ASN:HD22	1:D:88:ASN:N	2.04	0.54
1:A:72:VAL:HG23	1:A:73:ASN:ND2	2.22	0.54
1:A:88:ASN:HD22	1:A:88:ASN:N	2.04	0.54
1:A:166:GLU:H	1:A:166:GLU:CD	2.15	0.54
1:A:125:ILE:HD12	1:A:125:ILE:N	2.23	0.54
1:A:127:VAL:HG12	3:A:320:HOH:O	1.94	0.54
1:A:43:SER:HA	1:B:43:SER:HA	1.90	0.54
1:C:166:GLU:H	1:C:166:GLU:CD	2.15	0.54
1:C:88:ASN:N	1:C:88:ASN:ND2	2.56	0.54
1:C:100:GLU:HB3	1:C:101:PRO:HD3	1.89	0.54
1:A:238:TYR:CE2	1:A:261:ILE:HD11	2.43	0.53
1:B:57:ASN:C	1:B:57:ASN:ND2	2.57	0.53
1:B:88:ASN:HD22	1:B:88:ASN:N	2.06	0.53
1:B:166:GLU:CD	1:B:166:GLU:H	2.16	0.53
1:D:100:GLU:HB3	1:D:101:PRO:HD3	1.90	0.53
1:A:126:GLU:HA	1:A:126:GLU:OE1	2.08	0.53
1:C:233:ASP:O	1:C:237:ASN:HB2	2.08	0.53
1:C:139:LYS:O	1:C:143:ASP:HB2	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:241:GLN:HB3	1:D:257:ALA:HB2	1.90	0.53
1:A:92:PHE:O	1:A:93:ASP:C	2.52	0.53
1:A:282:LYS:HD3	1:A:287:GLU:HG3	1.90	0.53
1:B:90:ASP:OD2	3:B:320:HOH:O	2.19	0.53
1:D:57:ASN:C	1:D:57:ASN:ND2	2.59	0.53
1:D:72:VAL:HG23	1:D:73:ASN:ND2	2.24	0.53
1:D:123:TYR:O	1:D:125:ILE:HD12	2.09	0.53
1:C:274:ARG:CA	3:C:322:HOH:O	2.56	0.53
1:A:91:LEU:O	1:A:92:PHE:C	2.51	0.53
1:C:92:PHE:O	1:C:93:ASP:C	2.52	0.53
1:D:159:LEU:HD13	1:D:163:LEU:HD12	1.90	0.53
1:B:216:GLN:HA	1:B:216:GLN:NE2	2.23	0.52
1:D:233:ASP:O	1:D:237:ASN:HB2	2.08	0.52
1:B:72:VAL:HG23	1:B:73:ASN:ND2	2.24	0.52
1:B:161:ASN:ND2	2:E:4:LEU:HD21	2.23	0.52
1:C:88:ASN:HB2	1:C:91:LEU:HD11	1.91	0.52
1:D:114:LEU:HD11	1:D:159:LEU:HD23	1.91	0.52
1:D:57:ASN:ND2	1:D:58:PHE:N	2.43	0.52
1:D:88:ASN:N	1:D:88:ASN:ND2	2.57	0.52
1:B:88:ASN:O	1:B:89:PRO:C	2.52	0.52
1:A:100:GLU:HB3	1:A:101:PRO:HD3	1.90	0.52
1:A:114:LEU:HD11	1:A:159:LEU:HD23	1.92	0.52
1:B:88:ASN:HB2	1:B:91:LEU:HD11	1.92	0.52
1:D:166:GLU:CD	1:D:166:GLU:H	2.16	0.52
1:B:142:TYR:HA	1:B:145:ARG:HG2	1.92	0.52
1:A:263:ILE:HD12	1:B:260:ILE:HG12	1.91	0.52
1:B:114:LEU:HD11	1:B:159:LEU:CD2	2.40	0.52
1:D:126:GLU:OE1	1:D:126:GLU:HA	2.09	0.52
1:C:1:MET:HE3	1:D:45:GLU:HG3	1.91	0.52
1:C:72:VAL:HG23	1:C:73:ASN:ND2	2.25	0.52
1:C:241:GLN:HB3	1:C:257:ALA:HB2	1.90	0.52
1:A:134:ILE:HD12	1:A:135:THR:H	1.75	0.51
1:D:91:LEU:CD1	3:D:320:HOH:O	2.58	0.51
1:B:29:LYS:O	1:B:33:ILE:HG13	2.10	0.51
1:A:88:ASN:HB2	1:A:91:LEU:HD11	1.92	0.51
1:A:114:LEU:HD11	1:A:159:LEU:CD2	2.40	0.51
1:A:123:TYR:HB2	1:A:125:ILE:HD13	1.92	0.51
1:A:159:LEU:HD13	1:A:163:LEU:HD12	1.91	0.51
1:B:92:PHE:O	1:B:93:ASP:C	2.53	0.51
1:B:114:LEU:HD11	1:B:159:LEU:HD23	1.91	0.51
1:C:70:LYS:H	1:C:70:LYS:CD	2.20	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:138:LEU:HD21	1:C:159:LEU:HD21	1.92	0.51
1:D:70:LYS:H	1:D:70:LYS:CD	2.18	0.51
1:A:88:ASN:N	1:A:88:ASN:ND2	2.58	0.51
1:D:92:PHE:O	1:D:93:ASP:C	2.52	0.51
1:D:249:LYS:HA	1:D:249:LYS:CE	2.40	0.51
1:A:273:HIS:O	1:A:277:VAL:HG23	2.10	0.51
1:C:1:MET:CE	1:D:45:GLU:HG3	2.41	0.51
1:C:114:LEU:HD11	1:C:159:LEU:HD23	1.93	0.51
1:D:142:TYR:HA	1:D:145:ARG:HG2	1.92	0.51
1:D:114:LEU:HD11	1:D:159:LEU:CD2	2.41	0.51
1:B:127:VAL:HG22	3:B:322:HOH:O	2.11	0.51
1:B:249:LYS:HA	1:B:249:LYS:CE	2.40	0.51
1:D:273:HIS:O	1:D:277:VAL:HG23	2.10	0.51
1:C:216:GLN:HA	1:C:216:GLN:NE2	2.25	0.50
1:A:88:ASN:O	1:A:89:PRO:C	2.54	0.50
1:C:224:LYS:HG2	1:C:225:ASN:ND2	2.27	0.50
1:C:123:TYR:HB2	1:C:125:ILE:CD1	2.41	0.50
1:A:142:TYR:HA	1:A:145:ARG:HG2	1.93	0.50
1:A:187:ASP:O	1:A:190:ILE:HG12	2.12	0.50
1:B:57:ASN:ND2	1:B:58:PHE:N	2.43	0.50
1:C:114:LEU:HD11	1:C:159:LEU:CD2	2.42	0.50
1:D:91:LEU:O	1:D:92:PHE:C	2.54	0.50
1:B:70:LYS:H	1:B:70:LYS:CD	2.19	0.50
1:D:123:TYR:HB2	1:D:125:ILE:CD1	2.41	0.50
1:D:134:ILE:HD12	1:D:135:THR:H	1.77	0.50
1:B:138:LEU:HD21	1:B:159:LEU:HD21	1.94	0.50
1:B:159:LEU:HD13	1:B:163:LEU:HD12	1.94	0.50
1:C:125:ILE:HD12	1:C:125:ILE:N	2.27	0.50
1:B:139:LYS:HE3	3:B:333:HOH:O	2.12	0.50
1:B:233:ASP:O	1:B:237:ASN:HB2	2.11	0.50
1:C:45:GLU:HG3	1:D:1:MET:CE	2.41	0.50
1:D:138:LEU:HD21	1:D:159:LEU:HD21	1.94	0.50
1:C:249:LYS:HA	1:C:249:LYS:CE	2.42	0.50
1:A:89:PRO:O	1:A:91:LEU:N	2.45	0.49
1:A:216:GLN:NE2	1:A:216:GLN:HA	2.26	0.49
1:B:123:TYR:HB2	1:B:125:ILE:HD13	1.94	0.49
1:C:29:LYS:O	1:C:33:ILE:HG13	2.12	0.49
1:A:52:GLU:CD	1:B:73:ASN:HB2	2.37	0.49
1:B:224:LYS:HG2	1:B:225:ASN:ND2	2.27	0.49
1:C:45:GLU:HG3	1:D:1:MET:HE3	1.94	0.49
1:C:263:ILE:HG13	1:D:263:ILE:HG13	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:70:LYS:H	1:A:70:LYS:CD	2.19	0.49
1:C:20:ILE:CD1	3:C:318:HOH:O	2.60	0.49
1:A:230:GLY:HA2	1:B:231:TYR:CZ	2.48	0.49
1:C:91:LEU:O	1:C:92:PHE:C	2.55	0.49
1:D:85:ILE:CG1	3:D:320:HOH:O	2.58	0.49
1:A:98:ARG:HB3	1:A:98:ARG:NH1	2.28	0.49
1:B:88:ASN:CA	3:B:320:HOH:O	2.60	0.49
1:C:89:PRO:O	1:C:91:LEU:N	2.46	0.49
1:D:187:ASP:O	1:D:190:ILE:HG12	2.13	0.49
1:D:224:LYS:HG2	1:D:225:ASN:ND2	2.27	0.49
1:A:233:ASP:O	1:A:237:ASN:HB2	2.13	0.49
1:A:138:LEU:HD21	1:A:159:LEU:HD21	1.94	0.49
1:B:91:LEU:O	1:B:92:PHE:C	2.55	0.49
1:D:125:ILE:HD12	1:D:125:ILE:N	2.28	0.49
1:A:130:PHE:O	1:A:134:ILE:HG13	2.13	0.49
1:B:18:HIS:O	1:B:19:GLN:C	2.55	0.49
1:D:91:LEU:HD12	3:D:320:HOH:O	2.12	0.49
1:B:88:ASN:N	1:B:88:ASN:ND2	2.60	0.48
1:C:274:ARG:HA	3:C:322:HOH:O	2.12	0.48
1:C:88:ASN:O	1:C:89:PRO:C	2.55	0.48
1:C:134:ILE:HD12	1:C:135:THR:H	1.76	0.48
1:B:273:HIS:O	1:B:277:VAL:HG23	2.12	0.48
1:D:89:PRO:O	1:D:91:LEU:N	2.46	0.48
1:D:241:GLN:CG	1:D:256:ASN:HB2	2.43	0.48
1:B:189:THR:HG22	2:E:5:ILE:HG21	1.95	0.48
1:D:98:ARG:NH1	1:D:98:ARG:HB3	2.28	0.48
1:A:286:LYS:HD3	1:A:287:GLU:N	2.28	0.48
1:B:187:ASP:O	1:B:190:ILE:HG12	2.12	0.48
1:C:87:THR:C	1:C:88:ASN:ND2	2.70	0.48
1:A:87:THR:C	1:A:88:ASN:ND2	2.70	0.48
1:B:89:PRO:O	1:B:90:ASP:C	2.57	0.48
1:C:93:ASP:O	1:C:97:GLN:NE2	2.47	0.48
1:C:187:ASP:O	1:C:190:ILE:HG12	2.14	0.48
1:D:88:ASN:O	1:D:89:PRO:C	2.56	0.48
1:A:282:LYS:HD3	1:A:287:GLU:CG	2.44	0.48
1:A:249:LYS:HA	1:A:249:LYS:CE	2.42	0.48
1:B:139:LYS:CD	3:B:333:HOH:O	2.61	0.48
1:B:125:ILE:N	1:B:125:ILE:HD12	2.27	0.48
1:B:126:GLU:CA	3:B:322:HOH:O	2.49	0.48
1:A:241:GLN:HB3	1:A:257:ALA:HB2	1.96	0.47
1:B:90:ASP:CG	3:B:320:HOH:O	2.56	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:93:ASP:O	1:A:97:GLN:NE2	2.47	0.47
1:A:224:LYS:HG2	1:A:225:ASN:ND2	2.29	0.47
1:B:75:THR:HG21	1:B:108:GLN:CB	2.43	0.47
1:B:98:ARG:NH1	1:B:98:ARG:HB3	2.28	0.47
1:D:216:GLN:HA	1:D:216:GLN:NE2	2.29	0.47
1:B:123:TYR:HB2	1:B:125:ILE:CD1	2.44	0.47
1:C:103:ARG:HG2	1:C:103:ARG:NH1	2.28	0.47
1:A:123:TYR:HB2	1:A:125:ILE:CD1	2.44	0.47
1:D:93:ASP:O	1:D:97:GLN:NE2	2.48	0.47
1:C:199:THR:O	1:C:203:MET:HG2	2.15	0.47
1:C:108:GLN:NE2	1:C:151:ILE:HD13	2.29	0.47
1:C:274:ARG:N	3:C:322:HOH:O	2.47	0.47
1:B:90:ASP:O	1:B:94:LYS:NZ	2.46	0.47
1:D:90:ASP:O	1:D:94:LYS:NZ	2.43	0.47
1:B:130:PHE:O	1:B:134:ILE:HG13	2.15	0.47
1:C:18:HIS:O	1:C:19:GLN:C	2.57	0.47
1:A:139:LYS:HD3	1:A:139:LYS:HA	1.82	0.47
1:C:123:TYR:O	1:C:125:ILE:HD12	2.14	0.47
1:A:267:ILE:CG2	1:B:234:LEU:HD23	2.34	0.46
1:B:241:GLN:HB3	1:B:257:ALA:HB2	1.96	0.46
1:A:18:HIS:O	1:A:19:GLN:C	2.57	0.46
1:B:125:ILE:O	3:B:322:HOH:O	2.21	0.46
1:A:57:ASN:O	1:A:61:ILE:HG13	2.14	0.46
1:A:272:ILE:HG12	3:A:322:HOH:O	2.14	0.46
1:A:94:LYS:CD	1:C:13:GLN:OE1	2.58	0.46
1:B:241:GLN:CG	1:B:256:ASN:HB2	2.45	0.46
1:C:90:ASP:O	1:C:94:LYS:NZ	2.44	0.46
1:C:130:PHE:O	1:C:134:ILE:HG13	2.16	0.46
1:C:98:ARG:HB3	1:C:98:ARG:NH1	2.30	0.46
1:B:93:ASP:O	1:B:94:LYS:C	2.58	0.46
1:A:97:GLN:HE21	1:A:97:GLN:HB2	1.50	0.45
1:B:161:ASN:CG	2:E:4:LEU:HD21	2.41	0.45
1:D:103:ARG:HG2	1:D:103:ARG:NH1	2.29	0.45
1:A:70:LYS:HB3	1:A:76:GLY:CA	2.45	0.45
1:B:93:ASP:O	1:B:97:GLN:NE2	2.49	0.45
1:B:245:PHE:O	1:B:249:LYS:HA	2.16	0.45
1:C:241:GLN:CG	1:C:256:ASN:HB2	2.47	0.45
1:A:70:LYS:HB3	1:A:76:GLY:HA2	1.98	0.45
1:B:283:ILE:C	1:B:285:ALA:H	2.25	0.45
1:C:138:LEU:HD11	1:C:159:LEU:HD11	1.99	0.45
1:D:103:ARG:HD2	1:D:113:TYR:CE2	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:240:LYS:O	1:A:243:TYR:HB3	2.17	0.45
1:D:130:PHE:O	1:D:134:ILE:HG13	2.16	0.45
1:A:260:ILE:HG12	1:B:263:ILE:HD12	1.99	0.45
1:B:140:HIS:HB2	3:B:319:HOH:O	2.16	0.45
1:B:265:LYS:HB2	1:B:273:HIS:CD2	2.52	0.45
1:C:70:LYS:HB3	1:C:76:GLY:CA	2.46	0.45
1:C:88:ASN:HB2	1:C:91:LEU:HG	1.98	0.45
1:D:138:LEU:HD11	1:D:159:LEU:HD11	1.97	0.45
1:B:138:LEU:HD11	1:B:159:LEU:HD11	1.99	0.45
1:D:81:LEU:O	1:D:84:LYS:HB3	2.17	0.45
1:A:103:ARG:HG2	1:A:103:ARG:NH1	2.30	0.44
1:A:241:GLN:CG	1:A:256:ASN:HB2	2.47	0.44
1:A:52:GLU:OE2	1:B:73:ASN:HB2	2.16	0.44
1:A:81:LEU:O	1:A:84:LYS:HB3	2.17	0.44
1:D:70:LYS:HB3	1:D:76:GLY:CA	2.47	0.44
1:B:188:LEU:CD1	2:E:5:ILE:CD1	2.94	0.44
1:D:87:THR:C	1:D:88:ASN:ND2	2.70	0.44
1:A:93:ASP:O	1:A:94:LYS:C	2.60	0.44
1:A:98:ARG:NH1	1:A:98:ARG:CB	2.81	0.44
1:B:62:LEU:O	1:B:67:MET:HG2	2.17	0.44
1:B:88:ASN:CB	3:B:320:HOH:O	2.62	0.44
1:B:210:ALA:O	1:B:214:ILE:HG13	2.18	0.44
1:A:245:PHE:O	1:A:249:LYS:HA	2.18	0.44
1:A:283:ILE:C	1:A:285:ALA:H	2.26	0.44
1:B:251:ILE:CG2	1:B:252:ASP:N	2.80	0.44
1:B:70:LYS:HB3	1:B:76:GLY:CA	2.47	0.44
1:D:89:PRO:O	1:D:90:ASP:C	2.60	0.44
1:A:123:TYR:O	1:A:125:ILE:HD12	2.18	0.43
1:B:81:LEU:O	1:B:84:LYS:HB3	2.17	0.43
1:B:139:LYS:HG2	3:B:333:HOH:O	2.17	0.43
1:D:70:LYS:HB3	1:D:76:GLY:HA2	2.00	0.43
1:B:188:LEU:CD1	2:E:5:ILE:HD11	2.48	0.43
1:B:12:ARG:HH11	1:B:36:GLU:CD	2.26	0.43
1:B:263:ILE:HD13	1:B:263:ILE:HA	1.84	0.43
1:C:70:LYS:HB3	1:C:76:GLY:HA2	2.00	0.43
1:A:90:ASP:O	1:A:94:LYS:NZ	2.47	0.43
1:A:125:ILE:CD1	1:A:125:ILE:N	2.81	0.43
1:C:128:PRO:HG2	1:C:129:THR:H	1.83	0.43
1:D:210:ALA:O	1:D:214:ILE:HG13	2.18	0.43
1:A:98:ARG:CB	1:A:98:ARG:HH11	2.32	0.43
1:D:18:HIS:O	1:D:19:GLN:C	2.61	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:85:ILE:N	3:D:320:HOH:O	2.51	0.43
1:B:87:THR:C	1:B:88:ASN:ND2	2.73	0.43
1:C:81:LEU:O	1:C:84:LYS:HB3	2.18	0.43
1:C:89:PRO:O	1:C:90:ASP:C	2.60	0.43
1:A:251:ILE:CG2	1:A:252:ASP:N	2.82	0.43
1:A:263:ILE:HD13	1:A:263:ILE:HA	1.85	0.43
1:A:265:LYS:HB2	1:A:273:HIS:CD2	2.53	0.43
1:B:70:LYS:HB3	1:B:76:GLY:HA2	2.00	0.43
1:C:22:LEU:HD11	1:C:54:LEU:HG	2.01	0.43
1:C:209:GLU:O	1:C:212:TYR:HB3	2.18	0.43
1:C:251:ILE:CG2	1:C:252:ASP:N	2.82	0.43
1:C:283:ILE:C	1:C:285:ALA:H	2.27	0.43
1:D:199:THR:O	1:D:203:MET:HG2	2.19	0.43
1:D:265:LYS:HB2	1:D:273:HIS:CD2	2.54	0.43
1:A:210:ALA:O	1:A:214:ILE:HG13	2.18	0.43
1:D:251:ILE:CG2	1:D:252:ASP:N	2.82	0.43
1:B:22:LEU:HD11	1:B:54:LEU:HG	2.01	0.42
1:B:134:ILE:HD12	1:B:134:ILE:N	2.34	0.42
1:C:265:LYS:HB2	1:C:273:HIS:CD2	2.53	0.42
1:D:95:ASN:HA	1:D:98:ARG:HH12	1.84	0.42
1:D:241:GLN:HG2	1:D:256:ASN:HB2	2.01	0.42
1:C:93:ASP:O	1:C:94:LYS:C	2.61	0.42
1:C:97:GLN:HE21	1:C:97:GLN:HB2	1.53	0.42
1:D:57:ASN:O	1:D:61:ILE:HG13	2.19	0.42
1:D:245:PHE:O	1:D:249:LYS:HA	2.18	0.42
1:C:103:ARG:HD2	1:C:113:TYR:CE2	2.54	0.42
1:A:89:PRO:O	1:A:90:ASP:C	2.60	0.42
1:D:133:THR:O	1:D:134:ILE:C	2.62	0.42
1:D:209:GLU:O	1:D:212:TYR:HB3	2.19	0.42
1:A:92:PHE:HB3	1:A:93:ASP:H	1.68	0.42
1:C:245:PHE:O	1:C:249:LYS:HA	2.19	0.42
1:C:282:LYS:HE3	1:C:282:LYS:HB2	1.83	0.42
1:B:199:THR:O	1:B:203:MET:HG2	2.20	0.42
1:B:241:GLN:HG2	1:B:256:ASN:HB2	2.02	0.42
1:C:251:ILE:CD1	3:C:324:HOH:O	2.63	0.42
1:D:3:LYS:HB3	1:D:6:SER:OG	2.19	0.42
1:D:93:ASP:O	1:D:94:LYS:C	2.62	0.42
2:E:3:THR:CG2	2:E:4:LEU:N	2.82	0.42
1:A:88:ASN:HB2	1:A:91:LEU:HG	2.02	0.42
1:D:97:GLN:HE21	1:D:97:GLN:HB2	1.53	0.42
1:A:22:LEU:HD11	1:A:54:LEU:HG	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:12:ARG:NH1	1:B:36:GLU:OE2	2.53	0.42
1:B:240:LYS:O	1:B:243:TYR:HB3	2.20	0.42
1:A:103:ARG:HD2	1:A:113:TYR:CE2	2.55	0.41
1:B:103:ARG:HG2	1:B:103:ARG:NH1	2.32	0.41
1:D:68:ASN:O	1:D:69:THR:C	2.63	0.41
1:A:199:THR:O	1:A:203:MET:HG2	2.20	0.41
1:D:128:PRO:HG2	1:D:129:THR:H	1.84	0.41
1:A:95:ASN:HA	1:A:98:ARG:HH12	1.85	0.41
1:C:68:ASN:O	1:C:69:THR:C	2.63	0.41
1:C:139:LYS:HD3	1:C:139:LYS:HA	1.81	0.41
1:D:102:LYS:HB2	1:D:105:THR:OG1	2.20	0.41
1:B:123:TYR:O	1:B:125:ILE:HD12	2.21	0.41
1:D:85:ILE:HG23	1:D:91:LEU:HB2	2.02	0.41
1:A:87:THR:C	1:A:89:PRO:HD3	2.45	0.41
1:B:98:ARG:NH1	1:B:98:ARG:CB	2.83	0.41
1:B:241:GLN:HG3	1:B:253:SER:O	2.21	0.41
1:D:283:ILE:C	1:D:285:ALA:H	2.27	0.41
1:A:3:LYS:HB3	1:A:6:SER:OG	2.21	0.41
1:A:30:SER:O	1:A:33:ILE:HB	2.21	0.41
1:A:75:THR:HG21	1:A:108:GLN:CB	2.46	0.41
1:B:95:ASN:HA	1:B:98:ARG:HH12	1.86	0.41
1:D:88:ASN:HB2	1:D:91:LEU:HG	2.02	0.41
1:D:263:ILE:HD13	1:D:263:ILE:HA	1.85	0.41
1:C:70:LYS:C	1:C:72:VAL:H	2.29	0.41
1:C:210:ALA:O	1:C:214:ILE:HG13	2.21	0.41
1:D:139:LYS:HD3	1:D:139:LYS:HA	1.80	0.41
1:B:128:PRO:HG2	1:B:129:THR:H	1.85	0.41
1:C:12:ARG:HH11	1:C:36:GLU:CD	2.27	0.41
1:A:94:LYS:HA	1:C:13:GLN:NE2	2.36	0.41
1:A:156:VAL:HG11	1:A:172:ILE:HG12	2.03	0.41
1:B:57:ASN:O	1:B:61:ILE:HG13	2.21	0.41
1:B:70:LYS:C	1:B:72:VAL:H	2.29	0.41
1:C:31:VAL:O	1:C:34:LYS:HB2	2.21	0.41
1:C:263:ILE:HD13	1:C:263:ILE:HA	1.83	0.41
1:D:22:LEU:HD11	1:D:54:LEU:HG	2.03	0.41
1:D:75:THR:HG21	1:D:108:GLN:CB	2.45	0.41
1:D:241:GLN:HG3	1:D:253:SER:O	2.20	0.41
1:A:94:LYS:HG3	1:C:13:GLN:HG2	2.02	0.41
1:A:133:THR:O	1:A:134:ILE:C	2.62	0.41
1:A:231:TYR:OH	1:B:233:ASP:OD1	2.28	0.41
1:D:48:SER:O	1:D:51:SER:HB3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:108:GLN:HE22	1:C:151:ILE:HD13	1.86	0.40
1:A:108:GLN:NE2	1:A:151:ILE:HD13	2.36	0.40
1:B:68:ASN:O	1:B:69:THR:C	2.64	0.40
1:B:88:ASN:HB2	1:B:91:LEU:HG	2.04	0.40
1:C:57:ASN:ND2	1:C:58:PHE:N	2.46	0.40
1:C:87:THR:C	1:C:89:PRO:HD3	2.45	0.40
1:D:12:ARG:HH11	1:D:36:GLU:CD	2.29	0.40
1:A:282:LYS:HE3	1:A:282:LYS:HB2	1.83	0.40
1:B:98:ARG:CB	1:B:98:ARG:HH11	2.34	0.40
1:A:12:ARG:HH11	1:A:36:GLU:CD	2.28	0.40
1:A:138:LEU:HD11	1:A:159:LEU:HD11	2.02	0.40
1:B:89:PRO:C	1:B:91:LEU:N	2.79	0.40
1:C:125:ILE:HG22	1:C:126:GLU:N	2.36	0.40
1:D:240:LYS:O	1:D:243:TYR:HB3	2.21	0.40
1:A:107:LEU:CD2	3:A:324:HOH:O	2.70	0.40
1:A:112:ILE:O	1:A:115:GLY:N	2.53	0.40
1:C:3:LYS:HB3	1:C:6:SER:OG	2.20	0.40
1:C:125:ILE:CD1	1:C:125:ILE:N	2.84	0.40
1:D:70:LYS:C	1:D:72:VAL:H	2.30	0.40
1:D:87:THR:C	1:D:89:PRO:HD3	2.47	0.40
1:D:125:ILE:CG2	1:D:126:GLU:N	2.84	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	285/317 (90%)	257 (90%)	20 (7%)	8 (3%)	4	21
1	B	284/317 (90%)	257 (90%)	19 (7%)	8 (3%)	4	21
1	C	285/317 (90%)	258 (90%)	19 (7%)	8 (3%)	4	21
1	D	284/317 (90%)	257 (90%)	19 (7%)	8 (3%)	4	21

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	E	5/7 (71%)	4 (80%)	1 (20%)	0	100	100
All	All	1143/1275 (90%)	1033 (90%)	78 (7%)	32 (3%)	4	21

All (32) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	68	ASN
1	A	92	PHE
1	B	68	ASN
1	B	92	PHE
1	C	68	ASN
1	C	92	PHE
1	D	68	ASN
1	D	92	PHE
1	A	90	ASP
1	A	93	ASP
1	B	90	ASP
1	B	93	ASP
1	C	90	ASP
1	C	93	ASP
1	D	90	ASP
1	D	93	ASP
1	D	285	ALA
1	A	285	ALA
1	B	285	ALA
1	C	285	ALA
1	A	69	THR
1	B	69	THR
1	C	69	THR
1	D	69	THR
1	D	82	ILE
1	A	82	ILE
1	B	82	ILE
1	C	82	ILE
1	A	89	PRO
1	B	89	PRO
1	C	89	PRO
1	D	89	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	269/299 (90%)	251 (93%)	18 (7%)	15	46
1	B	268/299 (90%)	249 (93%)	19 (7%)	13	43
1	C	269/299 (90%)	250 (93%)	19 (7%)	13	43
1	D	268/299 (90%)	248 (92%)	20 (8%)	12	41
2	E	6/6 (100%)	5 (83%)	1 (17%)	2	12
All	All	1080/1202 (90%)	1003 (93%)	77 (7%)	13	43

All (77) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LYS
1	A	15	LEU
1	A	20	ILE
1	A	57	ASN
1	A	70	LYS
1	A	88	ASN
1	A	97	GLN
1	A	126	GLU
1	A	129	THR
1	A	134	ILE
1	A	139	LYS
1	A	143	ASP
1	A	159	LEU
1	A	179	VAL
1	A	237	ASN
1	A	238	TYR
1	A	241	GLN
1	A	280	LEU
1	B	3	LYS
1	B	15	LEU
1	B	20	ILE
1	B	57	ASN
1	B	70	LYS

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Mol	Chain	Res	Type
1	B	88	ASN
1	B	97	GLN
1	B	126	GLU
1	B	129	THR
1	B	134	ILE
1	B	139	LYS
1	B	143	ASP
1	B	159	LEU
1	B	179	VAL
1	B	237	ASN
1	B	238	TYR
1	B	241	GLN
1	B	263	ILE
1	B	280	LEU
1	C	3	LYS
1	C	15	LEU
1	C	20	ILE
1	C	57	ASN
1	C	70	LYS
1	C	88	ASN
1	C	97	GLN
1	C	126	GLU
1	C	129	THR
1	C	134	ILE
1	C	139	LYS
1	C	143	ASP
1	C	159	LEU
1	C	179	VAL
1	C	237	ASN
1	C	238	TYR
1	C	241	GLN
1	C	263	ILE
1	C	280	LEU
1	D	3	LYS
1	D	15	LEU
1	D	20	ILE
1	D	57	ASN
1	D	70	LYS
1	D	88	ASN
1	D	89	PRO
1	D	97	GLN
1	D	126	GLU

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Mol	Chain	Res	Type
1	D	129	THR
1	D	134	ILE
1	D	139	LYS
1	D	143	ASP
1	D	159	LEU
1	D	179	VAL
1	D	237	ASN
1	D	238	TYR
1	D	241	GLN
1	D	263	ILE
1	D	280	LEU
2	E	5	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (49) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	GLN
1	A	13	GLN
1	A	57	ASN
1	A	88	ASN
1	A	97	GLN
1	A	161	ASN
1	A	215	ASN
1	A	216	GLN
1	A	225	ASN
1	A	241	GLN
1	A	250	ASN
1	A	262	ASN
1	B	10	GLN
1	B	13	GLN
1	B	57	ASN
1	B	88	ASN
1	B	97	GLN
1	B	140	HIS
1	B	158	ASN
1	B	161	ASN
1	B	215	ASN
1	B	216	GLN
1	B	225	ASN
1	B	241	GLN
1	B	250	ASN
1	B	262	ASN

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Mol	Chain	Res	Type
1	C	10	GLN
1	C	13	GLN
1	C	57	ASN
1	C	88	ASN
1	C	97	GLN
1	C	161	ASN
1	C	215	ASN
1	C	216	GLN
1	C	225	ASN
1	C	250	ASN
1	C	262	ASN
1	D	10	GLN
1	D	13	GLN
1	D	57	ASN
1	D	88	ASN
1	D	97	GLN
1	D	161	ASN
1	D	215	ASN
1	D	216	GLN
1	D	225	ASN
1	D	241	GLN
1	D	250	ASN
1	D	262	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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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	A	287/317 (90%)	0.32	22 (7%)	19 10	19, 50, 128, 176	0
1	B	286/317 (90%)	0.32	16 (5%)	30 15	23, 50, 108, 194	0
1	C	287/317 (90%)	0.22	12 (4%)	40 22	28, 55, 122, 165	0
1	D	286/317 (90%)	0.47	25 (8%)	16 8	22, 63, 150, 200	0
2	E	7/7 (100%)	1.21	1 (14%)	6 3	69, 82, 106, 124	0
All	All	1153/1275 (90%)	0.34	76 (6%)	24 12	19, 56, 130, 200	0

All (76) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	92	PHE	5.6
1	B	126	GLU	4.5
1	A	86	PHE	4.5
1	B	88	ASN	4.4
1	A	82	ILE	4.1
1	A	94	LYS	4.0
1	D	96	PHE	4.0
1	D	95	ASN	3.9
1	C	144	LYS	3.7
1	A	116	TYR	3.6
1	D	89	PRO	3.6
1	D	86	PHE	3.5
1	B	70	LYS	3.4
1	A	96	PHE	3.4
1	B	90	ASP	3.3
1	A	92	PHE	3.2
1	C	139	LYS	3.2
1	A	93	ASP	3.1
1	C	92	PHE	3.0
1	D	87	THR	3.0

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Mol	Chain	Res	Type	RSRZ
1	C	69	THR	3.0
1	B	286	LYS	2.9
1	C	143	ASP	2.7
1	C	287	GLU	2.7
1	B	123	TYR	2.7
1	A	287	GLU	2.7
1	B	129	THR	2.7
1	A	119	ILE	2.6
1	A	72	VAL	2.6
1	D	123	TYR	2.6
1	B	203	MET	2.6
1	A	70	LYS	2.6
1	D	116	TYR	2.6
1	B	248	ASP	2.6
1	A	124	ASN	2.6
1	D	132	LYS	2.6
1	D	130	PHE	2.5
1	C	71	SER	2.5
1	D	286	LYS	2.5
1	D	100	GLU	2.4
1	C	250	ASN	2.4
1	A	284	SER	2.4
1	D	248	ASP	2.4
1	C	68	ASN	2.4
1	C	248	ASP	2.4
1	A	85	ILE	2.4
1	D	166	GLU	2.4
2	E	1	ALA	2.4
1	A	126	GLU	2.4
1	D	127	VAL	2.4
1	A	90	ASP	2.3
1	B	69	THR	2.3
1	D	160	LEU	2.3
1	D	126	GLU	2.3
1	B	95	ASN	2.3
1	D	82	ILE	2.3
1	A	97	GLN	2.3
1	B	68	ASN	2.3
1	D	80	LEU	2.2
1	A	84	LYS	2.2
1	A	224	LYS	2.2
1	D	98	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	251	ILE	2.1
1	C	80	LEU	2.1
1	C	285	ALA	2.1
1	B	128	PRO	2.1
1	D	105	THR	2.1
1	A	161	ASN	2.1
1	D	113	TYR	2.1
1	D	121	HIS	2.1
1	A	129	THR	2.1
1	D	279	GLU	2.1
1	D	72	VAL	2.0
1	A	1	MET	2.0
1	B	16	ASN	2.0
1	B	255	LEU	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 ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.