



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 11:06 PM UTC

PDB ID : 2FS3 / pdb_00002fs3
Title : Bacteriophage HK97 K169Y Head I
Authors : Gan, L.; Speir, J.A.; Conway, J.F.; Lander, G.; Cheng, N.; Firek, B.A.; Hendrix, R.W.; Duda, R.L.; Liljas, L.; Johnson, J.E.
Deposited on : 2006-01-20
Resolution : 4.20 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

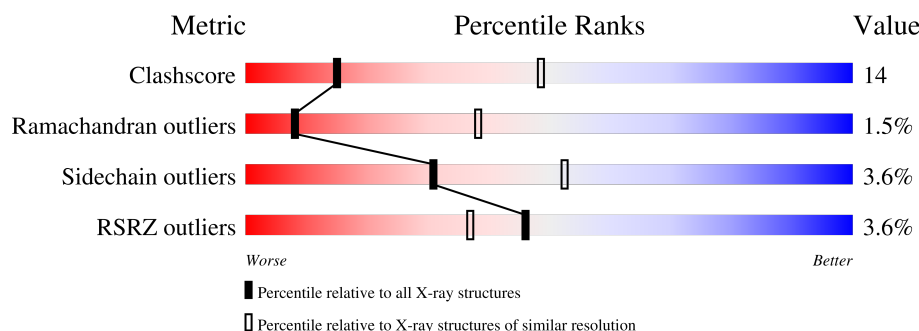
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.20 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))
Clashscore	190562	1019 (4.50-3.90)
Ramachandran outliers	187476	1020 (4.56-3.84)
Sidechain outliers	187428	1006 (4.56-3.84)
RSRZ outliers	180081	1001 (4.52-3.88)

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	282	
1	B	282	
1	C	282	
1	D	282	
1	E	282	
1	F	282	

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Mol	Chain	Length	Quality of chain
1	G	282	7% 56% 27% • 14%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 14664 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 Major capsid protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	280	Total	C	N	O	S	0	0	0
			2154	1347	374	423	10			
1	B	280	Total	C	N	O	S	0	0	0
			2154	1347	374	423	10			
1	C	280	Total	C	N	O	S	0	0	0
			2154	1347	374	423	10			
1	D	280	Total	C	N	O	S	0	0	0
			2154	1347	374	423	10			
1	E	280	Total	C	N	O	S	0	0	0
			2154	1347	374	423	10			
1	F	258	Total	C	N	O	S	0	0	0
			2004	1254	350	391	9			
1	G	243	Total	C	N	O	S	0	0	0
			1890	1181	333	368	8			

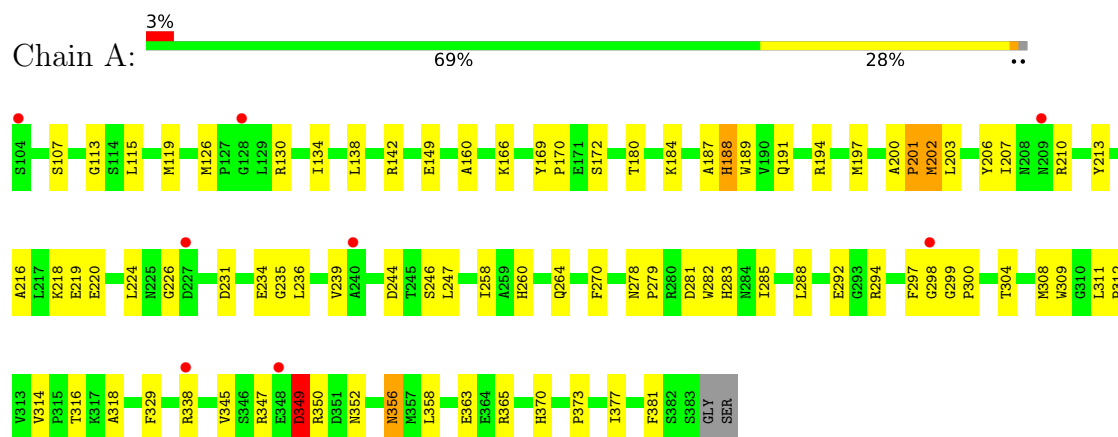
There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	169	TYR	LYS	engineered mutation	UNP P49861
B	169	TYR	LYS	engineered mutation	UNP P49861
C	169	TYR	LYS	engineered mutation	UNP P49861
D	169	TYR	LYS	engineered mutation	UNP P49861
E	169	TYR	LYS	engineered mutation	UNP P49861
F	169	TYR	LYS	engineered mutation	UNP P49861
G	169	TYR	LYS	engineered mutation	UNP P49861

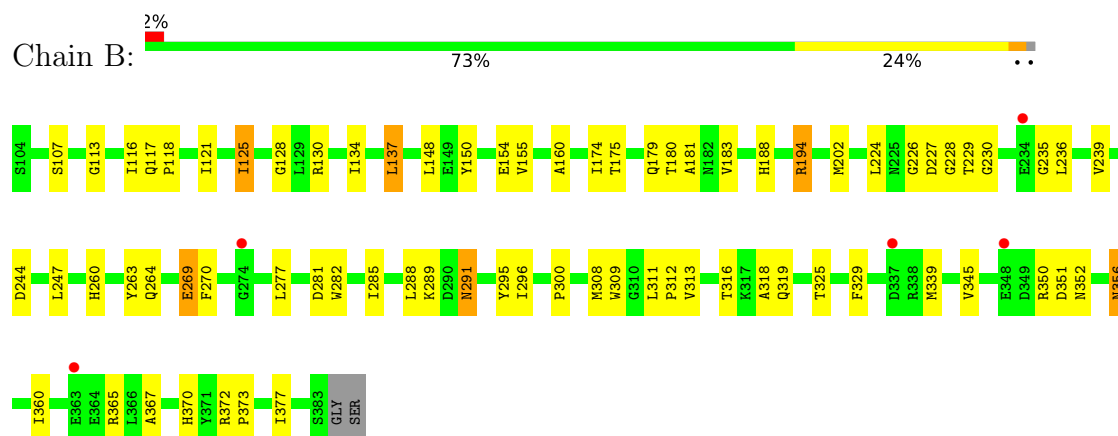
3 Residue-property plots [i](#)

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.

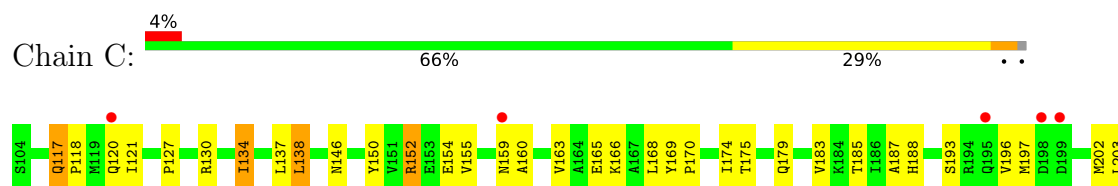
- Molecule 1: Major capsid protein

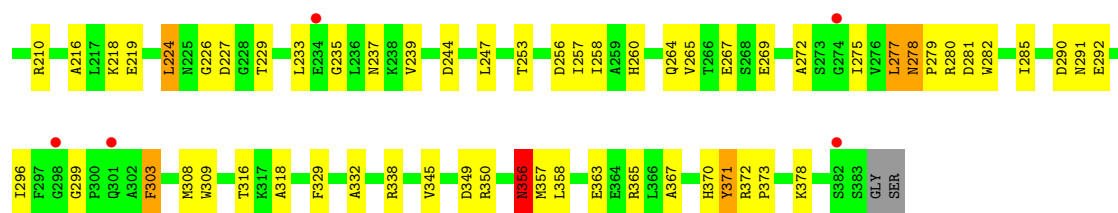


- Molecule 1: Major capsid protein

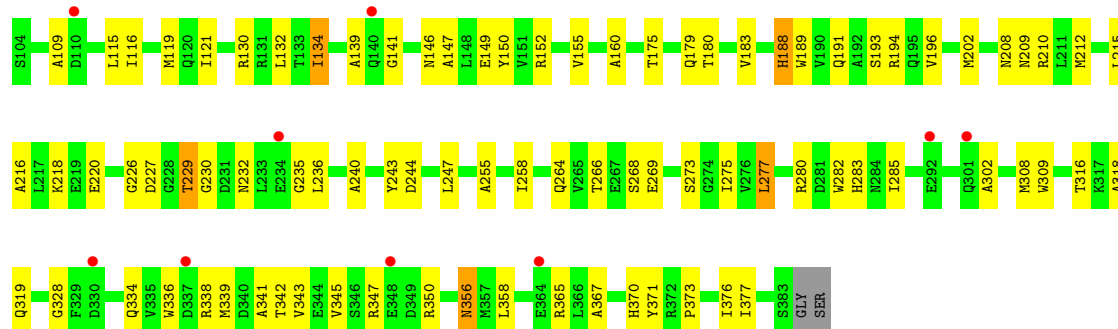


- Molecule 1: Major capsid protein

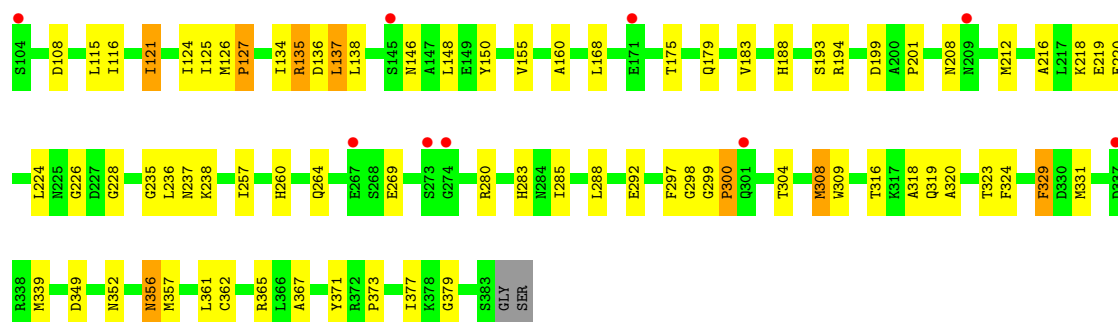




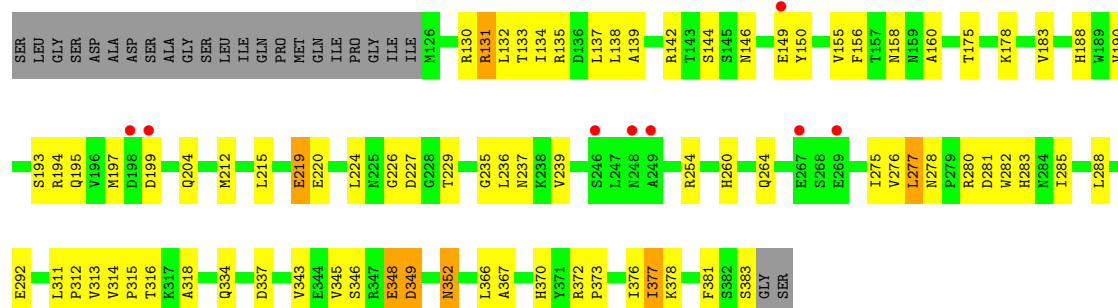
• Molecule 1: Major capsid protein



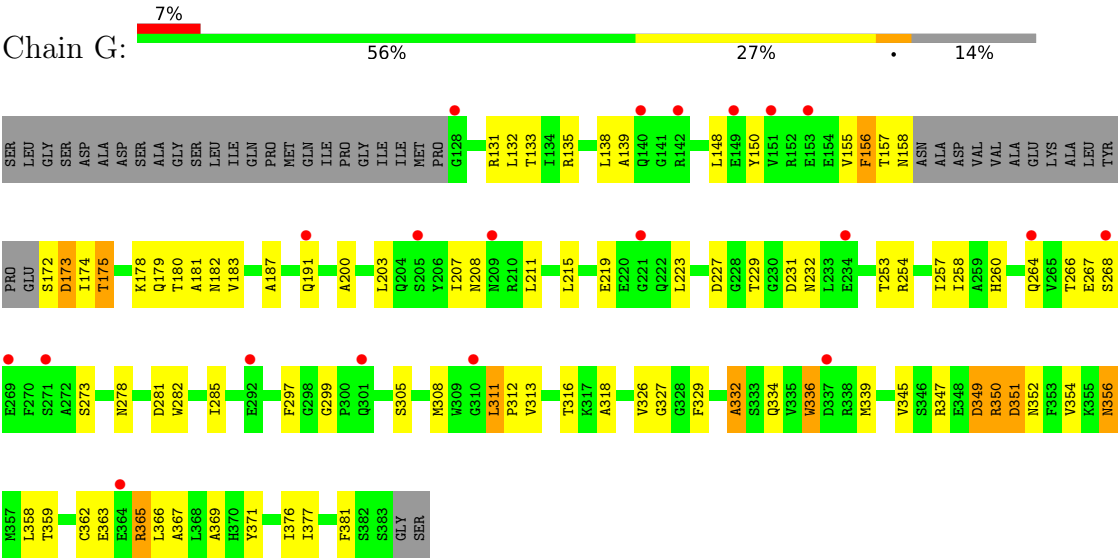
• Molecule 1: Major capsid protein



• Molecule 1: Major capsid protein



• Molecule 1: Major capsid protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	1009.64Å 1009.64Å 729.81Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 4.20 30.00 – 4.20	Depositor EDS
% Data completeness (in resolution range)	63.1 (30.00-4.20) 62.9 (30.00-4.20)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.95 (at 4.26Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.384 , (Not available) 0.356 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	20.0	Xtriage
Anisotropy	2.024	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.21 , 0.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.18	EDS
Total number of atoms	14664	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.10% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.27	0/2192	0.80	4/2976 (0.1%)
1	B	0.28	0/2192	0.83	2/2976 (0.1%)
1	C	0.27	0/2192	0.84	9/2976 (0.3%)
1	D	0.28	0/2192	0.82	1/2976 (0.0%)
1	E	0.28	0/2192	0.87	5/2976 (0.2%)
1	F	0.28	0/2040	0.82	3/2769 (0.1%)
1	G	0.35	0/1922	0.85	6/2605 (0.2%)
All	All	0.29	0/14922	0.83	30/20254 (0.1%)

There are no bond length outliers.

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	299	GLY	CA-C-N	8.86	130.91	119.84
1	E	299	GLY	C-N-CA	8.86	130.91	119.84
1	E	228	GLY	N-CA-C	-6.78	106.40	115.21
1	G	347	ARG	N-CA-C	-6.12	105.67	113.02
1	C	117	GLN	CA-C-N	6.08	126.09	119.89
1	C	117	GLN	C-N-CA	6.08	126.09	119.89
1	C	356	ASN	CB-CA-C	6.07	122.50	110.42
1	G	299	GLY	CA-C-N	5.78	126.18	119.47
1	G	299	GLY	C-N-CA	5.78	126.18	119.47
1	F	219	GLU	N-CA-C	-5.77	104.99	111.28
1	A	314	VAL	N-CA-C	5.75	113.84	108.15
1	B	228	GLY	N-CA-C	-5.58	108.17	115.47
1	B	125	ILE	N-CA-C	5.48	115.14	106.32
1	D	338	ARG	N-CA-C	-5.40	104.81	111.40
1	F	372	ARG	CA-C-N	5.35	125.17	119.28
1	F	372	ARG	C-N-CA	5.35	125.17	119.28
1	C	372	ARG	CA-C-N	5.27	124.78	119.19
1	C	372	ARG	C-N-CA	5.27	124.78	119.19
1	A	200	ALA	CA-C-N	5.21	126.35	119.84
1	A	200	ALA	C-N-CA	5.21	126.35	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	121	ILE	CA-C-N	5.18	126.32	119.84
1	E	121	ILE	C-N-CA	5.18	126.32	119.84
1	G	351	ASP	N-CA-C	5.18	117.62	107.57
1	C	338	ARG	N-CA-C	-5.14	106.70	113.12
1	C	356	ASN	CA-CB-CG	5.13	117.73	112.60
1	A	278	ASN	N-CA-C	-5.12	103.20	109.65
1	G	311	LEU	CA-C-N	5.07	125.00	119.78
1	G	311	LEU	C-N-CA	5.07	125.00	119.78
1	C	299	GLY	CA-C-N	5.06	126.16	119.84
1	C	299	GLY	C-N-CA	5.06	126.16	119.84

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	2154	0	2115	66	0
1	B	2154	0	2115	55	0
1	C	2154	0	2115	67	0
1	D	2154	0	2115	72	0
1	E	2154	0	2115	55	0
1	F	2004	0	1963	61	0
1	G	1890	0	1851	70	0
All	All	14664	0	14389	399	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 14.

All (399) 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:F:130:ARG:HD3	1:F:131:ARG:H	1.33	0.92
1:D:264:GLN:HE21	1:D:377:ILE:HD12	1.40	0.85
1:E:297:PHE:HB3	1:E:304:THR:HG21	1.59	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:157:THR:HB	1:G:173:ASP:O	1.76	0.83
1:G:191:GLN:HG3	1:G:359:THR:HG22	1.61	0.83
1:D:121:ILE:HD12	1:E:150:TYR:HB3	1.60	0.83
1:G:345:VAL:HG13	1:G:358:LEU:HD21	1.60	0.83
1:A:130:ARG:HA	1:B:269:GLU:HG2	1.63	0.79
1:F:142:ARG:HH11	1:F:142:ARG:HB3	1.47	0.79
1:F:316:THR:HG22	1:F:318:ALA:H	1.48	0.79
1:F:226:GLY:H	1:F:235:GLY:HA3	1.48	0.78
1:G:158:ASN:HA	1:G:172:SER:HA	1.64	0.78
1:E:116:ILE:HD12	1:F:146:ASN:HB2	1.66	0.78
1:A:194:ARG:HB3	1:A:356:ASN:ND2	2.00	0.77
1:B:116:ILE:HD12	1:C:146:ASN:HB2	1.68	0.75
1:D:194:ARG:HH21	1:D:347:ARG:HD3	1.53	0.74
1:G:336:TRP:HE1	1:G:369:ALA:HB2	1.52	0.73
1:G:345:VAL:CG1	1:G:358:LEU:HD21	2.17	0.73
1:A:244:ASP:HB2	1:A:264:GLN:HE22	1.53	0.73
1:D:277:LEU:HA	1:D:319:GLN:HG2	1.72	0.72
1:B:183:VAL:HG22	1:B:367:ALA:HB2	1.72	0.71
1:F:254:ARG:HH21	1:F:383:SER:HB2	1.54	0.71
1:G:264:GLN:HB3	1:G:377:ILE:HD13	1.71	0.71
1:G:183:VAL:HG22	1:G:367:ALA:HB2	1.73	0.71
1:G:227:ASP:HB2	1:G:232:ASN:HD22	1.56	0.70
1:E:226:GLY:H	1:E:235:GLY:HA3	1.56	0.70
1:G:350:ARG:HG3	1:G:351:ASP:H	1.56	0.70
1:B:277:LEU:HA	1:B:319:GLN:HG2	1.74	0.69
1:D:258:ILE:HD11	1:D:275:ILE:HD13	1.74	0.69
1:C:316:THR:HG22	1:C:318:ALA:H	1.58	0.69
1:G:155:VAL:HB	1:G:175:THR:HB	1.76	0.68
1:A:297:PHE:HB3	1:A:304:THR:HG21	1.75	0.68
1:G:316:THR:HG22	1:G:318:ALA:H	1.59	0.68
1:D:258:ILE:HD11	1:D:275:ILE:HG21	1.76	0.67
1:A:184:LYS:NZ	1:A:231:ASP:HA	2.10	0.67
1:D:149:GLU:HG2	1:D:180:THR:HG22	1.77	0.67
1:G:349:ASP:N	1:G:352:ASN:ND2	2.43	0.67
1:D:316:THR:HG22	1:D:318:ALA:H	1.60	0.66
1:E:316:THR:HG22	1:E:318:ALA:H	1.60	0.66
1:A:189:TRP:HZ3	1:A:191:GLN:HB2	1.59	0.66
1:A:142:ARG:HH11	1:A:142:ARG:HB3	1.59	0.66
1:B:150:TYR:CE1	1:B:179:GLN:HB2	2.30	0.66
1:G:157:THR:H	1:G:174:ILE:HD13	1.60	0.65
1:F:142:ARG:HB3	1:F:142:ARG:NH1	2.11	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:150:TYR:CE1	1:D:179:GLN:HB2	2.32	0.65
1:A:244:ASP:HB2	1:A:264:GLN:NE2	2.10	0.65
1:B:121:ILE:HD12	1:C:150:TYR:HB3	1.79	0.65
1:D:339:MET:HE2	1:D:365:ARG:HG3	1.79	0.64
1:A:345:VAL:HB	1:A:358:LEU:HD21	1.78	0.64
1:G:257:ILE:HA	1:G:260:HIS:HD2	1.62	0.64
1:E:339:MET:HE2	1:E:365:ARG:HG3	1.78	0.63
1:F:275:ILE:HB	1:F:313:VAL:HG12	1.81	0.63
1:A:258:ILE:HD11	1:A:381:PHE:HZ	1.62	0.63
1:B:339:MET:HB3	1:B:365:ARG:H	1.64	0.63
1:D:229:THR:HG23	1:D:230:GLY:H	1.63	0.63
1:B:239:VAL:HG12	1:B:373:PRO:HB3	1.80	0.63
1:C:152:ARG:HH11	1:C:152:ARG:HB2	1.64	0.63
1:C:244:ASP:HB2	1:C:264:GLN:HE22	1.63	0.63
1:G:139:ALA:O	1:G:334:GLN:HB2	1.98	0.62
1:A:142:ARG:HB3	1:A:142:ARG:NH1	2.14	0.62
1:C:278:ASN:C	1:C:278:ASN:HD22	2.08	0.61
1:F:130:ARG:CD	1:F:131:ARG:H	2.07	0.61
1:E:183:VAL:HG22	1:E:367:ALA:HB2	1.81	0.61
1:C:130:ARG:HA	1:D:269:GLU:HG2	1.82	0.61
1:D:193:SER:HB3	1:D:196:VAL:HG23	1.82	0.61
1:G:282:TRP:HA	1:G:285:ILE:HD12	1.82	0.61
1:D:191:GLN:HE22	1:D:350:ARG:HH21	1.49	0.60
1:E:124:ILE:HG22	1:E:125:ILE:H	1.67	0.59
1:F:132:LEU:HD23	1:F:132:LEU:O	2.02	0.59
1:B:236:LEU:HD23	1:B:370:HIS:HE1	1.67	0.59
1:G:229:THR:HG23	1:G:231:ASP:H	1.66	0.59
1:G:227:ASP:HB2	1:G:232:ASN:ND2	2.16	0.59
1:E:264:GLN:HB3	1:E:377:ILE:HD13	1.84	0.59
1:C:218:LYS:HG3	1:D:160:ALA:O	2.02	0.59
1:F:197:MET:HE1	1:F:204:GLN:HA	1.85	0.59
1:B:137:LEU:HD22	1:B:329:PHE:HB2	1.85	0.59
1:D:218:LYS:HG3	1:E:160:ALA:O	2.02	0.58
1:F:236:LEU:HD23	1:F:370:HIS:HE1	1.68	0.58
1:B:270:PHE:CZ	1:B:372:ARG:HD3	2.37	0.58
1:C:127:PRO:HD2	1:C:210:ARG:HH21	1.68	0.58
1:G:200:ALA:O	1:G:203:LEU:HB3	2.04	0.58
1:F:239:VAL:HG12	1:F:373:PRO:HB3	1.86	0.58
1:D:134:ILE:HD12	1:D:220:GLU:HG3	1.84	0.58
1:A:236:LEU:HD23	1:A:370:HIS:HE1	1.69	0.58
1:A:356:ASN:C	1:A:356:ASN:HD22	2.10	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:300:PRO:HG2	1:B:296:ILE:HG23	1.86	0.57
1:A:194:ARG:HB3	1:A:356:ASN:HD22	1.67	0.57
1:E:121:ILE:HD12	1:F:150:TYR:HB3	1.86	0.57
1:E:349:ASP:O	1:E:352:ASN:HB2	2.04	0.57
1:F:130:ARG:HD3	1:F:131:ARG:N	2.13	0.57
1:C:150:TYR:CE1	1:C:179:GLN:HB2	2.39	0.57
1:F:282:TRP:HA	1:F:285:ILE:HD12	1.85	0.57
1:D:255:ALA:O	1:D:258:ILE:HG22	2.04	0.57
1:D:243:TYR:HA	1:D:264:GLN:HE22	1.69	0.57
1:G:336:TRP:HZ2	1:G:371:TYR:HH	1.52	0.56
1:F:183:VAL:HG22	1:F:367:ALA:HB2	1.86	0.56
1:G:207:ILE:O	1:G:211:LEU:HG	2.04	0.56
1:D:189:TRP:HZ3	1:D:191:GLN:HB2	1.70	0.56
1:G:155:VAL:HB	1:G:175:THR:CB	2.35	0.56
1:A:338:ARG:HB3	1:A:365:ARG:HB2	1.88	0.56
1:G:264:GLN:HB3	1:G:377:ILE:CD1	2.34	0.56
1:D:229:THR:HG23	1:D:230:GLY:N	2.20	0.55
1:E:371:TYR:O	1:E:373:PRO:HD3	2.06	0.55
1:G:257:ILE:HA	1:G:260:HIS:CD2	2.41	0.55
1:C:197:MET:SD	1:C:203:LEU:HD23	2.46	0.55
1:E:218:LYS:HG3	1:F:160:ALA:O	2.07	0.55
1:A:149:GLU:HG2	1:A:180:THR:HG23	1.88	0.55
1:C:121:ILE:HD12	1:D:150:TYR:HB3	1.87	0.55
1:F:155:VAL:H	1:F:175:THR:HB	1.72	0.55
1:D:191:GLN:HE22	1:D:350:ARG:NH2	2.04	0.55
1:G:349:ASP:CG	1:G:352:ASN:HD21	2.15	0.55
1:F:239:VAL:HG21	1:F:370:HIS:CD2	2.42	0.55
1:G:349:ASP:H	1:G:352:ASN:ND2	2.06	0.54
1:E:193:SER:HA	1:E:357:MET:HG2	1.90	0.54
1:E:264:GLN:HB3	1:E:377:ILE:CD1	2.38	0.54
1:A:316:THR:HG22	1:A:318:ALA:H	1.71	0.54
1:D:155:VAL:H	1:D:175:THR:HB	1.72	0.54
1:D:264:GLN:HE21	1:D:377:ILE:CD1	2.18	0.54
1:E:134:ILE:HB	1:E:220:GLU:HG3	1.89	0.54
1:C:120:GLN:NE2	1:D:149:GLU:HB2	2.23	0.53
1:B:128:GLY:HA3	1:C:269:GLU:HB3	1.89	0.53
1:A:184:LYS:HZ1	1:A:231:ASP:HA	1.73	0.53
1:A:308:MET:HG2	1:A:309:TRP:CD1	2.44	0.53
1:C:239:VAL:HG12	1:C:373:PRO:HB3	1.91	0.53
1:D:273:SER:H	1:D:328:GLY:HA2	1.72	0.53
1:G:349:ASP:N	1:G:352:ASN:HD21	2.05	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:260:HIS:HA	1:F:283:HIS:NE2	2.24	0.53
1:C:154:GLU:HG3	1:C:155:VAL:HG23	1.89	0.53
1:G:229:THR:HG22	1:G:232:ASN:ND2	2.23	0.53
1:G:138:LEU:HD23	1:G:329:PHE:HB3	1.91	0.53
1:B:350:ARG:HG3	1:B:351:ASP:H	1.73	0.52
1:A:264:GLN:HB3	1:A:377:ILE:HD13	1.90	0.52
1:C:183:VAL:HG22	1:C:367:ALA:HB2	1.92	0.52
1:C:329:PHE:HA	1:C:332:ALA:HB3	1.92	0.52
1:E:194:ARG:HB3	1:E:356:ASN:ND2	2.25	0.52
1:F:219:GLU:HG3	1:F:366:LEU:HD11	1.90	0.52
1:G:352:ASN:C	1:G:354:VAL:H	2.16	0.52
1:G:215:LEU:HD22	1:G:362:CYS:SG	2.49	0.52
1:A:279:PRO:HB2	1:B:263:TYR:OH	2.09	0.52
1:G:376:ILE:C	1:G:377:ILE:HG13	2.34	0.52
1:A:258:ILE:HD11	1:A:381:PHE:CZ	2.44	0.52
1:D:146:ASN:O	1:D:183:VAL:HG12	2.09	0.52
1:G:174:ILE:HG22	1:G:175:THR:N	2.25	0.52
1:E:124:ILE:HG22	1:E:125:ILE:N	2.25	0.51
1:A:130:ARG:HA	1:B:269:GLU:CG	2.35	0.51
1:E:135:ARG:HG2	1:E:135:ARG:HH11	1.75	0.51
1:D:188:HIS:CE1	1:E:160:ALA:HB2	2.46	0.51
1:E:138:LEU:H	1:E:138:LEU:HD12	1.74	0.51
1:G:138:LEU:HB3	1:G:334:GLN:HA	1.92	0.51
1:G:150:TYR:O	1:G:178:LYS:HG2	2.11	0.51
1:C:282:TRP:HA	1:C:285:ILE:HD12	1.92	0.51
1:D:229:THR:CG2	1:D:232:ASN:HD22	2.24	0.51
1:F:156:PHE:CE2	1:F:158:ASN:HB2	2.46	0.50
1:A:138:LEU:HD23	1:A:329:PHE:HB3	1.93	0.50
1:B:188:HIS:ND1	1:C:160:ALA:HB2	2.26	0.50
1:B:289:LYS:HE2	1:B:295:TYR:HE2	1.74	0.50
1:D:345:VAL:HG13	1:D:358:LEU:HD21	1.92	0.50
1:E:150:TYR:CE1	1:E:179:GLN:HB2	2.46	0.50
1:B:308:MET:HG2	1:B:309:TRP:CD1	2.46	0.50
1:C:278:ASN:HD22	1:C:280:ARG:H	1.59	0.50
1:F:237:ASN:HB3	1:F:378:LYS:HD3	1.94	0.50
1:G:336:TRP:HZ2	1:G:371:TYR:OH	1.94	0.50
1:A:160:ALA:HB2	1:F:188:HIS:ND1	2.26	0.50
1:A:188:HIS:CE1	1:B:160:ALA:HB2	2.47	0.50
1:D:189:TRP:CZ3	1:D:191:GLN:HB2	2.45	0.50
1:E:308:MET:HE2	1:E:309:TRP:HE1	1.75	0.50
1:E:236:LEU:C	1:E:238:LYS:H	2.20	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:283:HIS:NE2	1:F:260:HIS:HA	2.27	0.50
1:D:152:ARG:HE	1:D:179:GLN:HG3	1.77	0.49
1:D:308:MET:HE2	1:D:309:TRP:HE1	1.77	0.49
1:D:342:THR:HG22	1:D:343:VAL:N	2.26	0.49
1:F:193:SER:HB3	1:F:195:GLN:HG2	1.94	0.49
1:B:130:ARG:HA	1:C:269:GLU:CD	2.37	0.49
1:G:334:GLN:HG2	1:G:371:TYR:HE2	1.76	0.49
1:A:226:GLY:H	1:A:235:GLY:HA3	1.77	0.49
1:D:227:ASP:HB3	1:D:229:THR:HG22	1.93	0.49
1:E:115:LEU:HD12	1:E:115:LEU:N	2.28	0.49
1:F:236:LEU:HD23	1:F:370:HIS:CE1	2.45	0.49
1:G:180:THR:HG22	1:G:181:ALA:H	1.78	0.49
1:A:187:ALA:HB2	1:A:363:GLU:HB3	1.95	0.49
1:D:139:ALA:O	1:D:334:GLN:HG3	2.13	0.49
1:F:130:ARG:HH11	1:F:131:ARG:HD3	1.77	0.49
1:A:218:LYS:HG3	1:B:160:ALA:O	2.13	0.49
1:A:281:ASP:O	1:A:285:ILE:HG13	2.12	0.49
1:E:208:ASN:O	1:E:212:MET:HG2	2.12	0.49
1:C:244:ASP:HB2	1:C:264:GLN:NE2	2.26	0.48
1:C:193:SER:OG	1:C:196:VAL:HG23	2.13	0.48
1:C:239:VAL:HG21	1:C:370:HIS:CD2	2.49	0.48
1:F:134:ILE:N	1:F:134:ILE:HD12	2.29	0.48
1:F:212:MET:SD	1:F:343:VAL:HG23	2.53	0.48
1:G:191:GLN:HG3	1:G:359:THR:CG2	2.39	0.48
1:B:325:THR:HA	1:B:377:ILE:O	2.13	0.48
1:D:188:HIS:ND1	1:E:160:ALA:HB2	2.29	0.48
1:A:264:GLN:HB3	1:A:377:ILE:CD1	2.44	0.48
1:C:290:ASP:C	1:C:292:GLU:H	2.21	0.48
1:C:278:ASN:ND2	1:C:280:ARG:H	2.12	0.48
1:F:264:GLN:HG2	1:F:377:ILE:HG21	1.96	0.48
1:A:247:LEU:HD23	1:F:280:ARG:NH2	2.29	0.48
1:D:236:LEU:HD23	1:D:370:HIS:HE1	1.79	0.47
1:C:258:ILE:HD12	1:C:308:MET:HE1	1.95	0.47
1:F:132:LEU:HD11	1:F:315:PRO:O	2.15	0.47
1:G:133:THR:HG22	1:G:135:ARG:H	1.79	0.47
1:G:187:ALA:HB2	1:G:363:GLU:HA	1.96	0.47
1:E:135:ARG:HD2	1:E:135:ARG:C	2.40	0.47
1:C:187:ALA:HB2	1:C:363:GLU:HA	1.96	0.47
1:C:278:ASN:HD22	1:C:279:PRO:N	2.13	0.47
1:G:349:ASP:O	1:G:352:ASN:ND2	2.48	0.47
1:C:227:ASP:OD1	1:C:229:THR:HB	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:371:TYR:O	1:D:373:PRO:HD3	2.14	0.47
1:G:138:LEU:CD2	1:G:329:PHE:HB3	2.45	0.47
1:G:219:GLU:O	1:G:223:LEU:HG	2.14	0.47
1:G:336:TRP:CZ2	1:G:371:TYR:OH	2.66	0.47
1:D:130:ARG:HA	1:E:269:GLU:CD	2.40	0.47
1:G:254:ARG:HD3	1:G:381:PHE:HE2	1.80	0.47
1:B:350:ARG:HG3	1:B:351:ASP:N	2.29	0.47
1:G:332:ALA:O	1:G:371:TYR:HD2	1.97	0.47
1:C:118:PRO:HG3	1:D:147:ALA:HB3	1.97	0.47
1:E:138:LEU:HD12	1:E:138:LEU:N	2.30	0.47
1:A:338:ARG:HH11	1:A:338:ARG:HG2	1.80	0.47
1:B:130:ARG:NH2	1:B:318:ALA:HB2	2.30	0.47
1:G:258:ILE:HD12	1:G:308:MET:HE1	1.97	0.46
1:C:356:ASN:ND2	1:C:356:ASN:O	2.49	0.46
1:D:210:ARG:HG3	1:D:210:ARG:HH11	1.81	0.46
1:F:134:ILE:HD13	1:F:220:GLU:CD	2.40	0.46
1:A:126:MET:HE2	1:A:206:TYR:HE1	1.80	0.46
1:A:282:TRP:HZ3	1:A:308:MET:HE3	1.80	0.46
1:B:226:GLY:HA3	1:B:235:GLY:H	1.80	0.46
1:G:326:VAL:HG12	1:G:327:GLY:N	2.31	0.46
1:A:134:ILE:HD12	1:A:220:GLU:HB3	1.97	0.46
1:A:189:TRP:CZ3	1:A:191:GLN:HB2	2.43	0.46
1:A:297:PHE:HB3	1:A:304:THR:CG2	2.43	0.46
1:F:376:ILE:C	1:F:377:ILE:HD13	2.40	0.46
1:A:166:LYS:O	1:A:166:LYS:HG2	2.16	0.46
1:C:185:THR:HG22	1:C:365:ARG:HG2	1.98	0.46
1:E:324:PHE:CZ	1:E:379:GLY:HA3	2.51	0.46
1:G:352:ASN:O	1:G:356:ASN:N	2.46	0.46
1:C:257:ILE:O	1:C:260:HIS:HB2	2.16	0.46
1:G:156:PHE:CD1	1:G:156:PHE:N	2.82	0.46
1:C:224:LEU:HD12	1:C:237:ASN:HD21	1.81	0.46
1:D:226:GLY:H	1:D:235:GLY:HA3	1.81	0.46
1:F:139:ALA:O	1:F:334:GLN:HG3	2.17	0.45
1:F:264:GLN:HG2	1:F:377:ILE:HD12	1.97	0.45
1:F:281:ASP:O	1:F:285:ILE:HG13	2.15	0.45
1:E:188:HIS:HB3	1:F:160:ALA:HA	1.98	0.45
1:D:141:GLY:O	1:D:336:TRP:HA	2.17	0.45
1:F:348:GLU:O	1:F:349:ASP:HB2	2.16	0.45
1:B:155:VAL:H	1:B:175:THR:HB	1.80	0.45
1:A:107:SER:O	1:A:113:GLY:HA3	2.15	0.45
1:B:226:GLY:H	1:B:235:GLY:HA3	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:300:PRO:HD2	1:C:296:ILE:HG22	1.99	0.45
1:C:165:GLU:HG2	1:C:166:LYS:HG3	1.99	0.45
1:C:265:VAL:HG21	1:C:272:ALA:HB2	1.99	0.45
1:D:308:MET:HE2	1:D:309:TRP:NE1	2.31	0.45
1:D:376:ILE:O	1:D:377:ILE:HD13	2.17	0.45
1:C:174:ILE:HG22	1:C:175:THR:N	2.31	0.45
1:E:135:ARG:C	1:E:137:LEU:H	2.25	0.45
1:G:157:THR:H	1:G:174:ILE:CD1	2.28	0.45
1:A:349:ASP:O	1:A:350:ARG:C	2.60	0.45
1:B:194:ARG:HB3	1:B:356:ASN:ND2	2.31	0.45
1:D:345:VAL:CG1	1:D:358:LEU:HD21	2.47	0.45
1:G:131:ARG:HG3	1:G:132:LEU:N	2.32	0.45
1:A:347:ARG:H	1:A:347:ARG:HD2	1.82	0.45
1:D:115:LEU:HD23	1:D:115:LEU:O	2.17	0.45
1:G:358:LEU:C	1:G:358:LEU:HD23	2.42	0.45
1:C:168:LEU:HD23	1:C:169:TYR:O	2.16	0.45
1:E:199:ASP:O	1:E:201:PRO:HD3	2.17	0.45
1:C:371:TYR:HD1	1:C:371:TYR:H	1.65	0.44
1:F:227:ASP:C	1:F:229:THR:H	2.25	0.44
1:B:117:GLN:HA	1:B:118:PRO:HD3	1.87	0.44
1:C:155:VAL:H	1:C:175:THR:HB	1.81	0.44
1:B:281:ASP:O	1:B:285:ILE:HG13	2.16	0.44
1:D:130:ARG:NH2	1:D:318:ALA:HB2	2.32	0.44
1:F:345:VAL:HG12	1:F:346:SER:N	2.31	0.44
1:G:203:LEU:HG	1:G:207:ILE:HD11	1.99	0.44
1:C:264:GLN:O	1:C:267:GLU:HB2	2.18	0.44
1:C:275:ILE:HG22	1:C:277:LEU:HD11	1.99	0.44
1:D:183:VAL:HG23	1:D:367:ALA:HB2	1.98	0.44
1:E:155:VAL:H	1:E:175:THR:HB	1.83	0.44
1:F:130:ARG:NH1	1:F:131:ARG:HD3	2.33	0.44
1:F:133:THR:C	1:F:134:ILE:HD12	2.43	0.44
1:B:316:THR:HG22	1:B:318:ALA:H	1.82	0.44
1:C:371:TYR:N	1:C:371:TYR:CD1	2.86	0.44
1:E:137:LEU:HD22	1:E:329:PHE:HB2	2.00	0.44
1:E:188:HIS:ND1	1:F:160:ALA:HB2	2.33	0.44
1:F:276:VAL:HG22	1:F:314:VAL:HG23	1.99	0.44
1:B:174:ILE:HG22	1:B:175:THR:N	2.33	0.44
1:C:349:ASP:CG	1:C:350:ARG:HG2	2.43	0.44
1:D:116:ILE:HG21	1:E:146:ASN:HB2	1.98	0.44
1:G:349:ASP:O	1:G:351:ASP:N	2.50	0.44
1:A:244:ASP:OD1	1:A:246:SER:HB3	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:149:GLU:OE2	1:F:178:LYS:HD3	2.18	0.44
1:G:183:VAL:HG13	1:G:366:LEU:O	2.17	0.44
1:G:339:MET:HB3	1:G:365:ARG:HG2	2.00	0.44
1:C:188:HIS:ND1	1:D:160:ALA:HB2	2.32	0.43
1:C:277:LEU:N	1:C:277:LEU:HD12	2.33	0.43
1:F:138:LEU:HD12	1:F:138:LEU:N	2.33	0.43
1:D:244:ASP:OD2	1:D:247:LEU:HG	2.18	0.43
1:E:292:GLU:OE1	1:F:292:GLU:HG3	2.18	0.43
1:C:120:GLN:HE22	1:D:149:GLU:HB2	1.83	0.43
1:D:132:LEU:H	1:D:132:LEU:HD12	1.83	0.43
1:G:282:TRP:CZ3	1:G:313:VAL:HG11	2.53	0.43
1:A:210:ARG:HH12	1:A:213:TYR:HD2	1.67	0.43
1:C:216:ALA:O	1:C:219:GLU:HB3	2.18	0.43
1:A:349:ASP:O	1:A:352:ASN:HB2	2.18	0.43
1:B:107:SER:O	1:B:113:GLY:HA3	2.19	0.43
1:C:193:SER:HA	1:C:357:MET:HA	2.01	0.43
1:B:345:VAL:HG12	1:B:360:ILE:HA	2.01	0.43
1:D:194:ARG:HB2	1:D:356:ASN:O	2.18	0.43
1:G:180:THR:HG22	1:G:181:ALA:N	2.34	0.43
1:A:216:ALA:O	1:A:219:GLU:HB3	2.18	0.43
1:D:119:MET:HB3	1:E:148:LEU:CD2	2.49	0.43
1:C:308:MET:HG2	1:C:309:TRP:CD1	2.53	0.43
1:D:212:MET:HE1	1:D:341:ALA:O	2.19	0.43
1:E:216:ALA:O	1:E:219:GLU:HB3	2.19	0.43
1:A:285:ILE:O	1:A:288:LEU:HB2	2.19	0.43
1:A:349:ASP:CG	1:A:350:ARG:HG2	2.44	0.42
1:C:138:LEU:HD12	1:C:138:LEU:H	1.83	0.42
1:D:210:ARG:HD2	1:D:210:ARG:HA	1.87	0.42
1:A:201:PRO:C	1:A:203:LEU:H	2.27	0.42
1:C:278:ASN:HB3	1:C:281:ASP:OD2	2.18	0.42
1:F:215:LEU:C	1:F:215:LEU:HD23	2.44	0.42
1:F:264:GLN:HG2	1:F:377:ILE:CG2	2.49	0.42
1:G:266:THR:C	1:G:268:SER:H	2.28	0.42
1:C:345:VAL:HB	1:C:358:LEU:HD11	2.00	0.42
1:A:119:MET:HB3	1:B:148:LEU:CD2	2.49	0.42
1:B:137:LEU:CD2	1:B:329:PHE:HB2	2.48	0.42
1:B:282:TRP:CZ3	1:B:313:VAL:HG11	2.54	0.42
1:B:311:LEU:HA	1:B:312:PRO:HD3	1.91	0.42
1:A:283:HIS:NE2	1:B:260:HIS:HA	2.35	0.42
1:C:303:PHE:HD1	1:C:303:PHE:H	1.66	0.42
1:C:371:TYR:O	1:C:373:PRO:HD3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:172:SER:O	1:F:190:VAL:HG22	2.20	0.42
1:C:134:ILE:O	1:C:137:LEU:HB2	2.19	0.42
1:F:349:ASP:O	1:F:352:ASN:HB2	2.19	0.42
1:G:273:SER:O	1:G:312:PRO:HD2	2.20	0.42
1:G:278:ASN:HB3	1:G:281:ASP:OD2	2.20	0.42
1:A:169:TYR:HA	1:A:170:PRO:HD3	1.87	0.42
1:B:288:LEU:O	1:B:296:ILE:HG12	2.20	0.42
1:E:361:LEU:HD12	1:E:362:CYS:H	1.83	0.42
1:B:244:ASP:OD1	1:B:247:LEU:HG	2.20	0.42
1:B:264:GLN:HB3	1:B:377:ILE:HD13	2.01	0.42
1:A:300:PRO:HG2	1:B:296:ILE:CG2	2.50	0.41
1:B:202:MET:N	1:B:202:MET:SD	2.93	0.41
1:D:302:ALA:O	1:E:309:TRP:HA	2.20	0.41
1:A:311:LEU:HA	1:A:312:PRO:HD3	1.89	0.41
1:D:208:ASN:O	1:D:212:MET:HG2	2.19	0.41
1:E:280:ARG:O	1:E:283:HIS:HB3	2.19	0.41
1:E:329:PHE:C	1:E:331:MET:H	2.28	0.41
1:B:264:GLN:HB3	1:B:377:ILE:CD1	2.50	0.41
1:D:215:LEU:HD23	1:D:216:ALA:N	2.35	0.41
1:B:125:ILE:HB	1:C:152:ARG:HA	2.03	0.41
1:B:227:ASP:C	1:B:229:THR:H	2.29	0.41
1:B:339:MET:HB3	1:B:365:ARG:HB2	2.00	0.41
1:D:280:ARG:O	1:D:283:HIS:HB3	2.20	0.41
1:D:342:THR:HG22	1:D:343:VAL:H	1.84	0.41
1:F:254:ARG:HB3	1:F:381:PHE:HE2	1.84	0.41
1:C:226:GLY:HA3	1:C:235:GLY:HA3	2.01	0.41
1:D:116:ILE:HG21	1:E:146:ASN:CB	2.51	0.41
1:D:132:LEU:HD12	1:D:132:LEU:N	2.36	0.41
1:B:154:GLU:HG3	1:B:155:VAL:HG23	2.02	0.41
1:F:311:LEU:HA	1:F:312:PRO:HD3	1.86	0.41
1:G:311:LEU:HA	1:G:312:PRO:HD3	1.87	0.41
1:C:163:VAL:CG2	1:C:170:PRO:HD3	2.50	0.41
1:G:349:ASP:C	1:G:350:ARG:HG2	2.46	0.41
1:A:234:GLU:HG2	1:A:239:VAL:CG2	2.51	0.41
1:E:257:ILE:O	1:E:260:HIS:HB2	2.21	0.41
1:F:135:ARG:HH21	1:F:337:ASP:CG	2.28	0.41
1:A:239:VAL:HG12	1:A:373:PRO:HB3	2.02	0.41
1:B:188:HIS:HB3	1:C:160:ALA:HA	2.02	0.41
1:C:253:THR:OG1	1:C:256:ASP:HB2	2.21	0.41
1:D:134:ILE:HD12	1:D:220:GLU:CG	2.51	0.41
1:D:266:THR:C	1:D:268:SER:H	2.29	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:126:MET:HA	1:E:127:PRO:HD3	1.94	0.41
1:E:135:ARG:HH11	1:E:135:ARG:CG	2.33	0.41
1:E:226:GLY:HA3	1:E:235:GLY:H	1.85	0.41
1:E:285:ILE:O	1:E:288:LEU:HG	2.21	0.41
1:E:320:ALA:HB3	1:E:323:THR:OG1	2.21	0.41
1:G:174:ILE:CG2	1:G:175:THR:N	2.84	0.41
1:A:130:ARG:CA	1:B:269:GLU:HG2	2.43	0.41
1:C:244:ASP:OD2	1:C:247:LEU:HG	2.21	0.41
1:C:281:ASP:O	1:C:285:ILE:HG13	2.21	0.41
1:G:345:VAL:HG11	1:G:358:LEU:HD21	2.02	0.41
1:A:197:MET:SD	1:A:203:LEU:HD23	2.61	0.40
1:A:203:LEU:O	1:A:207:ILE:HG12	2.21	0.40
1:C:130:ARG:HA	1:D:269:GLU:CG	2.49	0.40
1:E:224:LEU:HD21	1:E:319:GLN:HA	2.02	0.40
1:F:285:ILE:O	1:F:288:LEU:HG	2.22	0.40
1:A:210:ARG:HA	1:A:210:ARG:HD2	1.88	0.40
1:F:130:ARG:CG	1:F:131:ARG:H	2.33	0.40
1:F:277:LEU:N	1:F:277:LEU:HD12	2.35	0.40
1:A:184:LYS:HZ2	1:A:231:ASP:HA	1.86	0.40
1:A:292:GLU:O	1:B:291:ASN:HB2	2.21	0.40
1:A:297:PHE:O	1:A:299:GLY:N	2.52	0.40
1:B:180:THR:HG22	1:B:181:ALA:N	2.36	0.40
1:F:278:ASN:HB3	1:F:281:ASP:OD2	2.21	0.40
1:D:229:THR:CG2	1:D:230:GLY:H	2.27	0.40
1:D:282:TRP:HA	1:D:285:ILE:HD12	2.04	0.40
1:G:253:THR:O	1:G:257:ILE:HG13	2.21	0.40
1:G:336:TRP:HE1	1:G:369:ALA:CB	2.25	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	278/282 (99%)	241 (87%)	32 (12%)	5 (2%)	6	33
1	B	278/282 (99%)	239 (86%)	36 (13%)	3 (1%)	11	45
1	C	278/282 (99%)	248 (89%)	27 (10%)	3 (1%)	11	45
1	D	278/282 (99%)	247 (89%)	27 (10%)	4 (1%)	9	39
1	E	278/282 (99%)	244 (88%)	29 (10%)	5 (2%)	6	33
1	F	256/282 (91%)	228 (89%)	24 (9%)	4 (2%)	7	37
1	G	239/282 (85%)	204 (85%)	30 (13%)	5 (2%)	5	30
All	All	1885/1974 (96%)	1651 (88%)	205 (11%)	29 (2%)	8	38

All (29) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	201	PRO
1	E	300	PRO
1	F	352	ASN
1	A	202	MET
1	B	352	ASN
1	D	109	ALA
1	D	229	THR
1	E	237	ASN
1	E	298	GLY
1	F	349	ASP
1	G	305	SER
1	G	332	ALA
1	G	349	ASP
1	G	350	ARG
1	A	298	GLY
1	A	349	ASP
1	C	291	ASN
1	E	136	ASP
1	F	131	ARG
1	F	144	SER
1	G	267	GLU
1	C	202	MET
1	A	294	ARG
1	D	240	ALA
1	E	127	PRO
1	D	134	ILE
1	B	134	ILE
1	B	230	GLY
1	C	134	ILE

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	230/231 (100%)	223 (97%)	7 (3%)	36	57
1	B	230/231 (100%)	224 (97%)	6 (3%)	40	61
1	C	230/231 (100%)	218 (95%)	12 (5%)	21	44
1	D	230/231 (100%)	225 (98%)	5 (2%)	45	64
1	E	230/231 (100%)	222 (96%)	8 (4%)	32	53
1	F	213/231 (92%)	206 (97%)	7 (3%)	33	55
1	G	201/231 (87%)	190 (94%)	11 (6%)	19	43
All	All	1564/1617 (97%)	1508 (96%)	56 (4%)	31	52

All (56) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	115	LEU
1	A	188	HIS
1	A	202	MET
1	A	224	LEU
1	A	270	PHE
1	A	349	ASP
1	A	356	ASN
1	B	137	LEU
1	B	194	ARG
1	B	224	LEU
1	B	269	GLU
1	B	291	ASN
1	B	356	ASN
1	C	117	GLN
1	C	138	LEU
1	C	152	ARG
1	C	159	ASN
1	C	224	LEU
1	C	233	LEU
1	C	277	LEU

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Mol	Chain	Res	Type
1	C	278	ASN
1	C	303	PHE
1	C	356	ASN
1	C	371	TYR
1	C	378	LYS
1	D	188	HIS
1	D	202	MET
1	D	209	ASN
1	D	277	LEU
1	D	356	ASN
1	E	108	ASP
1	E	135	ARG
1	E	137	LEU
1	E	168	LEU
1	E	300	PRO
1	E	308	MET
1	E	329	PHE
1	E	356	ASN
1	F	137	LEU
1	F	194	ARG
1	F	199	ASP
1	F	224	LEU
1	F	277	LEU
1	F	348	GLU
1	F	377	ILE
1	G	148	LEU
1	G	156	PHE
1	G	173	ASP
1	G	175	THR
1	G	179	GLN
1	G	182	ASN
1	G	208	ASN
1	G	297	PHE
1	G	336	TRP
1	G	356	ASN
1	G	365	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (59) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	195	GLN
1	A	222	GLN

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Mol	Chain	Res	Type
1	A	264	GLN
1	A	291	ASN
1	A	306	ASN
1	A	334	GLN
1	A	356	ASN
1	B	120	GLN
1	B	158	ASN
1	B	191	GLN
1	B	195	GLN
1	B	306	ASN
1	B	334	GLN
1	B	352	ASN
1	B	356	ASN
1	B	370	HIS
1	C	120	GLN
1	C	158	ASN
1	C	195	GLN
1	C	278	ASN
1	C	291	ASN
1	C	334	GLN
1	C	356	ASN
1	D	140	GLN
1	D	191	GLN
1	D	195	GLN
1	D	208	ASN
1	D	232	ASN
1	D	237	ASN
1	D	260	HIS
1	D	264	GLN
1	D	306	ASN
1	D	334	GLN
1	E	158	ASN
1	E	182	ASN
1	E	188	HIS
1	E	191	GLN
1	E	195	GLN
1	E	204	GLN
1	E	208	ASN
1	E	222	GLN
1	E	291	ASN
1	E	306	ASN
1	E	334	GLN

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Mol	Chain	Res	Type
1	E	352	ASN
1	F	158	ASN
1	F	159	ASN
1	F	204	GLN
1	F	248	ASN
1	F	291	ASN
1	F	306	ASN
1	F	334	GLN
1	G	179	GLN
1	G	182	ASN
1	G	222	GLN
1	G	232	ASN
1	G	260	HIS
1	G	334	GLN
1	G	352	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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	280/282 (99%)	0.28	8 (2%)	53	41	8, 74, 127, 208	0
1	B	280/282 (99%)	0.37	5 (1%)	67	52	1, 68, 117, 152	0
1	C	280/282 (99%)	0.30	10 (3%)	46	37	1, 69, 114, 163	0
1	D	280/282 (99%)	0.40	9 (3%)	50	39	1, 69, 117, 187	0
1	E	280/282 (99%)	0.43	9 (3%)	50	39	8, 68, 119, 151	0
1	F	258/282 (91%)	0.28	8 (3%)	51	39	5, 72, 140, 226	0
1	G	243/282 (86%)	0.75	20 (8%)	17	21	41, 122, 182, 225	0
All	All	1901/1974 (96%)	0.40	69 (3%)	46	37	1, 74, 141, 226	0

All (69) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	199	ASP	4.6
1	G	153	GLU	4.4
1	E	337	ASP	4.3
1	F	149	GLU	4.2
1	B	363	GLU	3.9
1	G	128	GLY	3.8
1	D	301	GLN	3.6
1	B	234	GLU	3.4
1	G	140	GLN	3.4
1	G	301	GLN	3.3
1	E	145	SER	3.2
1	D	337	ASP	3.0
1	A	338	ARG	2.9
1	B	337	ASP	2.8
1	E	301	GLN	2.8
1	G	142	ARG	2.8
1	A	227	ASP	2.7

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Mol	Chain	Res	Type	RSRZ
1	G	209	ASN	2.7
1	F	269	GLU	2.7
1	C	159	ASN	2.6
1	A	348	GLU	2.6
1	B	348	GLU	2.6
1	C	120	GLN	2.6
1	C	195	GLN	2.6
1	G	151	VAL	2.5
1	D	348	GLU	2.5
1	D	330	ASP	2.5
1	C	274	GLY	2.5
1	F	248	ASN	2.5
1	G	310	GLY	2.4
1	E	267	GLU	2.4
1	C	298	GLY	2.4
1	G	271	SER	2.4
1	G	264	GLN	2.4
1	G	337	ASP	2.4
1	D	140	GLN	2.3
1	C	199	ASP	2.3
1	F	198	ASP	2.3
1	E	209	ASN	2.3
1	A	240	ALA	2.3
1	D	110	ASP	2.3
1	A	128	GLY	2.3
1	E	274	GLY	2.3
1	C	301	GLN	2.3
1	C	382	SER	2.2
1	B	274	GLY	2.2
1	D	364	GLU	2.2
1	A	209	ASN	2.2
1	E	273	SER	2.2
1	D	292	GLU	2.2
1	F	267	GLU	2.2
1	G	191	GLN	2.2
1	F	249	ALA	2.2
1	G	364	GLU	2.2
1	G	205	SER	2.2
1	G	269	GLU	2.2
1	F	246	SER	2.1
1	D	234	GLU	2.1
1	G	292	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	234	GLU	2.1
1	A	298	GLY	2.1
1	G	149	GLU	2.1
1	E	104	SER	2.1
1	E	171	GLU	2.1
1	C	198	ASP	2.0
1	G	221	GLY	2.0
1	A	104	SER	2.0
1	G	268	SER	2.0
1	G	234	GLU	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.