



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 05:37 PM UTC

PDB ID : 2R3Y / pdb_00002r3y
Title : Crystal structure of the DegS protease in complex with the YWF activating peptide
Authors : Clausen, T.; Hasselblatt, H.
Deposited on : 2007-08-30
Resolution : 2.50 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

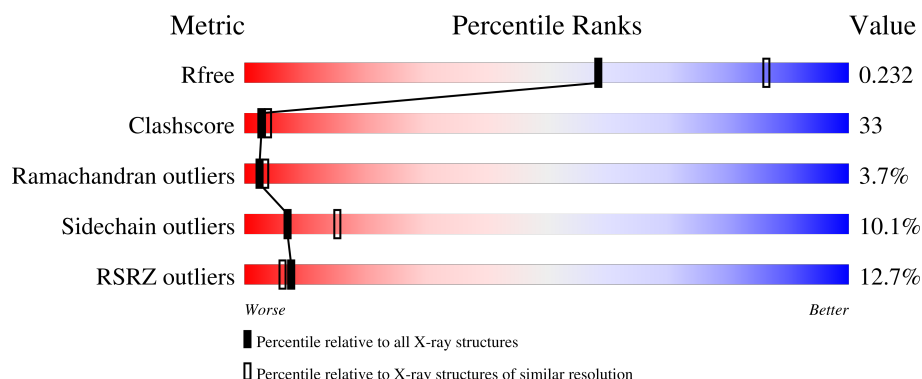
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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.



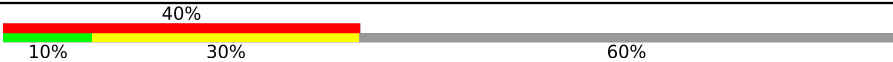
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	314	9% 49% 29% 11% 11%
1	B	314	13% 46% 33% 7% 13%
1	C	314	9% 47% 35% • 12%
2	D	10	30% 10% 30% 60%
2	E	10	40% 10% 30% 60%

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Mol	Chain	Length	Quality of chain
2	F	10	 A horizontal bar chart showing the quality of chain F. The bar is divided into four segments: green (0-10%), yellow (10-30%), red (30-40%), and grey (40-60%). The segments are labeled with their respective percentage values: 10%, 30%, 40%, and 60%.

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6446 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 Protease degS.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	280	Total	C	N	O	S	0	0	0
			2080	1302	372	401	5			
1	B	274	Total	C	N	O	S	0	0	0
			2033	1277	361	390	5			
1	C	275	Total	C	N	O	S	0	0	0
			2041	1281	363	392	5			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	42	MET	-	initiating methionine	UNP P0AEE3
B	42	MET	-	initiating methionine	UNP P0AEE3
C	42	MET	-	initiating methionine	UNP P0AEE3

- Molecule 2 is a protein called Synthetic peptide YWF.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	D	4	Total	C	N	O	0	0	0
			45	34	5	6			
2	E	4	Total	C	N	O	0	0	0
			45	34	5	6			
2	F	4	Total	C	N	O	0	0	0
			45	34	5	6			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	71	Total	O	0	0
			71	71		
3	B	45	Total	O	0	0
			45	45		

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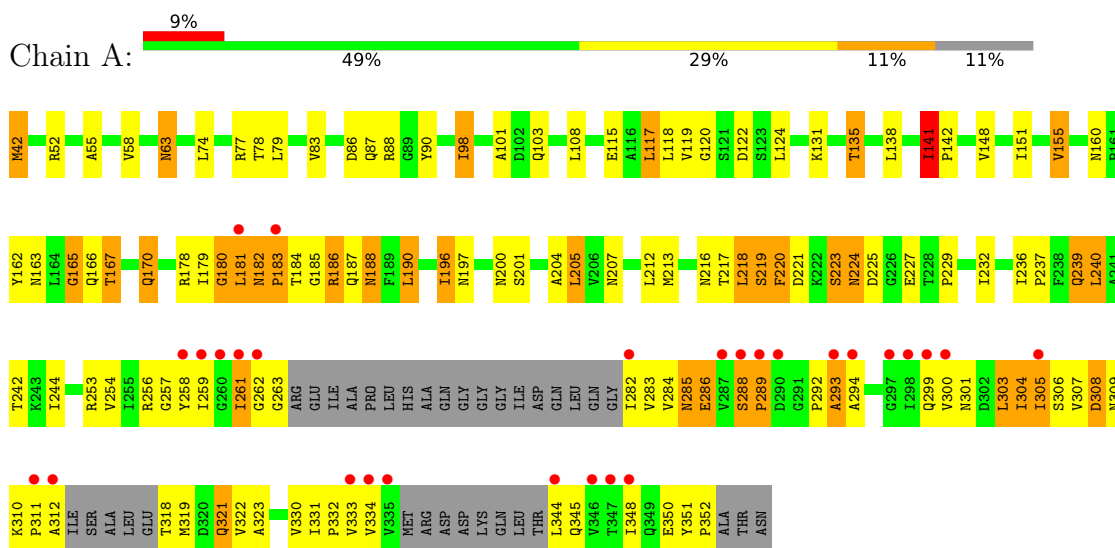
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	41	Total	O	0	0
			41	41		

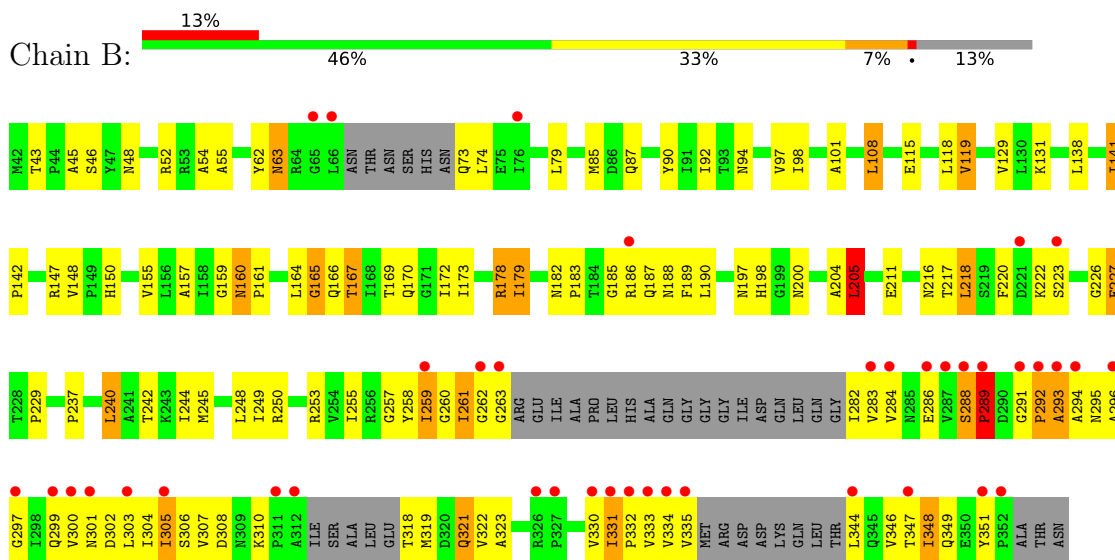
3 Residue-property plots

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: Protease degS

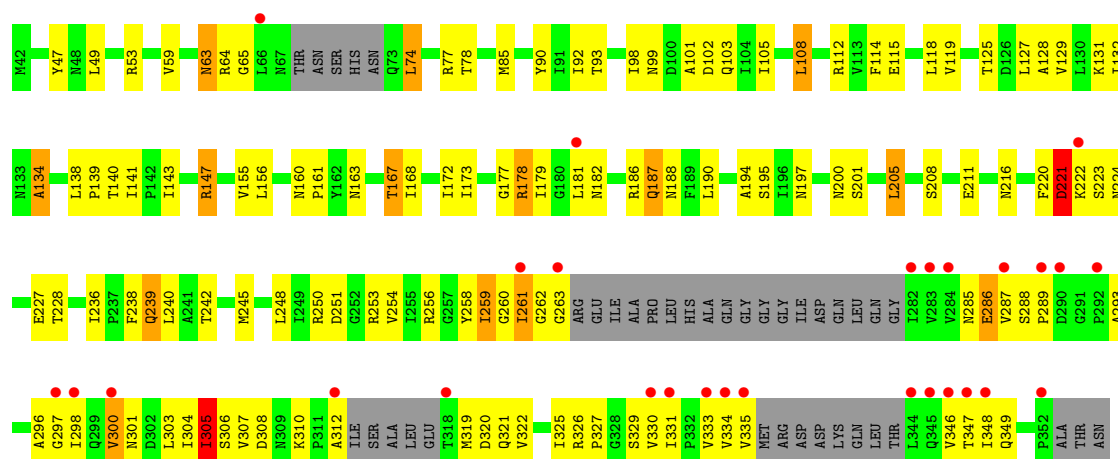


• Molecule 1: Protease degS



• Molecule 1: Protease degS





• Molecule 2: Synthetic peptide YWF



• Molecule 2: Synthetic peptide YWF



• Molecule 2: Synthetic peptide YWF



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	205.80Å 142.70Å 41.10Å 90.00° 90.68° 90.00°	Depositor
Resolution (Å)	15.00 – 2.50 15.00 – 2.50	Depositor EDS
% Data completeness (in resolution range)	95.0 (15.00-2.50) 94.5 (15.00-2.50)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.09 (at 2.51Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.204 , 0.234 0.204 , 0.232	Depositor DCC
R_{free} test set	1923 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	44.0	Xtriage
Anisotropy	0.212	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 65.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.038 for -h,-k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6446	wwPDB-VP
Average B, all atoms (Å ²)	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.17% 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	0.53	0/2106	1.05	11/2865 (0.4%)
1	B	0.47	0/2057	1.02	15/2796 (0.5%)
1	C	0.50	0/2065	1.01	10/2807 (0.4%)
2	D	0.42	0/48	0.49	0/64
2	E	0.47	0/48	0.60	0/64
2	F	0.42	0/48	0.55	0/64
All	All	0.50	0/6372	1.02	36/8660 (0.4%)

There are no bond length outliers.

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	115	GLU	N-CA-C	-7.78	96.90	109.96
1	A	141	ILE	N-CA-C	7.42	116.22	108.95
1	C	222	LYS	N-CA-C	6.79	120.52	110.46
1	A	165	GLY	N-CA-C	-6.63	105.65	111.95
1	A	77	ARG	N-CA-C	-6.59	105.24	113.55
1	C	190	LEU	N-CA-C	-6.59	98.96	109.76
1	C	115	GLU	N-CA-C	-6.41	99.56	109.76
1	A	115	GLU	N-CA-C	-6.26	99.49	109.76
1	B	165	GLY	N-CA-C	-6.26	105.76	112.08
1	A	135	THR	N-CA-C	-6.16	100.12	109.85
1	C	287	VAL	N-CA-C	-6.11	105.78	112.80
1	B	291	GLY	CA-C-N	6.07	127.43	119.84
1	B	291	GLY	C-N-CA	6.07	127.43	119.84
1	C	221	ASP	N-CA-C	6.07	123.74	110.80
1	A	98	ILE	N-CA-C	6.05	117.92	112.17
1	C	102	ASP	N-CA-C	-5.93	106.20	113.50
1	B	160	ASN	CA-C-N	5.78	126.08	119.83
1	B	160	ASN	C-N-CA	5.78	126.08	119.83
1	C	194	ALA	N-CA-C	-5.76	101.52	110.10
1	A	288	SER	CA-C-N	5.49	126.71	119.84
1	A	288	SER	C-N-CA	5.49	126.71	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	54	ALA	N-CA-C	5.45	119.93	113.12
1	C	139	PRO	N-CA-C	-5.39	102.73	111.19
1	A	190	LEU	N-CA-C	-5.32	101.02	109.96
1	A	204	ALA	N-CA-C	5.30	118.70	110.17
1	B	288	SER	CA-C-N	5.29	126.45	119.84
1	B	288	SER	C-N-CA	5.29	126.45	119.84
1	B	204	ALA	N-CA-C	5.23	118.59	110.17
1	B	250	ARG	N-CA-C	5.21	118.11	111.69
1	B	205	LEU	N-CA-C	-5.19	99.95	108.41
1	C	134	ALA	N-CA-C	5.19	117.17	107.99
1	B	348	ILE	N-CA-C	5.18	115.67	108.84
1	B	331	ILE	N-CA-C	5.17	113.77	107.61
1	B	46	SER	N-CA-C	5.16	116.92	108.76
1	A	223	SER	N-CA-C	-5.16	97.46	107.62
1	C	195	SER	N-CA-C	5.12	117.12	109.59

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	2080	0	2118	156	0
1	B	2033	0	2080	131	0
1	C	2041	0	2086	145	0
2	D	45	0	36	9	0
2	E	45	0	36	5	0
2	F	45	0	36	9	0
3	A	71	0	0	7	0
3	B	45	0	0	2	0
3	C	41	0	0	4	0
All	All	6446	0	6392	419	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 33.

All (419) 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:A:305:ILE:HA	1:A:312:ALA:HB2	1.41	1.03
1:B:305:ILE:HG12	1:B:306:SER:H	1.24	1.02
1:C:223:SER:HB3	1:C:227:GLU:O	1.60	1.00
1:C:63:ASN:C	1:C:63:ASN:HD22	1.76	0.94
1:B:300:VAL:HG13	1:B:301:ASN:H	1.32	0.94
1:A:305:ILE:HG12	1:A:306:SER:H	1.34	0.92
1:C:300:VAL:HG13	1:C:301:ASN:H	1.31	0.91
1:A:300:VAL:HG13	1:A:301:ASN:H	1.34	0.90
1:A:141:ILE:HD13	1:A:212:LEU:HD13	1.52	0.90
1:C:65:GLY:HA3	1:C:77:ARG:HD2	1.53	0.89
1:B:63:ASN:C	1:B:63:ASN:HD22	1.82	0.87
1:B:257:GLY:H	1:B:323:ALA:HA	1.40	0.87
1:A:257:GLY:H	1:A:323:ALA:HA	1.40	0.86
1:B:141:ILE:HD13	1:B:142:PRO:HD2	1.59	0.85
1:B:147:ARG:HD2	1:B:211:GLU:OE2	1.75	0.85
1:C:197:ASN:H	1:C:200:ASN:HD22	1.20	0.84
1:B:330:VAL:HG22	1:B:347:THR:HG22	1.60	0.83
1:C:319:MET:HE1	2:F:410:PHE:HA	1.62	0.82
1:A:63:ASN:C	1:A:63:ASN:HD22	1.88	0.80
1:B:307:VAL:HG12	1:B:331:ILE:HD11	1.62	0.79
1:C:303:LEU:H	1:C:303:LEU:HD23	1.47	0.79
1:B:305:ILE:HG12	1:B:306:SER:N	1.98	0.79
1:A:155:VAL:HG13	1:A:205:LEU:HD21	1.64	0.79
1:A:182:ASN:H	1:A:183:PRO:HD2	1.47	0.78
1:C:64:ARG:HD3	1:C:105:ILE:HD13	1.65	0.77
1:B:187:GLN:HG3	1:B:188:ASN:H	1.48	0.77
1:C:348:ILE:HD12	1:C:348:ILE:H	1.49	0.77
1:C:239:GLN:HB2	3:C:358:HOH:O	1.84	0.77
1:A:220:PHE:HD1	1:A:229:PRO:HG2	1.50	0.77
1:A:258:TYR:HB2	1:A:351:TYR:HA	1.67	0.77
1:A:141:ILE:CD1	1:A:212:LEU:HD13	2.16	0.76
1:C:178:ARG:O	1:C:188:ASN:HA	1.86	0.75
1:B:305:ILE:HD13	1:B:305:ILE:H	1.51	0.75
1:C:63:ASN:ND2	1:C:77:ARG:HD3	2.02	0.74
1:C:308:ASP:HB2	1:C:331:ILE:HG13	1.68	0.74
1:B:197:ASN:H	1:B:200:ASN:HD22	1.33	0.74
1:A:308:ASP:HB2	1:A:331:ILE:HD11	1.69	0.74
1:A:305:ILE:HD13	1:A:305:ILE:H	1.54	0.72
1:B:286:GLU:HB3	1:B:288:SER:O	1.90	0.71
1:A:310:LYS:HG3	1:A:311:PRO:HD2	1.72	0.71
1:C:293:ALA:HB2	1:C:349:GLN:OE1	1.89	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:296:ALA:HB3	1:C:346:VAL:HG13	1.73	0.71
1:A:257:GLY:N	1:A:323:ALA:HA	2.06	0.70
1:A:155:VAL:CG1	1:A:205:LEU:HD21	2.21	0.70
1:C:186:ARG:HB2	2:F:409:TRP:HE1	1.57	0.70
1:B:263:GLY:HA2	2:E:407:VAL:HA	1.74	0.69
1:A:160:ASN:ND2	1:A:165:GLY:H	1.90	0.69
1:A:167:THR:HG22	1:B:178:ARG:NH2	2.08	0.69
1:B:283:VAL:HG12	1:B:284:VAL:H	1.58	0.69
1:A:155:VAL:HG13	1:A:205:LEU:CD2	2.22	0.68
1:C:63:ASN:HD21	1:C:77:ARG:HD3	1.58	0.68
1:A:308:ASP:HB2	1:A:331:ILE:CD1	2.24	0.68
1:B:257:GLY:N	1:B:323:ALA:HA	2.08	0.68
1:C:177:GLY:HA2	1:C:188:ASN:HB2	1.76	0.68
1:B:161:PRO:HD2	1:B:167:THR:HG23	1.74	0.68
1:C:197:ASN:H	1:C:200:ASN:ND2	1.92	0.68
1:C:298:ILE:HG23	1:C:333:VAL:HG21	1.77	0.67
1:A:239:GLN:HE21	1:A:239:GLN:HA	1.59	0.67
1:A:263:GLY:C	2:D:408:TYR:H	2.01	0.67
1:A:300:VAL:HG22	1:A:301:ASN:ND2	2.09	0.67
1:A:118:LEU:C	1:A:118:LEU:HD23	2.19	0.67
1:B:155:VAL:HB	1:B:205:LEU:HD22	1.76	0.67
1:C:334:VAL:HG12	1:C:335:VAL:HG23	1.77	0.67
1:C:305:ILE:HD13	1:C:305:ILE:N	2.09	0.67
1:A:160:ASN:HD21	1:A:165:GLY:H	1.39	0.67
1:A:167:THR:HG22	1:B:178:ARG:HH21	1.60	0.67
1:B:141:ILE:HD13	1:B:142:PRO:CD	2.24	0.66
1:A:257:GLY:H	1:A:323:ALA:CA	2.08	0.66
1:B:293:ALA:HB2	1:B:349:GLN:OE1	1.94	0.66
1:C:307:VAL:HG12	1:C:331:ILE:HD11	1.78	0.66
1:A:300:VAL:HG13	1:A:301:ASN:N	2.10	0.66
1:B:303:LEU:HD23	1:B:303:LEU:H	1.61	0.66
1:C:296:ALA:HB1	1:C:346:VAL:HA	1.76	0.66
1:B:283:VAL:HG12	1:B:284:VAL:N	2.12	0.65
1:B:288:SER:O	1:B:289:PRO:O	2.14	0.65
1:C:286:GLU:HB3	1:C:288:SER:O	1.96	0.65
1:C:304:ILE:HG13	1:C:334:VAL:O	1.97	0.65
1:A:178:ARG:NH2	1:C:167:THR:HG22	2.11	0.65
1:A:303:LEU:H	1:A:303:LEU:HD23	1.61	0.65
1:A:184:THR:HG23	1:A:186:ARG:HD3	1.77	0.65
1:A:223:SER:O	1:A:225:ASP:N	2.30	0.65
1:A:185:GLY:O	1:A:187:GLN:N	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:307:VAL:HG13	1:A:333:VAL:HG12	1.77	0.64
1:B:308:ASP:HB2	1:B:331:ILE:CD1	2.27	0.64
1:C:98:ILE:HD11	1:C:128:ALA:HB1	1.79	0.64
1:A:219:SER:C	1:A:221:ASP:H	2.04	0.64
1:B:223:SER:HB3	1:B:227:GLU:OE2	1.98	0.64
1:C:262:GLY:C	1:C:286:GLU:HG2	2.23	0.64
1:B:262:GLY:O	1:B:286:GLU:HG2	1.98	0.64
1:C:147:ARG:HD2	1:C:211:GLU:OE2	1.98	0.63
1:B:63:ASN:HD21	1:B:101:ALA:HA	1.64	0.63
1:B:197:ASN:H	1:B:200:ASN:ND2	1.96	0.63
1:B:205:LEU:HG	1:B:216:ASN:HD21	1.64	0.62
1:B:305:ILE:HD13	1:B:305:ILE:N	2.13	0.62
1:C:186:ARG:H	2:F:409:TRP:HZ2	1.48	0.62
1:A:306:SER:HA	1:A:310:LYS:O	1.99	0.62
1:A:261:ILE:HD13	1:A:261:ILE:H	1.65	0.62
1:A:305:ILE:HD13	1:A:305:ILE:N	2.13	0.62
1:C:305:ILE:HG12	1:C:306:SER:H	1.65	0.62
1:C:250:ARG:HH11	1:C:250:ARG:HG2	1.64	0.61
1:A:318:THR:O	1:A:321:GLN:HB2	2.01	0.61
1:B:305:ILE:CG1	1:B:306:SER:H	2.07	0.61
1:A:254:VAL:HG12	3:A:385:HOH:O	2.00	0.61
1:C:305:ILE:HA	1:C:312:ALA:HB3	1.83	0.61
1:A:87:GLN:HE21	1:A:138:LEU:H	1.49	0.61
1:B:257:GLY:H	1:B:323:ALA:CA	2.13	0.61
1:A:217:THR:O	1:A:218:LEU:HD13	2.01	0.60
1:C:53:ARG:HG2	1:C:53:ARG:HH11	1.66	0.60
1:C:259:ILE:HG22	1:C:260:GLY:N	2.16	0.60
1:B:222:LYS:HG3	1:B:227:GLU:O	2.00	0.60
1:C:63:ASN:C	1:C:63:ASN:ND2	2.50	0.60
1:C:155:VAL:HB	1:C:205:LEU:CD2	2.31	0.60
1:B:63:ASN:C	1:B:63:ASN:ND2	2.53	0.60
1:B:319:MET:HE1	2:E:410:PHE:HA	1.83	0.60
1:C:64:ARG:HH21	1:C:74:LEU:HB3	1.66	0.60
1:B:178:ARG:O	1:B:189:PHE:HB2	2.02	0.60
1:A:322:VAL:HG21	2:D:410:PHE:HD2	1.67	0.60
1:C:155:VAL:HG11	1:C:173:ILE:HD11	1.83	0.60
1:C:181:LEU:HD23	1:C:182:ASN:H	1.66	0.59
1:C:103:GLN:CD	1:C:105:ILE:HD11	2.27	0.59
1:C:329:SER:O	1:C:347:THR:HA	2.02	0.59
1:A:304:ILE:HG13	1:A:334:VAL:O	2.03	0.59
1:C:300:VAL:HG22	1:C:301:ASN:ND2	2.18	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:55:ALA:HB1	1:B:166:GLN:NE2	2.18	0.59
1:B:259:ILE:O	1:B:293:ALA:HB3	2.02	0.59
1:A:182:ASN:N	1:A:183:PRO:HD2	2.17	0.59
1:B:261:ILE:HD13	1:B:261:ILE:N	2.18	0.59
1:B:296:ALA:HB3	1:B:346:VAL:HG13	1.85	0.59
1:B:87:GLN:HE22	1:B:138:LEU:H	1.50	0.59
1:C:346:VAL:HG12	1:C:347:THR:N	2.17	0.59
1:A:305:ILE:HG12	1:A:306:SER:N	2.11	0.58
1:A:197:ASN:H	1:A:200:ASN:HD22	1.52	0.58
1:B:129:VAL:HG23	1:B:248:LEU:HD12	1.86	0.58
1:A:261:ILE:HD13	1:A:261:ILE:N	2.19	0.58
1:A:220:PHE:CD1	1:A:229:PRO:HG2	2.34	0.58
1:A:307:VAL:HG12	1:A:331:ILE:CD1	2.33	0.58
1:C:65:GLY:CA	1:C:77:ARG:HD2	2.28	0.58
1:B:240:LEU:O	1:B:240:LEU:HD22	2.04	0.58
1:B:292:PRO:O	1:B:294:ALA:N	2.36	0.58
1:B:304:ILE:HG12	1:B:305:ILE:N	2.19	0.57
1:B:94:ASN:HB2	1:B:97:VAL:HG23	1.86	0.57
1:B:296:ALA:CB	1:B:346:VAL:HG13	2.34	0.57
1:B:348:ILE:HD12	1:B:348:ILE:N	2.18	0.57
1:C:261:ILE:HD13	1:C:261:ILE:N	2.19	0.57
1:A:305:ILE:HD11	1:A:334:VAL:HG12	1.85	0.57
1:A:223:SER:HB2	1:A:229:PRO:HD3	1.87	0.57
1:C:178:ARG:HG3	1:C:178:ARG:HH11	1.69	0.57
1:C:300:VAL:HG13	1:C:301:ASN:N	2.10	0.57
1:A:282:ILE:HG22	1:A:283:VAL:N	2.19	0.57
1:B:160:ASN:ND2	1:B:165:GLY:H	2.03	0.57
1:A:184:THR:CG2	1:A:186:ARG:HD3	2.35	0.57
1:A:257:GLY:O	1:A:322:VAL:HG12	2.05	0.56
1:B:159:GLY:C	1:B:161:PRO:HD3	2.31	0.56
1:B:262:GLY:HA2	2:E:408:TYR:O	2.05	0.56
1:C:179:ILE:HG22	1:C:179:ILE:O	2.04	0.56
1:C:205:LEU:HG	1:C:216:ASN:HD21	1.70	0.56
1:A:135:THR:HA	3:A:368:HOH:O	2.05	0.56
1:A:286:GLU:HB3	1:A:288:SER:O	2.06	0.56
1:A:319:MET:HA	2:D:410:PHE:CZ	2.40	0.56
1:A:348:ILE:N	1:A:348:ILE:HD12	2.21	0.56
1:B:296:ALA:HB3	1:B:346:VAL:HG22	1.86	0.56
1:C:262:GLY:O	1:C:286:GLU:HG2	2.06	0.56
1:C:147:ARG:CD	1:C:211:GLU:OE2	2.54	0.55
1:B:304:ILE:HG12	1:B:305:ILE:H	1.70	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:259:ILE:HG13	1:A:322:VAL:HG13	1.88	0.55
1:B:308:ASP:HB2	1:B:331:ILE:HD11	1.88	0.55
1:C:155:VAL:HB	1:C:205:LEU:HD22	1.87	0.55
1:C:307:VAL:HG13	1:C:333:VAL:HG12	1.88	0.55
1:B:260:GLY:C	1:B:261:ILE:HD13	2.33	0.54
1:C:296:ALA:CB	1:C:346:VAL:HG13	2.37	0.54
1:C:263:GLY:N	2:F:408:TYR:HB2	2.23	0.54
1:A:303:LEU:O	1:A:304:ILE:HB	2.07	0.54
1:C:348:ILE:HD12	1:C:348:ILE:N	2.19	0.54
1:A:319:MET:HE3	1:A:319:MET:O	2.08	0.54
1:B:165:GLY:C	1:C:178:ARG:NH2	2.66	0.54
1:B:300:VAL:HG13	1:B:301:ASN:N	2.12	0.54
1:C:160:ASN:HD21	1:C:163:ASN:HD22	1.56	0.54
1:B:334:VAL:HG12	1:B:335:VAL:HG23	1.89	0.53
1:A:283:VAL:HG12	1:A:284:VAL:N	2.24	0.53
1:A:118:LEU:HD23	1:A:120:GLY:N	2.24	0.53
1:A:322:VAL:HG21	2:D:410:PHE:CD2	2.43	0.53
1:B:260:GLY:O	1:B:261:ILE:HG23	2.09	0.53
1:B:318:THR:HG22	2:E:410:PHE:HE2	1.73	0.53
1:A:188:ASN:N	1:A:188:ASN:HD22	2.07	0.53
1:B:260:GLY:H	1:B:261:ILE:HD13	1.72	0.53
1:B:150:HIS:HD2	3:B:360:HOH:O	1.91	0.53
1:C:305:ILE:O	1:C:312:ALA:HB2	2.09	0.53
1:B:164:LEU:HD21	1:C:220:PHE:CE2	2.44	0.53
1:A:83:VAL:CG1	1:A:141:ILE:HD12	2.39	0.52
1:C:223:SER:CB	1:C:227:GLU:O	2.47	0.52
1:C:259:ILE:O	1:C:293:ALA:HB3	2.09	0.52
1:C:296:ALA:CB	1:C:346:VAL:HA	2.38	0.52
1:A:117:LEU:HD22	1:A:118:LEU:N	2.24	0.52
1:A:42:MET:HE3	1:A:42:MET:N	2.25	0.52
1:A:300:VAL:C	1:A:301:ASN:HD22	2.18	0.52
1:C:308:ASP:HB2	1:C:331:ILE:CG1	2.38	0.52
1:C:178:ARG:HG3	1:C:178:ARG:NH1	2.24	0.52
1:C:300:VAL:C	1:C:301:ASN:HD22	2.18	0.52
1:A:282:ILE:HG22	1:A:283:VAL:H	1.75	0.52
1:A:307:VAL:HG12	1:A:331:ILE:HD11	1.90	0.52
1:B:170:GLN:HG2	1:C:172:ILE:HG23	1.90	0.52
1:B:79:LEU:N	1:B:79:LEU:HD22	2.25	0.52
1:B:282:ILE:HG22	1:B:283:VAL:N	2.25	0.52
1:B:173:ILE:HG23	1:B:190:LEU:HD21	1.92	0.51
1:B:260:GLY:HA3	1:B:294:ALA:HB2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:122:ASP:OD1	1:A:254:VAL:HG11	2.10	0.51
1:B:198:HIS:HB2	3:C:395:HOH:O	2.09	0.51
1:B:157:ALA:HB3	1:B:169:THR:OG1	2.10	0.51
1:C:254:VAL:HG11	1:C:256:ARG:CZ	2.40	0.51
1:A:87:GLN:NE2	1:A:138:LEU:H	2.08	0.51
1:C:161:PRO:HD2	1:C:167:THR:HG23	1.93	0.51
1:A:292:PRO:C	1:A:294:ALA:H	2.19	0.51
1:C:223:SER:HB2	1:C:227:GLU:CD	2.34	0.51
1:B:303:LEU:H	1:B:303:LEU:CD2	2.23	0.51
1:B:160:ASN:HD21	1:B:165:GLY:H	1.58	0.50
1:C:125:THR:HA	1:C:187:GLN:HE21	1.75	0.50
1:A:74:LEU:HD13	1:A:103:GLN:OE1	2.10	0.50
1:A:79:LEU:C	1:A:79:LEU:HD12	2.36	0.50
1:B:55:ALA:HB1	1:B:166:GLN:HE22	1.75	0.50
1:C:177:GLY:HA2	1:C:188:ASN:HD22	1.76	0.50
1:C:303:LEU:O	1:C:335:VAL:HG12	2.10	0.50
1:A:330:VAL:CG1	1:A:345:GLN:HB3	2.42	0.50
1:C:250:ARG:HG2	1:C:250:ARG:NH1	2.27	0.50
1:A:52:ARG:HG3	1:A:52:ARG:HH11	1.77	0.50
1:A:184:THR:HG23	1:A:186:ARG:HH11	1.77	0.50
1:B:332:PRO:HA	1:B:344:LEU:O	2.12	0.50
1:C:238:PHE:CZ	1:C:239:GLN:NE2	2.79	0.50
1:B:73:GLN:HG2	1:B:74:LEU:N	2.27	0.50
1:A:185:GLY:HA2	2:D:409:TRP:HH2	1.77	0.49
1:A:283:VAL:HA	1:A:303:LEU:HA	1.94	0.49
1:A:292:PRO:O	1:A:294:ALA:N	2.45	0.49
1:A:305:ILE:CA	1:A:312:ALA:HB2	2.28	0.49
1:C:258:TYR:HD1	2:F:410:PHE:OXT	1.94	0.49
1:A:259:ILE:HG13	1:A:322:VAL:CG1	2.41	0.49
1:B:308:ASP:HB2	1:B:331:ILE:HG13	1.94	0.49
1:C:296:ALA:HB3	1:C:346:VAL:HG22	1.94	0.49
1:A:90:TYR:CE2	1:A:131:LYS:HD2	2.47	0.49
1:C:143:ILE:HD11	3:C:387:HOH:O	2.12	0.49
1:C:261:ILE:HD13	1:C:261:ILE:H	1.76	0.49
1:C:307:VAL:HG12	1:C:331:ILE:CD1	2.41	0.49
1:A:178:ARG:HH21	1:C:167:THR:HG22	1.74	0.49
1:C:53:ARG:HG2	1:C:53:ARG:NH1	2.28	0.49
1:C:298:ILE:HG23	1:C:333:VAL:CG2	2.42	0.49
1:A:300:VAL:CG1	1:A:301:ASN:H	2.17	0.49
1:A:303:LEU:H	1:A:303:LEU:CD2	2.26	0.49
1:B:63:ASN:ND2	1:B:101:ALA:HA	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:90:TYR:CE2	1:C:131:LYS:HD2	2.47	0.49
1:A:223:SER:HB3	1:A:227:GLU:O	2.12	0.48
1:C:251:ASP:C	1:C:253:ARG:H	2.20	0.48
1:A:333:VAL:O	1:A:344:LEU:HB3	2.13	0.48
1:C:186:ARG:CB	2:F:409:TRP:HE1	2.24	0.48
1:C:305:ILE:HA	1:C:312:ALA:CB	2.42	0.48
1:A:219:SER:C	1:A:221:ASP:N	2.69	0.48
1:A:258:TYR:HD1	2:D:410:PHE:OXT	1.97	0.48
1:C:98:ILE:HD11	1:C:128:ALA:CB	2.43	0.48
1:A:86:ASP:OD2	1:A:88:ARG:HB2	2.14	0.48
1:B:90:TYR:CE2	1:B:131:LYS:HD3	2.49	0.48
1:A:88:ARG:O	1:A:131:LYS:NZ	2.47	0.48
1:B:119:VAL:HG13	1:B:129:VAL:O	2.14	0.48
1:B:245:MET:HG2	1:B:249:ILE:HD13	1.94	0.48
1:A:63:ASN:C	1:A:63:ASN:ND2	2.62	0.47
1:A:148:VAL:HG12	3:A:416:HOH:O	2.14	0.47
1:A:218:LEU:HD12	1:A:218:LEU:HA	1.72	0.47
1:A:179:ILE:HG12	3:A:417:HOH:O	2.14	0.47
1:A:205:LEU:HG	1:A:216:ASN:HD21	1.79	0.47
1:A:220:PHE:HB2	1:A:232:ILE:HG22	1.96	0.47
1:A:319:MET:SD	2:D:409:TRP:HD1	2.38	0.47
1:B:253:ARG:CZ	1:B:255:ILE:HD11	2.44	0.47
1:C:92:ILE:HG22	1:C:93:THR:N	2.30	0.47
1:A:258:TYR:CD2	1:A:352:PRO:HD3	2.50	0.47
1:B:147:ARG:CD	1:B:211:GLU:OE2	2.57	0.47
1:B:333:VAL:O	1:B:344:LEU:HD22	2.14	0.47
1:C:155:VAL:HG11	1:C:173:ILE:CD1	2.45	0.47
1:C:348:ILE:H	1:C:348:ILE:CD1	2.22	0.47
1:A:118:LEU:C	1:A:118:LEU:CD2	2.88	0.47
1:A:254:VAL:HG13	1:A:254:VAL:O	2.14	0.47
1:A:307:VAL:O	1:A:308:ASP:HB3	2.15	0.47
1:C:129:VAL:HG23	1:C:248:LEU:HD12	1.96	0.47
1:A:262:GLY:C	1:A:286:GLU:HG2	2.40	0.47
1:B:303:LEU:HD23	1:B:303:LEU:N	2.30	0.47
1:C:186:ARG:HG3	1:C:319:MET:HG2	1.96	0.47
1:C:306:SER:HA	1:C:310:LYS:O	2.14	0.47
1:A:348:ILE:HD12	1:A:348:ILE:H	1.79	0.46
1:C:112:ARG:HB3	1:C:114:PHE:CE1	2.50	0.46
1:A:182:ASN:H	1:A:183:PRO:CD	2.21	0.46
1:B:108:LEU:HD23	1:B:108:LEU:N	2.30	0.46
1:B:284:VAL:HB	1:B:302:ASP:O	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:240:LEU:O	1:B:244:ILE:HG12	2.15	0.46
1:C:134:ALA:CB	1:C:138:LEU:HD21	2.45	0.46
1:A:179:ILE:HG23	1:A:184:THR:O	2.15	0.46
1:A:184:THR:O	1:A:185:GLY:C	2.58	0.46
1:C:59:VAL:CG1	1:C:108:LEU:HD22	2.46	0.46
1:C:304:ILE:HG12	1:C:305:ILE:N	2.31	0.46
1:B:98:ILE:C	1:B:98:ILE:HD12	2.41	0.46
1:C:49:LEU:HB3	3:C:364:HOH:O	2.16	0.46
1:B:220:PHE:O	1:B:229:PRO:HG2	2.16	0.45
1:B:292:PRO:C	1:B:294:ALA:H	2.24	0.45
1:B:94:ASN:OD1	1:B:217:THR:HA	2.16	0.45
1:B:306:SER:HA	1:B:310:LYS:O	2.16	0.45
1:A:223:SER:C	1:A:225:ASP:H	2.23	0.45
1:B:258:TYR:HB2	1:B:351:TYR:HA	1.98	0.45
1:A:207:ASN:HB2	3:A:358:HOH:O	2.16	0.45
1:C:259:ILE:HG13	1:C:322:VAL:HG11	1.99	0.45
1:B:170:GLN:HG2	1:C:172:ILE:CG2	2.46	0.45
1:B:305:ILE:N	1:B:305:ILE:CD1	2.79	0.45
1:B:321:GLN:OE1	1:B:321:GLN:N	2.50	0.45
2:D:408:TYR:HB3	2:D:410:PHE:CE1	2.52	0.45
1:A:124:LEU:HD12	1:A:256:ARG:CZ	2.47	0.45
1:A:188:ASN:ND2	1:A:188:ASN:O	2.49	0.45
1:A:223:SER:C	1:A:225:ASP:N	2.74	0.45
1:A:240:LEU:HD22	1:A:244:ILE:HG12	1.99	0.45
1:C:259:ILE:HG13	1:C:322:VAL:CG1	2.46	0.45
1:A:117:LEU:HD22	1:A:118:LEU:H	1.82	0.45
1:B:45:ALA:H	1:C:208:SER:HG	1.65	0.45
1:C:134:ALA:HB3	1:C:138:LEU:HD21	1.98	0.45
1:C:186:ARG:HD3	1:C:320:ASP:OD1	2.17	0.45
1:A:98:ILE:HD12	1:A:98:ILE:C	2.42	0.45
1:B:48:ASN:O	1:B:52:ARG:HG3	2.17	0.45
1:A:165:GLY:O	1:B:178:ARG:NH2	2.50	0.44
1:B:308:ASP:HB2	1:B:331:ILE:CG1	2.47	0.44
1:A:83:VAL:HG11	1:A:141:ILE:HD12	2.00	0.44
1:A:303:LEU:HG	1:A:304:ILE:N	2.32	0.44
1:A:307:VAL:O	1:A:308:ASP:CB	2.65	0.44
1:A:196:ILE:HD11	1:A:216:ASN:CG	2.42	0.44
1:C:236:ILE:CG2	1:C:240:LEU:HD12	2.47	0.44
1:A:239:GLN:HA	1:A:239:GLN:NE2	2.29	0.44
1:C:263:GLY:CA	2:F:408:TYR:HB2	2.48	0.44
1:C:47:TYR:HB3	1:C:156:LEU:HD11	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:240:LEU:HD13	1:C:240:LEU:C	2.43	0.44
1:C:263:GLY:H	2:F:408:TYR:HB2	1.82	0.44
1:C:305:ILE:CG1	1:C:306:SER:H	2.31	0.44
1:B:217:THR:HG23	1:B:218:LEU:N	2.32	0.44
1:C:303:LEU:HD23	1:C:303:LEU:N	2.24	0.44
1:C:305:ILE:HD13	1:C:305:ILE:H	1.82	0.44
1:C:253:ARG:HG2	1:C:254:VAL:N	2.33	0.44
1:A:151:ILE:HG21	1:C:168:ILE:HD13	2.00	0.43
1:A:284:VAL:O	1:A:285:ASN:HB3	2.18	0.43
1:B:62:TYR:CE2	1:B:79:LEU:HD12	2.53	0.43
1:B:161:PRO:HG3	1:B:200:ASN:ND2	2.33	0.43
1:B:292:PRO:C	1:B:294:ALA:N	2.76	0.43
1:C:346:VAL:CG1	1:C:347:THR:N	2.81	0.43
1:A:165:GLY:C	1:B:178:ARG:HH22	2.25	0.43
1:A:187:GLN:O	1:A:188:ASN:C	2.61	0.43
1:A:213:MET:HE2	1:A:213:MET:HA	2.00	0.43
1:A:42:MET:N	1:A:42:MET:SD	2.92	0.43
1:B:293:ALA:HB2	1:B:349:GLN:CD	2.44	0.43
1:C:331:ILE:O	1:C:331:ILE:HG23	2.17	0.43
1:A:141:ILE:HA	1:A:142:PRO:HD3	1.89	0.43
1:A:319:MET:SD	2:D:409:TRP:CD1	3.12	0.43
1:B:253:ARG:CZ	1:B:255:ILE:CD1	2.96	0.43
1:B:292:PRO:O	1:B:295:ASN:ND2	2.51	0.43
1:A:253:ARG:HH12	1:A:350:GLU:CD	2.26	0.43
1:A:182:ASN:N	1:A:183:PRO:CD	2.80	0.43
1:A:220:PHE:CD1	1:A:220:PHE:O	2.72	0.43
1:B:187:GLN:HG3	1:B:188:ASN:N	2.24	0.43
1:A:305:ILE:HD11	1:A:334:VAL:CG1	2.47	0.43
1:C:325:ILE:HD13	1:C:331:ILE:HD12	2.01	0.43
1:B:85:MET:HG3	1:B:245:MET:SD	2.59	0.43
1:B:220:PHE:HD2	1:B:229:PRO:HG3	1.83	0.43
1:A:55:ALA:HB1	1:A:166:GLN:NE2	2.34	0.42
1:A:170:GLN:HG2	1:B:172:ILE:HG23	2.01	0.42
1:C:326:ARG:HA	1:C:327:PRO:HD3	1.88	0.42
1:B:240:LEU:HD22	1:B:244:ILE:HG12	2.00	0.42
1:A:83:VAL:HG13	1:A:141:ILE:HD12	2.02	0.42
1:B:189:PHE:CE1	1:B:217:THR:HG21	2.54	0.42
1:B:248:LEU:HD23	1:B:248:LEU:HA	1.88	0.42
1:B:304:ILE:HG13	1:B:334:VAL:O	2.19	0.42
1:B:85:MET:SD	1:B:92:ILE:HD12	2.60	0.42
1:B:307:VAL:HG12	1:B:331:ILE:CD1	2.41	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:141:ILE:O	1:C:141:ILE:HG23	2.18	0.42
1:B:188:ASN:ND2	1:B:237:PRO:HG2	2.35	0.42
1:B:283:VAL:CG1	1:B:284:VAL:H	2.29	0.42
1:B:300:VAL:CG1	1:B:301:ASN:H	2.14	0.42
1:A:63:ASN:CG	1:A:101:ALA:HB2	2.45	0.42
1:A:259:ILE:O	1:A:293:ALA:HB3	2.19	0.42
1:C:127:LEU:HD23	1:C:127:LEU:HA	1.93	0.42
1:C:322:VAL:HG21	2:F:410:PHE:HD2	1.84	0.42
1:C:333:VAL:CG2	1:C:346:VAL:HG23	2.49	0.42
1:A:219:SER:O	1:A:221:ASP:N	2.49	0.42
1:A:258:TYR:CB	1:A:351:TYR:HA	2.42	0.42
1:A:307:VAL:HG12	1:A:331:ILE:HD13	2.01	0.42
1:B:348:ILE:HD12	1:B:348:ILE:H	1.85	0.42
1:C:132:ILE:O	1:C:132:ILE:HG13	2.19	0.42
1:B:165:GLY:CA	1:C:178:ARG:NH2	2.83	0.41
1:A:87:GLN:HG3	3:A:415:HOH:O	2.20	0.41
1:B:257:GLY:HA3	1:B:322:VAL:O	2.21	0.41
1:C:251:ASP:C	1:C:253:ARG:N	2.78	0.41
1:C:300:VAL:CG1	1:C:301:ASN:H	2.14	0.41
1:C:331:ILE:HB	1:C:348:ILE:HD11	2.01	0.41
1:A:257:GLY:H	1:A:323:ALA:C	2.26	0.41
1:A:331:ILE:CG2	1:A:348:ILE:HD11	2.51	0.41
1:C:59:VAL:HG12	1:C:108:LEU:HD22	2.02	0.41
1:C:248:LEU:CD2	1:C:253:ARG:HA	2.49	0.41
1:C:98:ILE:HD12	1:C:118:LEU:HD13	2.02	0.41
1:C:330:VAL:HA	1:C:346:VAL:O	2.20	0.41
1:A:179:ILE:O	1:A:181:LEU:N	2.53	0.41
1:C:168:ILE:N	1:C:168:ILE:HD12	2.35	0.41
1:C:160:ASN:HD21	1:C:163:ASN:ND2	2.17	0.41
1:A:188:ASN:N	1:A:188:ASN:ND2	2.68	0.41
1:A:257:GLY:CA	1:A:323:ALA:HA	2.51	0.41
1:A:309:ASN:O	1:A:310:LYS:HE2	2.20	0.41
1:A:331:ILE:HG13	1:A:332:PRO:HD2	2.03	0.41
1:B:182:ASN:HA	1:B:183:PRO:HD3	1.95	0.41
1:C:85:MET:HG3	1:C:245:MET:SD	2.61	0.41
1:C:305:ILE:HG12	1:C:306:SER:N	2.34	0.41
1:B:282:ILE:HG22	1:B:283:VAL:H	1.85	0.41
1:B:300:VAL:HG22	1:B:301:ASN:N	2.36	0.41
1:C:74:LEU:HA	1:C:74:LEU:HD12	1.86	0.41
1:C:333:VAL:HG23	1:C:333:VAL:O	2.21	0.41
1:A:236:ILE:HA	1:A:237:PRO:HD3	1.90	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:201:SER:HB2	3:A:406:HOH:O	2.21	0.40
1:C:63:ASN:CG	1:C:101:ALA:HB2	2.46	0.40
1:C:248:LEU:HD21	1:C:254:VAL:HG23	2.04	0.40
1:C:300:VAL:HG22	1:C:301:ASN:N	2.35	0.40
1:A:180:GLY:O	1:A:181:LEU:O	2.39	0.40
1:B:179:ILE:HD12	3:B:380:HOH:O	2.21	0.40
1:B:261:ILE:HG12	2:E:410:PHE:HB2	2.04	0.40
1:C:92:ILE:CG2	1:C:93:THR:N	2.85	0.40
1:C:105:ILE:HD12	1:C:105:ILE:N	2.37	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	272/314 (87%)	238 (88%)	19 (7%)	15 (6%)	1	1
1	B	264/314 (84%)	237 (90%)	19 (7%)	8 (3%)	3	5
1	C	265/314 (84%)	242 (91%)	16 (6%)	7 (3%)	4	7
2	D	2/10 (20%)	1 (50%)	1 (50%)	0	100	100
2	E	2/10 (20%)	2 (100%)	0	0	100	100
2	F	2/10 (20%)	1 (50%)	1 (50%)	0	100	100
All	All	807/972 (83%)	721 (89%)	56 (7%)	30 (4%)	2	3

All (30) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	181	LEU
1	A	183	PRO
1	A	186	ARG

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Mol	Chain	Res	Type
1	A	224	ASN
1	A	289	PRO
1	A	293	ALA
1	A	299	GLN
1	A	304	ILE
1	B	289	PRO
1	B	293	ALA
1	C	221	ASP
1	C	259	ILE
1	C	300	VAL
1	A	180	GLY
1	A	308	ASP
1	B	297	GLY
1	A	162	TYR
1	A	285	ASN
1	B	226	GLY
1	B	292	PRO
1	B	299	GLN
1	C	285	ASN
1	C	297	GLY
1	B	185	GLY
1	A	220	PHE
1	A	303	LEU
1	A	182	ASN
1	C	289	PRO
1	C	305	ILE
1	B	259	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	227/253 (90%)	200 (88%)	27 (12%)	5	11
1	B	221/253 (87%)	201 (91%)	20 (9%)	9	19
1	C	222/253 (88%)	200 (90%)	22 (10%)	7	16

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	D	4/9 (44%)	4 (100%)	0	100	100
2	E	4/9 (44%)	4 (100%)	0	100	100
2	F	4/9 (44%)	4 (100%)	0	100	100
All	All	682/786 (87%)	613 (90%)	69 (10%)	7	15

All (69) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	42	MET
1	A	58	VAL
1	A	63	ASN
1	A	78	THR
1	A	108	LEU
1	A	117	LEU
1	A	119	VAL
1	A	141	ILE
1	A	155	VAL
1	A	163	ASN
1	A	167	THR
1	A	170	GLN
1	A	188	ASN
1	A	190	LEU
1	A	196	ILE
1	A	205	LEU
1	A	218	LEU
1	A	219	SER
1	A	224	ASN
1	A	239	GLN
1	A	240	LEU
1	A	242	THR
1	A	261	ILE
1	A	286	GLU
1	A	289	PRO
1	A	305	ILE
1	A	321	GLN
1	B	43	THR
1	B	63	ASN
1	B	108	LEU
1	B	118	LEU
1	B	119	VAL
1	B	141	ILE

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Mol	Chain	Res	Type
1	B	148	VAL
1	B	167	THR
1	B	178	ARG
1	B	179	ILE
1	B	186	ARG
1	B	205	LEU
1	B	218	LEU
1	B	227	GLU
1	B	240	LEU
1	B	242	THR
1	B	261	ILE
1	B	289	PRO
1	B	305	ILE
1	B	321	GLN
1	C	63	ASN
1	C	74	LEU
1	C	78	THR
1	C	99	ASN
1	C	108	LEU
1	C	119	VAL
1	C	140	THR
1	C	147	ARG
1	C	167	THR
1	C	178	ARG
1	C	187	GLN
1	C	201	SER
1	C	205	LEU
1	C	221	ASP
1	C	224	ASN
1	C	228	THR
1	C	239	GLN
1	C	242	THR
1	C	261	ILE
1	C	286	GLU
1	C	305	ILE
1	C	321	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (41) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	60	ASN
1	A	63	ASN

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Mol	Chain	Res	Type
1	A	73	GLN
1	A	87	GLN
1	A	160	ASN
1	A	163	ASN
1	A	166	GLN
1	A	187	GLN
1	A	188	ASN
1	A	200	ASN
1	A	216	ASN
1	A	224	ASN
1	A	239	GLN
1	A	301	ASN
1	B	63	ASN
1	B	73	GLN
1	B	87	GLN
1	B	150	HIS
1	B	160	ASN
1	B	163	ASN
1	B	166	GLN
1	B	170	GLN
1	B	187	GLN
1	B	191	GLN
1	B	200	ASN
1	B	216	ASN
1	B	301	ASN
1	C	63	ASN
1	C	67	ASN
1	C	87	GLN
1	C	109	GLN
1	C	163	ASN
1	C	166	GLN
1	C	170	GLN
1	C	187	GLN
1	C	200	ASN
1	C	216	ASN
1	C	239	GLN
1	C	295	ASN
1	C	301	ASN
1	C	345	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](#)

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	280/314 (89%)	0.12	28 (10%)	12 10	18, 40, 163, 166	0
1	B	274/314 (87%)	0.34	40 (14%)	6 4	22, 51, 163, 166	0
1	C	275/314 (87%)	0.35	28 (10%)	12 10	24, 52, 160, 167	0
2	D	4/10 (40%)	2.80	3 (75%)	0 0	156, 157, 159, 161	0
2	E	4/10 (40%)	2.86	4 (100%)	0 0	152, 156, 157, 159	0
2	F	4/10 (40%)	3.28	4 (100%)	0 0	160, 160, 161, 163	0
All	All	841/972 (86%)	0.31	107 (12%)	8 6	18, 49, 163, 167	0

All (107) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	407	VAL	4.9
1	A	344	LEU	4.6
1	B	287	VAL	4.5
1	A	259	ILE	4.4
1	B	293	ALA	4.4
1	C	334	VAL	4.3
1	C	297	GLY	4.1
1	B	300	VAL	4.0
1	C	181	LEU	3.9
1	B	263	GLY	3.8
1	A	300	VAL	3.8
1	B	331	ILE	3.7
2	E	409	TRP	3.7
1	A	333	VAL	3.7
1	B	344	LEU	3.7
2	D	409	TRP	3.6
1	A	260	GLY	3.6
1	B	347	THR	3.6
2	E	407	VAL	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	181	LEU	3.5
1	B	65	GLY	3.5
1	C	331	ILE	3.5
1	A	297	GLY	3.4
1	A	293	ALA	3.4
1	B	283	VAL	3.4
2	F	409	TRP	3.3
1	C	282	ILE	3.3
1	B	292	PRO	3.3
1	A	305	ILE	3.3
1	C	284	VAL	3.2
1	C	287	VAL	3.2
1	C	300	VAL	3.2
2	D	407	VAL	3.2
1	B	352	PRO	3.2
1	B	330	VAL	3.2
1	B	286	GLU	3.1
1	C	344	LEU	3.1
1	A	335	VAL	3.1
1	A	261	ILE	3.1
1	C	261	ILE	3.1
1	C	292	PRO	3.1
1	B	262	GLY	3.1
1	B	335	VAL	3.1
1	C	333	VAL	3.1
1	C	222	LYS	3.0
1	B	291	GLY	3.0
1	C	346	VAL	3.0
1	C	263	GLY	3.0
1	B	312	ALA	2.9
1	B	289	PRO	2.9
1	A	287	VAL	2.9
1	A	258	TYR	2.9
1	B	333	VAL	2.8
1	B	296	ALA	2.8
1	A	334	VAL	2.8
1	A	346	VAL	2.8
1	A	282	ILE	2.8
1	A	289	PRO	2.8
1	A	311	PRO	2.8
1	A	347	THR	2.8
1	B	297	GLY	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	334	VAL	2.7
1	C	289	PRO	2.7
1	A	262	GLY	2.7
1	A	298	ILE	2.7
1	B	305	ILE	2.7
1	B	221	ASP	2.6
1	B	303	LEU	2.6
1	A	288	SER	2.6
1	B	284	VAL	2.6
1	C	347	THR	2.6
2	D	408	TYR	2.6
1	B	311	PRO	2.5
1	B	332	PRO	2.5
1	B	259	ILE	2.5
2	F	410	PHE	2.5
1	A	183	PRO	2.4
2	F	408	TYR	2.4
1	A	299	GLN	2.4
1	B	301	ASN	2.4
1	B	299	GLN	2.4
1	C	352	PRO	2.4
1	A	290	ASP	2.4
1	B	326	ARG	2.4
1	B	76	ILE	2.3
1	C	283	VAL	2.3
1	A	312	ALA	2.3
1	B	351	TYR	2.3
1	B	288	SER	2.3
1	A	294	ALA	2.2
1	B	186	ARG	2.2
1	C	330	VAL	2.2
1	C	298	ILE	2.2
1	C	348	ILE	2.2
1	B	327	PRO	2.2
1	B	66	LEU	2.1
2	E	408	TYR	2.1
1	C	335	VAL	2.1
1	B	294	ALA	2.1
1	A	348	ILE	2.1
1	C	66	LEU	2.1
1	B	223	SER	2.1
2	E	410	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	290	ASP	2.1
1	C	345	GLN	2.0
1	C	312	ALA	2.0
1	C	318	THR	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.