



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 07:51 AM UTC

PDB ID : 2WHB / pdb_00002whb
Title : Truncation and Optimisation of Peptide Inhibitors of CDK2, Cyclin A Through Structure Guided Design
Authors : Kontopidis, G.; Andrews, M.J.; McInnes, C.; Plater, A.; Innes, L.; Renachowski, S.; Cowan, A.; Fischer, P.M.
Deposited on : 2009-05-03
Resolution : 2.90 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

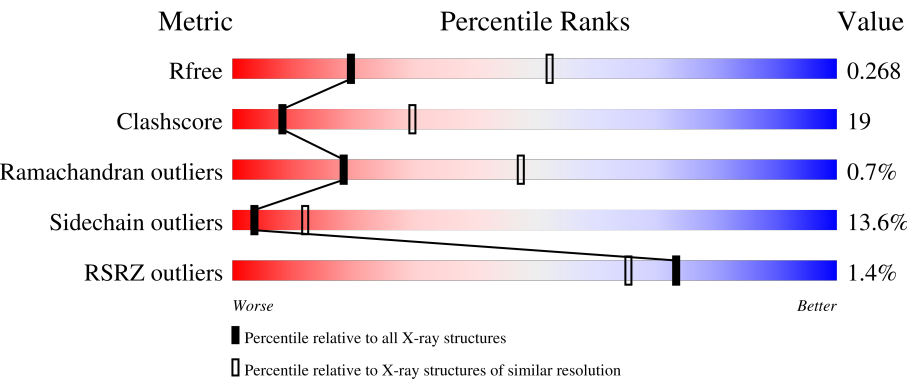
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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

Mol	Chain	Length	Quality of chain
1	A	298	50%37%12%..
1	C	298	3% 58%30%11%. .
2	B	260	2% 59%34%6%. .
2	D	260	% 55%36%7%..
3	E	5	40%40%20%

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Mol	Chain	Length	Quality of chain
3	F	5	20% 60% 20%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 9125 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 CELL DIVISION PROTEIN KINASE 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	296	Total	C	N	O	S	0	0	0
			2378	1547	403	420	8			
1	C	297	Total	C	N	O	S	0	0	1
			2379	1547	404	420	8			

- Molecule 2 is a protein called CYCLIN-A2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	258	Total	C	N	O	S	0	2	0
			2094	1358	341	384	11			
2	D	258	Total	C	N	O	S	0	0	0
			2084	1350	339	384	11			

- Molecule 3 is a protein called ARG-ARG-L3O-PFF.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	5	Total	C	F	N	O	0	0	1
			45	28	1	11	5			
3	F	5	Total	C	F	N	O	0	0	1
			45	28	1	11	5			

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	26	Total	O	0	0
			26	26		
4	B	18	Total	O	0	0
			18	18		
4	C	37	Total	O	0	0
			37	37		
4	D	17	Total	O	0	0
			17	17		

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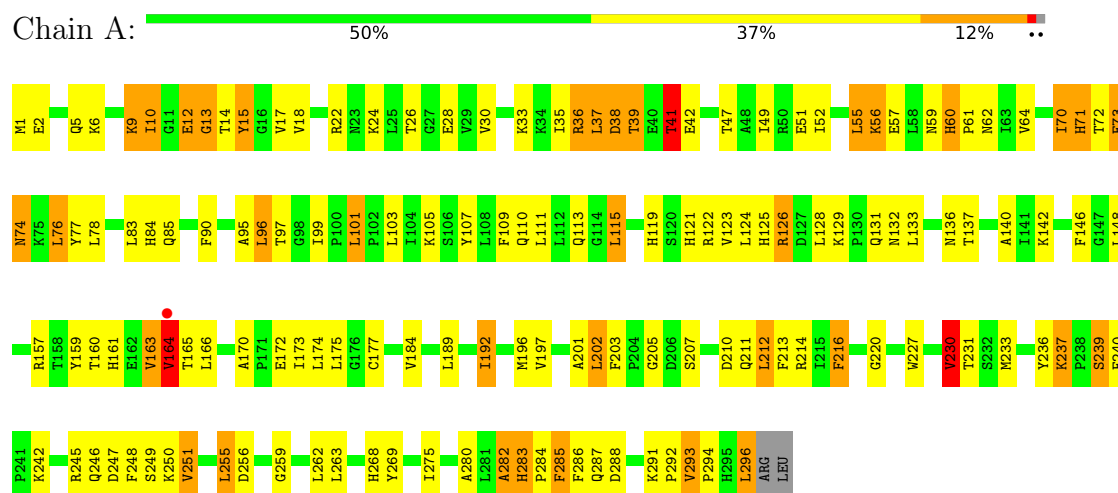
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	F	2	Total	O	0	0
			2	2		

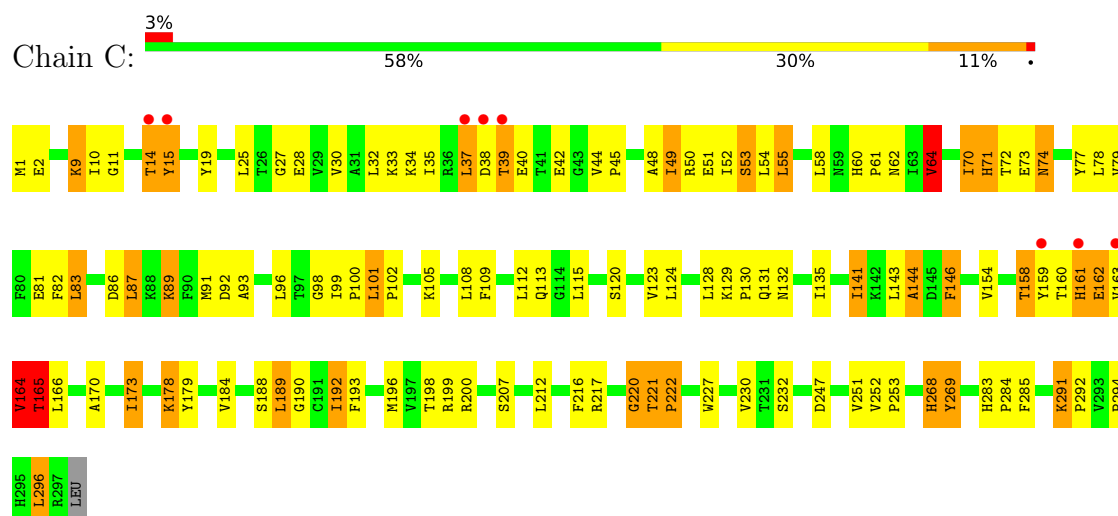
3 Residue-property plots

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: CELL DIVISION PROTEIN KINASE 2

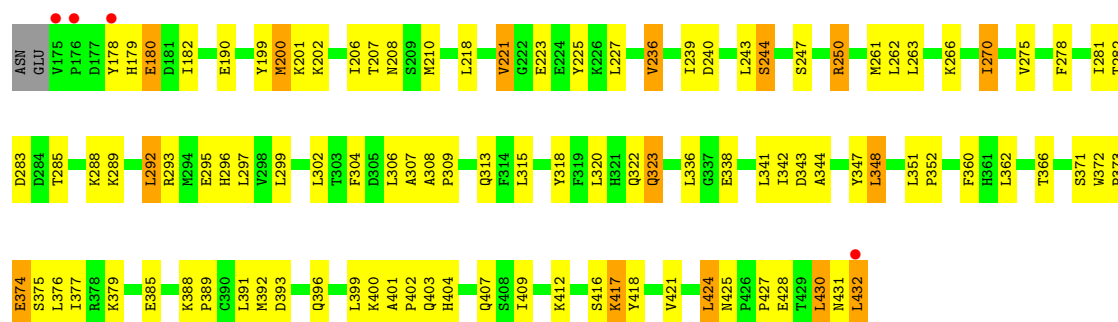


• Molecule 1: CELL DIVISION PROTEIN KINASE 2

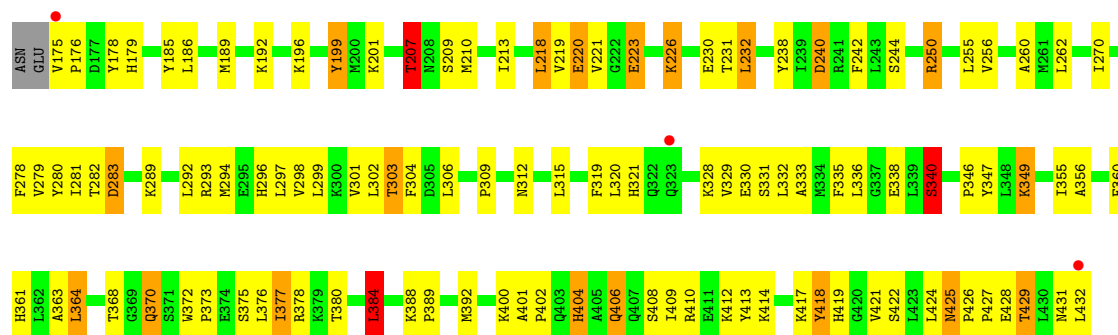


• Molecule 2: CYCLIN-A2

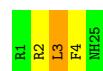




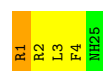
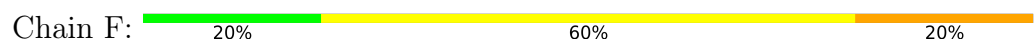
• Molecule 2: CYCLIN-A2



• Molecule 3: ARG-ARG-L3O-PFF



• Molecule 3: ARG-ARG-L3O-PFF



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	74.42Å 114.92Å 154.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.90 30.00 – 2.90	Depositor EDS
% Data completeness (in resolution range)	97.4 (30.00-2.90) 97.2 (30.00-2.90)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.59 (at 2.90Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.186 , 0.264 0.193 , 0.268	Depositor DCC
R_{free} test set	944 reflections (3.23%)	wwPDB-VP
Wilson B-factor (Å ²)	64.4	Xtriage
Anisotropy	0.229	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 74.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	9125	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.42% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: L3O, PFF, NH2

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	0.76	1/2440 (0.0%)	1.66	29/3313 (0.9%)
1	C	0.79	0/2441	1.64	39/3315 (1.2%)
2	B	0.70	0/2150	1.61	17/2920 (0.6%)
2	D	0.74	0/2134	1.66	30/2897 (1.0%)
3	E	0.55	0/21	2.28	0/25
3	F	0.73	0/21	2.15	1/25 (4.0%)
All	All	0.75	1/9207 (0.0%)	1.65	116/12495 (0.9%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
3	E	0	2
3	F	0	2
All	All	0	5

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	13	GLY	C-O	5.18	1.30	1.23

All (116) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	347	TYR	N-CA-C	8.75	121.97	111.82
1	A	12	GLU	CA-C-N	8.34	128.26	120.34
1	A	12	GLU	C-N-CA	8.34	128.26	120.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	196	MET	N-CA-C	-8.14	102.49	111.36
1	C	38	ASP	N-CA-C	-8.02	100.32	111.39
1	A	85	GLN	N-CA-C	8.00	118.80	108.24
2	D	360	PHE	N-CA-C	-7.97	101.89	111.69
1	A	2	GLU	N-CA-C	-7.96	103.57	113.28
1	A	90	PHE	N-CA-C	-7.73	102.49	112.23
1	A	13	GLY	N-CA-C	-7.59	102.35	112.14
1	C	44	VAL	CA-C-N	7.29	127.21	119.85
1	C	44	VAL	C-N-CA	7.29	127.21	119.85
2	D	425	ASN	CA-C-O	7.28	125.48	119.36
2	D	404	HIS	N-CA-C	7.27	120.49	110.24
1	A	84	HIS	N-CA-C	6.93	118.92	111.36
1	A	109	PHE	N-CA-C	-6.84	103.75	111.14
1	C	112	LEU	N-CA-C	-6.84	104.41	112.89
2	B	417	LYS	N-CA-C	-6.75	104.77	112.87
2	B	182	ILE	CB-CA-C	-6.74	103.08	111.70
2	D	255	LEU	N-CA-C	-6.73	103.41	111.69
1	A	60	HIS	CA-C-N	6.70	126.65	119.28
1	A	60	HIS	C-N-CA	6.70	126.65	119.28
1	A	26	THR	CA-C-O	6.49	126.27	119.14
1	A	283	HIS	N-CA-C	6.47	117.52	109.57
1	C	268	HIS	N-CA-C	6.46	119.14	110.35
2	B	270	ILE	CB-CA-C	-6.43	103.62	112.04
1	A	124	LEU	CB-CA-C	-6.34	99.41	109.80
1	C	11	GLY	N-CA-C	6.30	118.45	110.38
2	D	321	HIS	N-CA-C	-6.27	103.31	111.71
1	C	50	ARG	NE-CZ-NH1	-6.16	115.34	121.50
2	D	336	LEU	N-CA-C	-6.14	104.67	111.36
2	D	418	TYR	N-CA-C	-6.12	103.97	112.30
2	B	236	VAL	CA-C-O	6.10	127.32	120.85
1	C	120	SER	N-CA-C	-6.09	105.67	113.23
1	C	221	THR	CA-C-N	6.03	126.38	119.93
1	C	221	THR	C-N-CA	6.03	126.38	119.93
2	D	231	THR	N-CA-C	5.97	118.28	111.11
2	B	425	ASN	N-CA-C	5.95	117.51	109.24
1	C	64	VAL	CB-CA-C	-5.94	102.32	111.71
2	D	427	PRO	N-CA-C	-5.88	101.95	111.19
1	C	92	ASP	N-CA-C	5.86	118.42	111.33
1	C	179	TYR	N-CA-C	5.85	119.08	109.72
1	A	239	SER	N-CA-C	5.84	120.14	113.19
2	D	220	GLU	N-CA-C	5.82	117.71	111.36
2	B	371	SER	N-CA-C	5.79	117.02	108.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	406	GLN	N-CA-C	5.77	119.22	109.76
2	D	260	ALA	N-CA-C	-5.77	104.90	111.07
2	D	242	PHE	O-C-N	5.73	127.97	122.07
2	B	250	ARG	CA-C-O	5.72	126.41	119.38
1	C	123	VAL	N-CA-C	5.71	116.10	108.11
1	C	253	PRO	N-CA-C	5.69	117.64	110.70
2	D	347	TYR	N-CA-C	5.69	119.84	113.01
1	C	144	ALA	N-CA-C	5.69	115.62	108.45
1	A	113	GLN	N-CA-C	5.66	117.13	111.07
2	D	250	ARG	N-CA-C	5.64	117.42	111.28
1	C	93	ALA	N-CA-C	-5.62	105.07	111.14
1	C	222	PRO	N-CA-C	5.62	120.41	111.26
2	D	230	GLU	N-CA-C	-5.58	105.19	112.23
2	B	342	ILE	N-CA-C	5.57	117.08	111.00
2	B	318	TYR	N-CA-C	-5.57	105.21	111.28
2	D	262	LEU	N-CA-C	-5.57	105.11	111.07
1	A	12	GLU	N-CA-CB	5.54	119.81	110.77
2	B	302	LEU	N-CA-C	5.53	121.00	113.37
1	A	213	PHE	CA-C-O	5.51	126.15	119.31
2	D	185	TYR	N-CA-C	-5.50	105.37	111.36
2	D	340	SER	N-CA-C	-5.50	105.44	111.82
1	C	72	THR	N-CA-C	-5.49	101.78	109.69
2	D	242	PHE	CB-CA-C	-5.49	102.26	110.88
1	C	190	GLY	N-CA-C	5.48	119.28	112.64
1	C	173	ILE	CA-C-N	5.47	128.05	120.29
1	C	173	ILE	C-N-CA	5.47	128.05	120.29
2	D	207	THR	N-CA-C	5.46	117.69	109.23
2	D	384	LEU	N-CA-C	-5.45	105.44	111.71
1	C	89	LYS	N-CA-C	-5.45	104.75	111.40
2	D	414	LYS	N-CA-C	-5.42	106.16	112.89
2	B	236	VAL	O-C-N	-5.41	116.26	121.83
2	D	223	GLU	N-CA-C	5.38	116.83	111.07
1	A	107	TYR	N-CA-C	5.36	117.54	111.11
1	C	170	ALA	CA-C-N	5.36	125.17	119.28
1	C	170	ALA	C-N-CA	5.36	125.17	119.28
1	C	123	VAL	CA-C-O	-5.33	114.80	120.39
2	D	349	LYS	N-CA-C	-5.32	105.65	111.82
2	D	422	SER	N-CA-C	5.30	117.06	111.28
1	A	205	GLY	N-CA-C	5.29	121.25	112.89
1	C	54	LEU	N-CA-C	5.28	116.72	111.07
1	A	256	ASP	N-CA-C	5.28	116.90	110.41
1	A	101	LEU	O-C-N	-5.26	115.27	121.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	58	LEU	O-C-N	-5.25	116.41	122.87
2	D	240	ASP	CB-CG-OD1	-5.23	106.36	118.40
2	B	393	ASP	CA-C-O	5.23	125.97	120.42
1	C	269	TYR	N-CA-C	-5.22	105.03	111.40
1	A	201	ALA	CB-CA-C	5.21	118.22	109.89
2	D	419	HIS	N-CA-C	-5.21	105.57	112.24
1	C	124	LEU	CB-CA-C	-5.21	101.26	109.80
1	C	14	THR	N-CA-C	-5.20	105.29	111.69
1	A	6	LYS	CA-C-N	-5.20	117.83	123.08
1	A	6	LYS	C-N-CA	-5.20	117.83	123.08
1	A	216	PHE	N-CA-C	5.20	117.35	111.11
1	C	45	PRO	CB-CA-C	-5.19	104.18	110.98
2	B	221	VAL	CB-CA-C	-5.18	104.13	112.16
1	C	101	LEU	CA-C-O	5.18	123.09	118.33
1	C	83	LEU	CB-CG-CD1	-5.16	95.22	110.70
2	B	424	LEU	N-CA-C	5.15	116.93	110.24
1	A	230	VAL	CB-CA-C	-5.15	105.19	112.14
1	C	124	LEU	N-CA-CB	5.14	118.64	110.16
1	A	282	ALA	O-C-N	-5.13	116.22	122.22
2	D	333	ALA	O-C-N	5.13	127.56	122.12
1	A	72	THR	N-CA-C	-5.09	101.80	109.85
2	B	308	ALA	N-CA-C	-5.09	103.66	110.07
3	F	1	ARG	NE-CZ-NH1	-5.09	116.41	121.50
1	C	220	GLY	N-CA-C	5.06	119.05	112.68
2	B	424	LEU	CB-CG-CD2	-5.05	95.55	110.70
1	C	27	GLY	CA-C-O	5.04	124.70	119.06
1	C	146	PHE	CA-C-N	5.02	125.55	119.98
1	C	146	PHE	C-N-CA	5.02	125.55	119.98
2	D	218	LEU	N-CA-C	-5.01	105.89	111.36

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	163	VAL	Peptide
3	E	3	L3O	Mainchain,Peptide
3	F	3	L3O	Mainchain,Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2378	0	2426	124	0
1	C	2379	0	2426	88	0
2	B	2094	0	2123	84	0
2	D	2084	0	2107	73	0
3	E	45	0	47	0	0
3	F	45	0	47	0	0
4	A	26	0	0	0	0
4	B	18	0	0	0	0
4	C	37	0	0	0	0
4	D	17	0	0	1	0
4	F	2	0	0	0	0
All	All	9125	0	9176	351	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 19.

All (351) 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:38:ASP:CB	1:A:41:THR:HB	1.73	1.17
2:B:207:THR:HG22	2:B:210:MET:HG3	1.34	1.08
2:D:207:THR:HG22	2:D:210:MET:HG3	1.38	1.03
1:A:38:ASP:HB2	1:A:41:THR:HB	1.07	1.03
1:C:135:ILE:HG22	1:C:141:ILE:HG13	1.40	1.00
2:D:209:SER:O	2:D:213:ILE:HD12	1.63	0.97
1:A:163:VAL:HG13	1:A:163:VAL:O	1.70	0.92
1:C:15:TYR:C	1:C:15:TYR:HD2	1.75	0.91
2:B:282:THR:O	2:B:285:THR:HG22	1.70	0.90
1:A:137:THR:HG22	1:A:296:LEU:HD23	1.52	0.90
1:C:15:TYR:C	1:C:15:TYR:CD2	2.51	0.88
2:D:368:THR:OG1	2:D:370:GLN:HG3	1.73	0.88
1:A:71:HIS:NE2	2:B:296:HIS:CD2	2.42	0.87
1:A:71:HIS:ND1	1:A:76:LEU:HD23	1.90	0.87
1:C:83:LEU:N	1:C:83:LEU:HD12	1.90	0.86
2:B:266:LYS:NZ	2:B:295:GLU:OE2	2.09	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:227:TRP:CD2	1:A:230:VAL:HG13	2.10	0.85
2:D:361:HIS:HE1	2:D:384:LEU:HD21	1.41	0.84
1:A:212:LEU:HD22	1:A:216:PHE:CZ	2.13	0.84
2:B:179:HIS:NE2	2:B:379:LYS:NZ	2.23	0.83
2:D:404:HIS:NE2	2:D:406:GLN:OE1	2.11	0.83
2:B:282:THR:HB	2:B:285:THR:CG2	2.09	0.82
1:A:71:HIS:NE2	2:B:296:HIS:HD2	1.77	0.82
1:A:73:GLU:OE2	1:C:2:GLU:HG2	1.79	0.82
2:B:282:THR:HB	2:B:285:THR:HG22	1.61	0.81
1:C:15:TYR:OH	1:C:48:ALA:HB2	1.80	0.81
1:C:212:LEU:HD22	1:C:216:PHE:CZ	2.16	0.81
1:C:48:ALA:O	1:C:52:ILE:HG13	1.81	0.80
2:D:221:VAL:HG22	2:D:281:ILE:HG12	1.64	0.80
1:C:39:THR:O	1:C:40:GLU:HG2	1.83	0.79
1:C:162:GLU:HB3	1:C:164:VAL:HG23	1.62	0.79
2:B:225:TYR:HE1	2:B:281:ILE:HG21	1.46	0.79
1:C:60:HIS:CD2	1:C:61:PRO:HD2	2.18	0.79
2:D:219:VAL:HG22	2:D:232:LEU:HD11	1.63	0.79
2:B:430:LEU:O	2:B:431:ASN:HB2	1.83	0.79
1:A:227:TRP:O	1:A:230:VAL:HG22	1.83	0.77
2:B:282:THR:CB	2:B:285:THR:HG22	2.15	0.76
2:B:207:THR:CG2	2:B:210:MET:HG3	2.13	0.76
2:B:396[B]:GLN:NE2	2:B:400:LYS:NZ	2.37	0.73
2:B:179:HIS:CE1	2:B:320:LEU:HD12	2.24	0.73
1:A:95:ALA:O	1:A:96:LEU:HD23	1.89	0.72
1:A:60:HIS:HD2	1:A:62:ASN:H	1.37	0.72
1:A:52:ILE:HD11	1:A:78:LEU:HD21	1.69	0.72
2:B:431:ASN:O	2:B:432:LEU:HB2	1.90	0.72
1:C:64:VAL:HG23	1:C:143:LEU:O	1.91	0.71
2:B:282:THR:O	2:B:285:THR:CG2	2.38	0.71
2:B:309:PRO:HA	2:B:313:GLN:NE2	2.04	0.71
1:A:137:THR:HG22	1:A:296:LEU:CD2	2.21	0.71
1:C:128:LEU:HD13	1:C:189:LEU:HD13	1.74	0.70
1:A:39:THR:O	2:B:292:LEU:HD23	1.92	0.69
1:C:82:PHE:C	1:C:83:LEU:HD12	2.17	0.69
1:A:245:ARG:NH2	1:A:248:PHE:HE1	1.89	0.69
1:A:38:ASP:N	1:A:38:ASP:OD1	2.25	0.69
1:A:38:ASP:CB	1:A:41:THR:CB	2.63	0.69
1:A:60:HIS:CD2	1:A:62:ASN:H	2.10	0.68
2:D:361:HIS:CE1	2:D:384:LEU:HD21	2.26	0.68
1:A:288:ASP:OD1	1:A:288:ASP:N	2.23	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:71:HIS:CD2	2:B:296:HIS:CD2	2.82	0.67
1:A:177:CYS:HB2	1:A:233:MET:CE	2.24	0.67
1:C:1:MET:HE2	1:C:1:MET:HA	1.76	0.66
2:D:404:HIS:CD2	2:D:406:GLN:H	2.14	0.66
1:A:245:ARG:NH2	1:A:248:PHE:CE1	2.63	0.66
1:A:38:ASP:HB2	1:A:41:THR:CB	2.03	0.66
1:A:71:HIS:CD2	2:B:296:HIS:NE2	2.64	0.66
2:D:332:LEU:HD23	2:D:363:ALA:HA	1.78	0.65
1:A:227:TRP:CE3	1:A:230:VAL:CG1	2.80	0.65
2:D:207:THR:CG2	2:D:210:MET:HG3	2.23	0.65
1:A:165:THR:CG2	1:A:166:LEU:N	2.59	0.65
2:D:175:VAL:N	2:D:176:PRO:HD3	2.12	0.65
1:A:60:HIS:CD2	1:A:61:PRO:HD2	2.32	0.65
2:D:338:GLU:OE1	2:D:412:LYS:NZ	2.30	0.64
1:C:159:TYR:CE2	2:D:270:ILE:HG23	2.32	0.64
1:C:60:HIS:CG	1:C:61:PRO:HD2	2.32	0.64
2:D:388:LYS:HB3	2:D:389:PRO:HD3	1.79	0.64
1:C:162:GLU:HB3	1:C:164:VAL:CG2	2.27	0.64
2:D:278:PHE:O	2:D:281:ILE:HG22	1.97	0.64
1:C:70:ILE:HG22	1:C:70:ILE:O	1.97	0.64
2:D:175:VAL:HG12	2:D:175:VAL:O	1.99	0.63
1:A:41:THR:HG22	1:A:42:GLU:N	2.13	0.63
2:B:275:VAL:HG21	2:B:292:LEU:HD11	1.81	0.63
2:B:404:HIS:O	2:B:407:GLN:NE2	2.31	0.62
1:C:135:ILE:CG2	1:C:141:ILE:HG13	2.22	0.62
2:B:299:LEU:HD22	2:B:304:PHE:CD1	2.35	0.62
2:D:361:HIS:C	2:D:361:HIS:CD2	2.77	0.61
2:D:315:LEU:HD23	2:D:356:ALA:HB1	1.82	0.61
2:B:396[B]:GLN:NE2	2:B:400:LYS:HZ3	1.98	0.61
1:A:1:MET:HE3	1:A:77:TYR:CG	2.34	0.61
2:B:344:ALA:HB1	2:B:348:LEU:HD22	1.83	0.61
2:B:396[B]:GLN:HE22	2:B:400:LYS:NZ	1.97	0.61
2:D:299:LEU:HD22	2:D:304:PHE:CD1	2.35	0.61
1:A:60:HIS:CG	1:A:61:PRO:HD2	2.35	0.61
1:C:173:ILE:HD11	1:C:184:VAL:CG1	2.31	0.61
2:D:329:VAL:HG11	2:D:364:LEU:HD13	1.83	0.60
1:A:129:LYS:HA	1:A:192:ILE:HD11	1.82	0.60
1:A:13:GLY:C	1:A:15:TYR:N	2.58	0.60
1:C:32:LEU:HD23	1:C:79:VAL:HG22	1.82	0.60
1:A:227:TRP:CD2	1:A:230:VAL:CG1	2.83	0.60
2:D:404:HIS:ND1	4:D:2016:HOH:O	2.32	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:163:VAL:O	1:A:163:VAL:CG1	2.44	0.60
2:D:294:MET:O	2:D:298:VAL:HG23	2.02	0.60
1:A:38:ASP:HB3	1:A:41:THR:HB	1.79	0.59
2:B:227:LEU:CD1	2:B:261:MET:HE3	2.32	0.59
1:A:197:VAL:HG21	1:A:255:LEU:CD2	2.32	0.59
1:A:36:ARG:NH1	1:A:36:ARG:HG3	2.17	0.59
1:A:51:GLU:HG3	1:A:146:PHE:HB2	1.84	0.59
1:C:165:THR:O	1:C:165:THR:HG22	2.03	0.59
1:C:166:LEU:HD21	1:C:207:SER:C	2.28	0.59
2:B:373:PRO:HD2	2:B:376:LEU:HD12	1.85	0.59
1:C:173:ILE:HD11	1:C:184:VAL:HG11	1.83	0.59
2:D:207:THR:HG22	2:D:210:MET:CG	2.25	0.58
2:B:396[B]:GLN:NE2	2:B:400:LYS:HZ2	2.00	0.58
2:B:190:GLU:HG3	2:B:351:LEU:HD22	1.86	0.58
1:A:36:ARG:HG3	1:A:36:ARG:HH11	1.68	0.57
1:A:126:ARG:NH2	1:A:148:LEU:O	2.36	0.57
2:D:319:PHE:CE2	2:D:330:GLU:HG2	2.40	0.57
1:A:177:CYS:HB2	1:A:233:MET:HE1	1.85	0.57
2:B:225:TYR:CE1	2:B:281:ILE:HG21	2.35	0.57
2:D:335:PHE:CE1	2:D:409:ILE:HG22	2.39	0.57
1:C:105:LYS:HE2	1:C:285:PHE:O	2.05	0.57
2:B:178:TYR:O	2:B:179:HIS:C	2.48	0.57
2:B:309:PRO:HA	2:B:313:GLN:HE22	1.68	0.56
1:A:111:LEU:HD13	1:A:189:LEU:HD11	1.86	0.56
1:C:51:GLU:O	1:C:55:LEU:HB2	2.05	0.56
1:A:237:LYS:NZ	1:A:240:PHE:CE1	2.73	0.56
1:A:227:TRP:CE3	1:A:269:TYR:HB3	2.41	0.55
1:C:98:GLY:HA2	1:C:199:ARG:HE	1.70	0.55
1:A:71:HIS:CE1	1:A:76:LEU:HD23	2.41	0.55
1:C:251:VAL:HG12	1:C:252:VAL:HG13	1.87	0.55
1:A:122:ARG:HD2	1:A:122:ARG:O	2.07	0.55
2:B:374:GLU:HA	2:B:377:ILE:HD12	1.88	0.55
2:D:240:ASP:O	2:D:244:SER:OG	2.22	0.55
2:D:361:HIS:HE1	2:D:384:LEU:CD2	2.15	0.55
2:B:221:VAL:CG2	2:B:281:ILE:HD12	2.36	0.55
1:A:227:TRP:CE3	1:A:230:VAL:HG11	2.41	0.55
2:B:200:MET:HE3	2:B:207:THR:C	2.31	0.55
2:D:186:LEU:HD22	2:D:309:PRO:HB3	1.88	0.55
2:D:425:ASN:O	2:D:426:PRO:C	2.48	0.54
2:B:227:LEU:HD12	2:B:261:MET:HE3	1.90	0.54
1:A:59:ASN:C	1:A:59:ASN:OD1	2.51	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:49:ILE:O	1:C:53:SER:OG	2.26	0.54
2:D:207:THR:HG22	2:D:210:MET:H	1.72	0.54
2:B:336:LEU:HD13	2:B:362:LEU:HD23	1.90	0.53
1:C:37:LEU:HD12	1:C:39:THR:OG1	2.07	0.53
1:A:1:MET:HE3	1:A:77:TYR:CD1	2.43	0.53
1:C:37:LEU:HB2	1:C:74:ASN:O	2.08	0.53
1:C:291:LYS:N	1:C:292:PRO:CD	2.71	0.53
1:C:78:LEU:HD23	1:C:78:LEU:N	2.21	0.53
2:B:275:VAL:HG11	2:B:292:LEU:HD13	1.90	0.53
2:D:176:PRO:HD2	2:D:179:HIS:ND1	2.23	0.53
2:B:396[B]:GLN:HE22	2:B:400:LYS:HZ2	1.55	0.52
1:A:248:PHE:HA	1:A:251:VAL:HG23	1.90	0.52
2:B:416:SER:C	2:B:418:TYR:N	2.66	0.52
1:C:154:VAL:HG21	2:D:312:ASN:ND2	2.24	0.52
1:A:148:LEU:HD13	1:A:164:VAL:HG13	1.90	0.52
2:B:223:GLU:CD	2:B:412:LYS:HG3	2.35	0.52
1:C:132:ASN:O	1:C:144:ALA:HB3	2.10	0.52
1:C:71:HIS:CD2	2:D:296:HIS:CE1	2.97	0.52
2:B:240:ASP:O	2:B:244:SER:HB2	2.09	0.52
2:B:323:GLN:HE21	2:B:323:GLN:C	2.18	0.52
1:A:125:HIS:O	1:A:126:ARG:HB2	2.09	0.52
1:A:293:VAL:HG23	1:A:294:PRO:O	2.10	0.52
1:A:231:THR:HA	1:A:236:TYR:CD1	2.45	0.51
1:C:198:THR:O	1:C:199:ARG:HB2	2.09	0.51
1:A:291:LYS:N	1:A:292:PRO:CD	2.73	0.51
1:A:197:VAL:HG21	1:A:255:LEU:HD21	1.90	0.51
1:C:129:LYS:HB2	1:C:130:PRO:HD2	1.91	0.51
1:A:52:ILE:CD1	1:A:78:LEU:HD21	2.39	0.51
1:A:71:HIS:CE1	2:B:296:HIS:CD2	2.99	0.51
1:C:60:HIS:HD2	1:C:62:ASN:H	1.58	0.51
1:A:56:LYS:HZ2	1:A:56:LYS:HB3	1.76	0.51
1:C:15:TYR:HD2	1:C:15:TYR:O	1.91	0.51
1:C:129:LYS:HA	1:C:192:ILE:HD11	1.93	0.51
1:A:36:ARG:HH11	1:A:36:ARG:CG	2.23	0.51
1:A:165:THR:HG22	1:A:166:LEU:N	2.26	0.51
2:B:227:LEU:HD12	2:B:261:MET:CE	2.42	0.51
1:C:165:THR:HG23	1:C:166:LEU:N	2.26	0.50
2:B:416:SER:C	2:B:418:TYR:H	2.18	0.50
1:C:34:LYS:HG3	1:C:77:TYR:CE2	2.46	0.50
2:B:366:THR:HG23	2:B:427:PRO:HD3	1.93	0.50
2:B:263:LEU:HD21	2:B:295:GLU:HG2	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:121:HIS:O	1:A:123:VAL:HG23	2.11	0.50
1:C:159:TYR:O	1:C:160:THR:C	2.54	0.50
1:A:5:GLN:HB2	1:A:24:LYS:HD2	1.93	0.50
1:C:212:LEU:CD2	1:C:216:PHE:CZ	2.91	0.50
2:B:262:LEU:HD13	2:B:278:PHE:CD2	2.46	0.50
2:B:236:VAL:HG21	2:B:341:LEU:HD22	1.94	0.49
2:B:299:LEU:HD22	2:B:304:PHE:CE1	2.47	0.49
2:D:376:LEU:O	2:D:380:THR:HG23	2.12	0.49
1:A:60:HIS:CG	1:A:61:PRO:CD	2.95	0.49
1:A:212:LEU:CD2	1:A:216:PHE:CZ	2.92	0.49
2:D:256:VAL:HG23	2:D:294:MET:HE3	1.94	0.49
2:B:323:GLN:O	2:B:323:GLN:NE2	2.40	0.49
1:A:136:ASN:OD1	1:A:140:ALA:HB3	2.12	0.49
2:D:418:TYR:O	2:D:421:VAL:HG22	2.12	0.49
1:A:110:GLN:OE1	1:A:140:ALA:HA	2.13	0.49
2:D:361:HIS:CE1	2:D:384:LEU:CD2	2.93	0.49
2:B:179:HIS:HE1	2:B:320:LEU:HD12	1.74	0.49
2:D:384:LEU:HD12	2:D:384:LEU:O	2.13	0.49
2:B:221:VAL:CG2	2:B:281:ILE:CD1	2.91	0.48
2:B:179:HIS:CD2	2:B:379:LYS:HZ2	2.21	0.48
1:C:73:GLU:OE1	2:D:293:ARG:NH2	2.46	0.48
2:B:178:TYR:O	2:B:180:GLU:N	2.47	0.48
1:C:77:TYR:C	1:C:78:LEU:HD23	2.39	0.48
1:A:284:PRO:O	1:A:285:PHE:C	2.55	0.48
1:C:71:HIS:HE1	2:D:304:PHE:HZ	1.62	0.48
2:D:226:LYS:HB2	2:D:226:LYS:NZ	2.28	0.48
2:D:340:SER:OG	2:D:355:ILE:HD13	2.14	0.48
1:A:28:GLU:HG2	1:A:30:VAL:HG13	1.96	0.48
1:A:70:ILE:HB	1:A:77:TYR:HB2	1.96	0.48
1:A:175:LEU:HD23	1:A:212:LEU:HD11	1.95	0.48
2:B:297:LEU:HD12	2:B:297:LEU:O	2.14	0.48
2:B:199:TYR:CD1	2:B:199:TYR:C	2.91	0.47
1:A:159:TYR:CD1	2:B:270:ILE:HG23	2.49	0.47
1:C:60:HIS:CG	1:C:61:PRO:CD	2.97	0.47
1:A:115:LEU:HD13	1:A:119:HIS:CE1	2.49	0.47
2:D:335:PHE:HB2	2:D:413:TYR:CD2	2.50	0.47
1:A:170:ALA:HB3	1:A:173:ILE:HG13	1.97	0.47
2:B:221:VAL:HG22	2:B:281:ILE:HD12	1.96	0.47
2:B:239:ILE:HG22	2:B:243:LEU:HD12	1.96	0.46
2:B:388:LYS:O	2:B:389:PRO:C	2.57	0.46
1:C:2:GLU:CD	1:C:2:GLU:H	2.21	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:412:LYS:HD3	2:D:413:TYR:CE1	2.51	0.46
2:B:221:VAL:HG21	2:B:281:ILE:HD12	1.97	0.46
1:C:159:TYR:O	1:C:162:GLU:HG2	2.15	0.46
2:B:315:LEU:HD23	2:B:315:LEU:HA	1.54	0.46
1:C:291:LYS:N	1:C:292:PRO:HD3	2.31	0.46
1:C:161:HIS:O	1:C:162:GLU:C	2.58	0.46
2:B:190:GLU:OE1	2:B:352:PRO:HG2	2.16	0.46
1:A:121:HIS:O	1:A:122:ARG:C	2.58	0.46
1:C:252:VAL:O	1:C:252:VAL:HG23	2.16	0.46
1:A:159:TYR:HB3	1:A:161:HIS:O	2.15	0.45
1:C:51:GLU:HG3	1:C:146:PHE:HB2	1.98	0.45
1:A:115:LEU:HD22	1:A:115:LEU:HA	1.83	0.45
1:C:101:LEU:N	1:C:102:PRO:CD	2.80	0.45
2:D:335:PHE:HE1	2:D:409:ILE:HG22	1.81	0.45
1:C:39:THR:O	1:C:40:GLU:CG	2.60	0.45
2:D:302:LEU:C	2:D:303:THR:OG1	2.59	0.45
1:A:262:LEU:O	1:A:263:LEU:C	2.60	0.45
2:B:289:LYS:HE3	2:B:293:ARG:HH12	1.81	0.45
2:D:220:GLU:HG3	2:D:408:SER:OG	2.17	0.45
2:D:388:LYS:HB3	2:D:389:PRO:CD	2.47	0.45
2:D:238:TYR:OH	2:D:306:LEU:HB3	2.17	0.45
2:D:319:PHE:CZ	2:D:330:GLU:HA	2.51	0.45
1:C:188:SER:O	1:C:192:ILE:HG13	2.16	0.45
1:C:1:MET:HE3	1:C:77:TYR:CD1	2.52	0.45
2:D:210:MET:HE1	2:D:250:ARG:NH1	2.32	0.45
1:A:55:LEU:HD11	1:A:146:PHE:CE1	2.52	0.45
1:A:71:HIS:HE2	2:B:296:HIS:HD2	1.58	0.45
1:C:220:GLY:O	1:C:269:TYR:OH	2.27	0.45
1:A:275:ILE:HD11	1:A:280:ALA:HA	1.99	0.44
1:C:64:VAL:CG2	1:C:143:LEU:O	2.64	0.44
1:A:111:LEU:CD2	1:A:133:LEU:HD22	2.47	0.44
1:A:170:ALA:HB1	1:A:172:GLU:OE2	2.17	0.44
1:A:210:ASP:O	1:A:214:ARG:HG3	2.17	0.44
2:B:200:MET:HG2	2:B:208:ASN:ND2	2.31	0.44
2:B:360:PHE:HD2	2:B:372:TRP:CZ3	2.34	0.44
1:C:15:TYR:OH	1:C:35:ILE:HD13	2.18	0.44
1:C:28:GLU:HG2	1:C:30:VAL:CG1	2.46	0.44
1:A:9:LYS:C	1:A:10:ILE:CG2	2.90	0.44
1:C:158:THR:OG1	1:C:178:LYS:O	2.35	0.44
2:D:402:PRO:HB3	2:D:410:ARG:CZ	2.47	0.44
1:A:174:LEU:HD11	1:A:211:GLN:HG3	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:248:PHE:HE2	1:A:263:LEU:HG	1.83	0.44
2:B:338:GLU:HB3	2:B:409:ILE:HD13	1.99	0.44
2:D:373:PRO:O	2:D:377:ILE:HD12	2.17	0.44
1:C:35:ILE:HD13	1:C:35:ILE:HG21	1.61	0.44
1:A:284:PRO:O	1:A:286:PHE:N	2.51	0.44
1:C:158:THR:OG1	1:C:178:LYS:C	2.61	0.44
1:A:293:VAL:O	1:A:293:VAL:CG2	2.61	0.44
2:B:221:VAL:HG21	2:B:281:ILE:CD1	2.48	0.44
1:C:28:GLU:HG2	1:C:30:VAL:HG12	1.99	0.44
2:D:279:VAL:O	2:D:280:TYR:C	2.57	0.44
1:A:83:LEU:HD11	1:A:142:LYS:HD2	2.00	0.43
1:A:105:LYS:HE2	1:A:285:PHE:O	2.18	0.43
2:B:218:LEU:HD22	2:B:261:MET:SD	2.58	0.43
2:D:319:PHE:CD2	2:D:330:GLU:HG2	2.53	0.43
2:D:417:LYS:HD2	2:D:418:TYR:CE2	2.53	0.43
2:B:207:THR:HG23	2:B:210:MET:H	1.84	0.43
1:C:15:TYR:OH	1:C:35:ILE:CD1	2.66	0.43
1:C:64:VAL:CG2	1:C:144:ALA:HB2	2.49	0.43
1:C:163:VAL:HG13	1:C:163:VAL:O	2.19	0.43
1:A:49:ILE:HG23	2:B:306:LEU:HD12	2.00	0.43
1:C:227:TRP:O	1:C:230:VAL:HG12	2.18	0.43
1:A:165:THR:HG23	1:A:166:LEU:N	2.33	0.43
2:B:401:ALA:HB3	2:B:402:PRO:HD3	1.99	0.43
1:A:41:THR:HG22	1:A:42:GLU:H	1.82	0.43
1:A:55:LEU:HD11	1:A:146:PHE:CD1	2.54	0.43
1:A:159:TYR:CE2	1:A:163:VAL:HG12	2.54	0.43
1:C:221:THR:HA	1:C:222:PRO:HD2	1.76	0.43
2:D:207:THR:CG2	2:D:209:SER:HB3	2.48	0.43
2:D:428:GLU:O	2:D:429:THR:HB	2.19	0.43
1:C:91:MET:HE3	1:C:196:MET:HG3	2.00	0.43
1:C:222:PRO:HB2	1:C:230:VAL:HG21	2.00	0.43
1:A:284:PRO:C	1:A:286:PHE:N	2.76	0.43
1:C:294:PRO:HG2	1:C:296:LEU:HD22	2.01	0.42
2:D:428:GLU:O	2:D:429:THR:CB	2.67	0.42
1:A:255:LEU:HD13	1:A:255:LEU:HA	1.87	0.42
2:B:206:ILE:HD13	2:B:206:ILE:HG21	1.85	0.42
1:C:162:GLU:CB	1:C:164:VAL:HG23	2.41	0.42
2:D:346:PRO:O	2:D:349:LYS:HG3	2.19	0.42
2:D:425:ASN:HA	2:D:426:PRO:HD2	1.79	0.42
2:D:401:ALA:HB1	2:D:410:ARG:HD2	2.01	0.42
1:A:36:ARG:NH1	1:A:36:ARG:CG	2.82	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:49:ILE:HD11	2:B:299:LEU:HD11	2.02	0.42
1:C:60:HIS:CD2	1:C:62:ASN:H	2.37	0.42
2:D:178:TYR:C	2:D:178:TYR:CD2	2.97	0.42
2:D:218:LEU:O	2:D:219:VAL:C	2.61	0.42
1:A:282:ALA:O	1:A:283:HIS:C	2.61	0.42
1:A:41:THR:CG2	1:A:42:GLU:N	2.79	0.42
1:C:39:THR:CG2	1:C:40:GLU:N	2.82	0.42
1:C:55:LEU:HD12	1:C:55:LEU:HA	1.94	0.42
1:C:87:LEU:HD13	1:C:91:MET:SD	2.60	0.42
1:A:33:LYS:HB3	1:A:78:LEU:HB2	2.02	0.41
1:A:175:LEU:HD23	1:A:212:LEU:CD1	2.50	0.41
1:A:247:ASP:O	1:A:250:LYS:N	2.43	0.41
2:B:385:GLU:O	2:B:388:LYS:HB2	2.20	0.41
1:A:207:SER:H	1:A:210:ASP:HB3	1.85	0.41
1:C:25:LEU:HD23	1:C:25:LEU:HA	1.83	0.41
1:C:283:HIS:HA	1:C:284:PRO:HD2	1.88	0.41
2:D:297:LEU:O	2:D:301:VAL:HG23	2.19	0.41
1:A:172:GLU:OE2	1:A:172:GLU:N	2.48	0.41
2:D:199:TYR:CD1	2:D:199:TYR:C	2.98	0.41
1:A:115:LEU:HD21	1:A:128:LEU:HD11	2.03	0.41
1:C:99:ILE:O	1:C:100:PRO:C	2.62	0.41
1:A:37:LEU:HB2	1:A:74:ASN:O	2.20	0.41
2:D:302:LEU:C	2:D:303:THR:HG1	2.29	0.41
2:B:322:GLN:HG2	2:B:323:GLN:H	1.86	0.41
2:D:282:THR:O	2:D:283:ASP:HB2	2.20	0.41
2:D:331:SER:HB3	2:D:421:VAL:HG21	2.02	0.41
1:A:255:LEU:HD12	1:A:259:GLY:HA3	2.02	0.41
1:C:109:PHE:CE2	1:C:113:GLN:NE2	2.89	0.41
1:A:56:LYS:HZ3	1:A:56:LYS:HG2	1.73	0.41
1:A:99:ILE:HG23	1:A:103:LEU:HD23	2.02	0.41
1:C:81:GLU:HG3	1:C:83:LEU:HD11	2.02	0.41
1:C:108:LEU:HD22	1:C:193:PHE:CD1	2.56	0.41
1:A:95:ALA:O	1:A:96:LEU:CD2	2.65	0.41
1:A:231:THR:HA	1:A:236:TYR:CE1	2.56	0.41
1:A:83:LEU:HD23	1:A:136:ASN:HB3	2.03	0.40
1:A:49:ILE:HG23	2:B:306:LEU:CD1	2.51	0.40
1:A:159:TYR:CD2	1:A:163:VAL:HG12	2.56	0.40
1:A:220:GLY:O	1:A:269:TYR:OH	2.26	0.40
2:B:399:LEU:HA	2:B:399:LEU:HD23	1.85	0.40
1:C:9:LYS:HG3	1:C:19:TYR:CE2	2.56	0.40
1:A:64:VAL:O	1:A:64:VAL:HG13	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:129:LYS:HE3	1:A:132:ASN:HD21	1.87	0.40
2:B:323:GLN:HE21	2:B:323:GLN:CA	2.34	0.40
2:D:175:VAL:N	2:D:176:PRO:CD	2.82	0.40
2:D:372:TRP:HA	2:D:373:PRO:HD3	1.87	0.40
1:A:57:GLU:OE2	2:B:307:ALA:HB3	2.22	0.40
1:A:202:LEU:HD22	1:A:203:PHE:CE1	2.56	0.40
2:D:223:GLU:CD	2:D:412:LYS:HG3	2.47	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	294/298 (99%)	268 (91%)	22 (8%)	4 (1%)	9	30
1	C	295/298 (99%)	268 (91%)	25 (8%)	2 (1%)	18	48
2	B	258/260 (99%)	240 (93%)	18 (7%)	0	100	100
2	D	256/260 (98%)	240 (94%)	14 (6%)	2 (1%)	16	44
3	E	1/5 (20%)	1 (100%)	0	0	100	100
3	F	1/5 (20%)	1 (100%)	0	0	100	100
All	All	1105/1126 (98%)	1018 (92%)	79 (7%)	8 (1%)	18	48

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	41	THR
1	C	165	THR
2	D	320	LEU
1	A	14	THR
2	D	429	THR

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Mol	Chain	Res	Type
1	A	285	PHE
1	A	164	VAL
1	C	164	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	261/263 (99%)	215 (82%)	46 (18%)	2	6
1	C	261/263 (99%)	224 (86%)	37 (14%)	3	11
2	B	234/234 (100%)	209 (89%)	25 (11%)	6	22
2	D	232/234 (99%)	207 (89%)	25 (11%)	6	21
3	E	2/2 (100%)	1 (50%)	1 (50%)	0	0
3	F	2/2 (100%)	0	2 (100%)	0	0
All	All	992/998 (99%)	856 (86%)	136 (14%)	3	12

All (136) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	LYS
1	A	10	ILE
1	A	12	GLU
1	A	15	TYR
1	A	17	VAL
1	A	18	VAL
1	A	22	ARG
1	A	35	ILE
1	A	36	ARG
1	A	37	LEU
1	A	38	ASP
1	A	39	THR
1	A	41	THR
1	A	47	THR
1	A	55	LEU

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Mol	Chain	Res	Type
1	A	56	LYS
1	A	70	ILE
1	A	71	HIS
1	A	73	GLU
1	A	74	ASN
1	A	76	LEU
1	A	96	LEU
1	A	97	THR
1	A	101	LEU
1	A	115	LEU
1	A	126	ARG
1	A	131	GLN
1	A	157	ARG
1	A	160	THR
1	A	164	VAL
1	A	184	VAL
1	A	192	ILE
1	A	202	LEU
1	A	212	LEU
1	A	230	VAL
1	A	237	LYS
1	A	239	SER
1	A	242	LYS
1	A	246	GLN
1	A	249	SER
1	A	251	VAL
1	A	255	LEU
1	A	268	HIS
1	A	287	GLN
1	A	293	VAL
1	A	296	LEU
2	B	180	GLU
2	B	200	MET
2	B	201	LYS
2	B	202	LYS
2	B	244	SER
2	B	247	SER
2	B	250	ARG
2	B	283	ASP
2	B	288	LYS
2	B	292	LEU
2	B	323	GLN

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Mol	Chain	Res	Type
2	B	343	ASP
2	B	348	LEU
2	B	374	GLU
2	B	375	SER
2	B	391	LEU
2	B	392	MET
2	B	403[A]	GLN
2	B	403[B]	GLN
2	B	417	LYS
2	B	421	VAL
2	B	424	LEU
2	B	428	GLU
2	B	430	LEU
2	B	432	LEU
1	C	9	LYS
1	C	10	ILE
1	C	14	THR
1	C	15	TYR
1	C	33	LYS
1	C	37	LEU
1	C	39	THR
1	C	42	GLU
1	C	49	ILE
1	C	53	SER
1	C	55	LEU
1	C	64	VAL
1	C	70	ILE
1	C	71	HIS
1	C	74	ASN
1	C	86	ASP
1	C	87	LEU
1	C	89	LYS
1	C	96	LEU
1	C	115	LEU
1	C	131	GLN
1	C	141	ILE
1	C	158	THR
1	C	161	HIS
1	C	162	GLU
1	C	164	VAL
1	C	165	THR
1	C	178	LYS

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Mol	Chain	Res	Type
1	C	189	LEU
1	C	192	ILE
1	C	200	ARG
1	C	217	ARG
1	C	232	SER
1	C	247	ASP
1	C	268	HIS
1	C	291	LYS
1	C	296	LEU
2	D	189	MET
2	D	192	LYS
2	D	196	LYS
2	D	199	TYR
2	D	201	LYS
2	D	207	THR
2	D	226	LYS
2	D	232	LEU
2	D	283	ASP
2	D	289	LYS
2	D	292	LEU
2	D	303	THR
2	D	328	LYS
2	D	340	SER
2	D	364	LEU
2	D	370	GLN
2	D	375	SER
2	D	377	ILE
2	D	378	ARG
2	D	384	LEU
2	D	392	MET
2	D	400	LYS
2	D	424	LEU
2	D	431	ASN
2	D	432	LEU
3	E	2	ARG
3	F	1	ARG
3	F	2	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	60	HIS

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Mol	Chain	Res	Type
1	A	62	ASN
1	A	74	ASN
1	A	85	GLN
1	A	131	GLN
1	A	268	HIS
1	A	287	GLN
2	B	208	ASN
2	B	296	HIS
2	B	317	GLN
2	B	323	GLN
2	B	370	GLN
2	B	425	ASN
2	B	431	ASN
1	C	5	GLN
1	C	59	ASN
1	C	60	HIS
1	C	62	ASN
1	C	71	HIS
1	C	113	GLN
1	C	131	GLN
1	C	287	GLN
2	D	208	ASN
2	D	229	ASN
2	D	296	HIS
2	D	312	ASN
2	D	313	GLN
2	D	322	GLN
2	D	361	HIS
2	D	370	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

4 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond

length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	L3O	E	3	3	7,9,10	0.78	0	6,11,13	1.79	2 (33%)
3	PFF	E	4	3	11,12,13	0.78	0	10,15,17	2.08	5 (50%)
3	PFF	F	4	3	11,12,13	0.52	0	10,15,17	1.17	1 (10%)
3	L3O	F	3	3	7,9,10	0.56	0	6,11,13	0.93	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	L3O	E	3	3	-	0/9/10/12	-
3	PFF	E	4	3	-	0/5/6/8	0/1/1/1
3	PFF	F	4	3	-	0/5/6/8	0/1/1/1
3	L3O	F	3	3	-	1/9/10/12	-

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	3	L3O	OZ-CZ-C	-3.54	102.43	110.48
3	E	4	PFF	F-CZ-CE1	3.38	123.97	118.55
3	E	4	PFF	CE2-CD2-CG	-2.82	117.30	121.00
3	E	4	PFF	CD2-CG-CD1	2.56	122.04	118.23
3	E	4	PFF	CD2-CE2-CZ	2.50	120.95	118.38
3	E	3	L3O	CD1-CG-CB	2.35	119.52	111.08
3	E	4	PFF	F-CZ-CE2	-2.32	114.83	118.55
3	F	4	PFF	CD2-CG-CD1	2.06	121.30	118.23

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	F	3	L3O	O-C-CZ-CA

There are no ring outliers.

No monomer is involved in short contacts.

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	296/298 (99%)	-0.04	1 (0%) 90 87	29, 51, 78, 89	0
1	C	297/298 (99%)	-0.08	8 (2%) 56 47	27, 49, 78, 88	0
2	B	258/260 (99%)	-0.19	4 (1%) 70 62	25, 50, 76, 92	2 (0%)
2	D	258/260 (99%)	-0.17	3 (1%) 76 69	25, 50, 77, 89	0
3	E	2/5 (40%)	0.09	0 100 100	55, 55, 55, 89	0
3	F	2/5 (40%)	0.36	0 100 100	75, 75, 75, 87	0
All	All	1113/1126 (98%)	-0.11	16 (1%) 73 65	25, 50, 78, 92	2 (0%)

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	37	LEU	5.1
2	B	432	LEU	3.8
2	B	175	VAL	3.7
1	C	161	HIS	3.7
1	C	15	TYR	3.7
1	C	163	VAL	3.5
2	D	432	LEU	3.3
1	C	38	ASP	3.2
1	C	39	THR	3.0
2	D	175	VAL	2.9
2	B	178	TYR	2.4
1	C	14	THR	2.2
2	B	176	PRO	2.1
1	C	159	TYR	2.1
2	D	323	GLN	2.1
1	A	164	VAL	2.0

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	PFF	F	4	12/13	0.92	0.10	60,63,80,89	0
3	PFF	E	4	12/13	0.93	0.08	54,57,63,64	0
3	L3O	E	3	10/11	0.94	0.07	31,55,59,66	0
3	L3O	F	3	10/11	0.96	0.09	46,53,60,61	0

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.