



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 01:59 PM UTC

PDB ID : 3AEU / pdb_00003aeu
Title : Structure of the light-independent protochlorophyllide reductase catalyzing a key reduction for greening in the dark
Authors : Muraki, N.; Nomata, J.; Shiba, T.; Fujita, Y.; Kurisu, G.
Deposited on : 2010-02-10
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

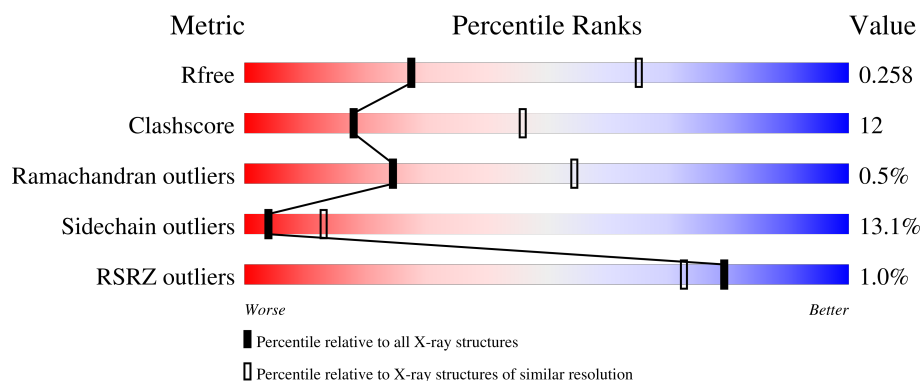
1 Overall quality at a glance

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	436	% 65% 25% • 5%
1	C	436	% 69% 22% • • 5%
2	B	525	57% 20% • 21%
2	D	525	% 54% 21% • 20%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 12752 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 Light-independent protochlorophyllide reductase subunit N.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	414	Total	C	N	O	S	0	0	0
			3160	2005	557	583	15			
1	C	414	Total	C	N	O	S	0	0	0
			3160	2005	557	583	15			

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	MET	-	expression tag	UNP P26164
A	-10	ALA	-	expression tag	UNP P26164
A	-9	SER	-	expression tag	UNP P26164
A	-8	TRP	-	expression tag	UNP P26164
A	-7	SER	-	expression tag	UNP P26164
A	-6	HIS	-	expression tag	UNP P26164
A	-5	PRO	-	expression tag	UNP P26164
A	-4	GLN	-	expression tag	UNP P26164
A	-3	PHE	-	expression tag	UNP P26164
A	-2	GLU	-	expression tag	UNP P26164
A	-1	LYS	-	expression tag	UNP P26164
A	0	GLY	-	expression tag	UNP P26164
A	1	ALA	-	expression tag	UNP P26164
C	-11	MET	-	expression tag	UNP P26164
C	-10	ALA	-	expression tag	UNP P26164
C	-9	SER	-	expression tag	UNP P26164
C	-8	TRP	-	expression tag	UNP P26164
C	-7	SER	-	expression tag	UNP P26164
C	-6	HIS	-	expression tag	UNP P26164
C	-5	PRO	-	expression tag	UNP P26164
C	-4	GLN	-	expression tag	UNP P26164
C	-3	PHE	-	expression tag	UNP P26164
C	-2	GLU	-	expression tag	UNP P26164
C	-1	LYS	-	expression tag	UNP P26164
C	0	GLY	-	expression tag	UNP P26164

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1	ALA	-	expression tag	UNP P26164

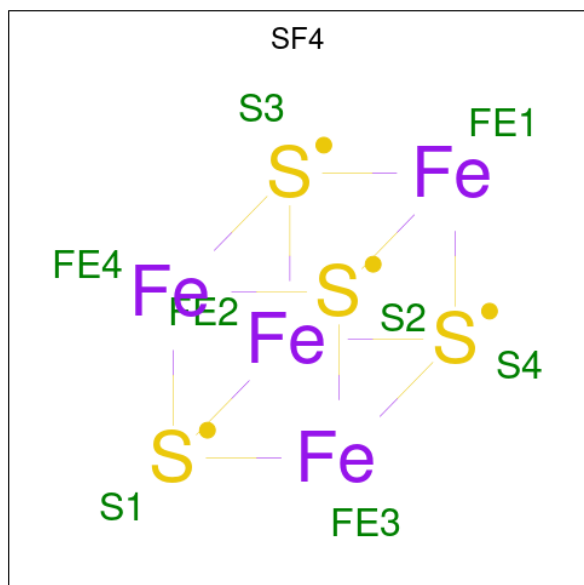
- Molecule 2 is a protein called Light-independent protochlorophyllide reductase subunit B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	417	Total	C	N	O	S	0	0	0
			3193	2035	554	583	21			
2	D	419	Total	C	N	O	S	0	0	0
			3208	2043	556	588	21			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	36	ALA	ASP	engineered mutation	UNP P26163
D	36	ALA	ASP	engineered mutation	UNP P26163

- Molecule 3 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	Fe	S	0	0
			8	4	4		
3	C	1	Total	Fe	S	0	0
			8	4	4		

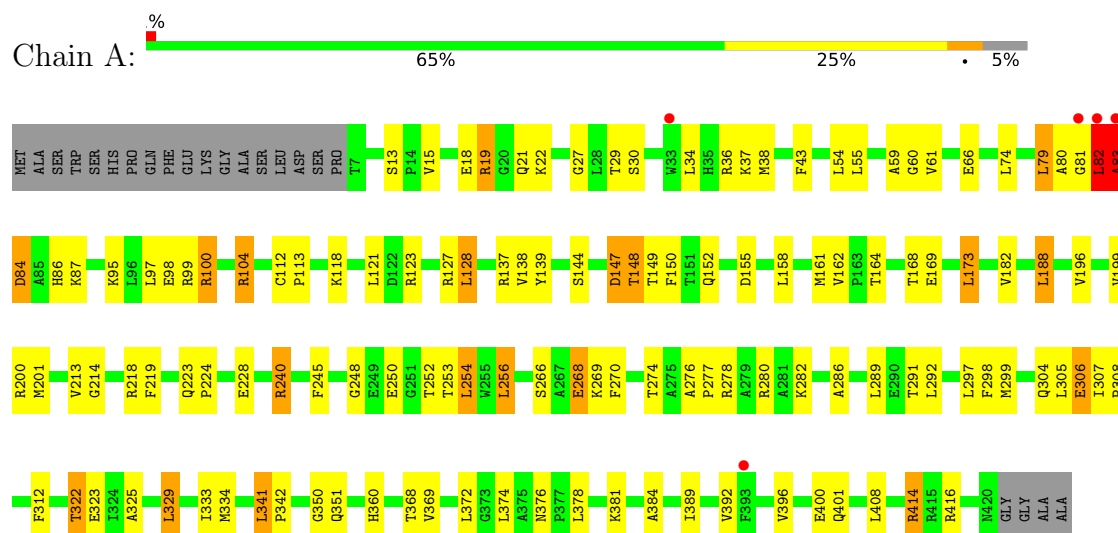
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total 1	O 1	0	0
4	B	5	Total 5	O 5	0	0
4	C	2	Total 2	O 2	0	0
4	D	7	Total 7	O 7	0	0

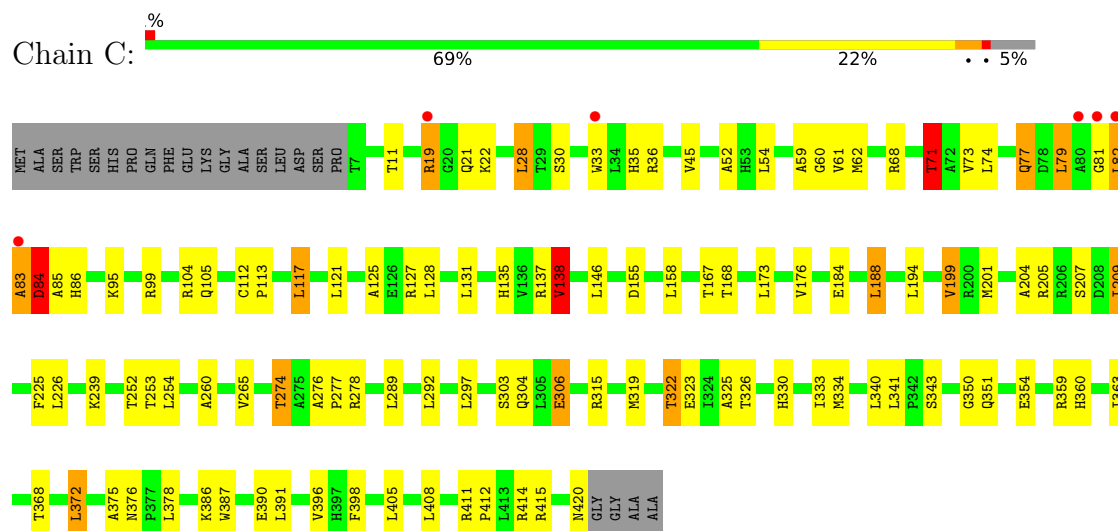
3 Residue-property plots [i](#)

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: Light-independent protochlorophyllide reductase subunit N

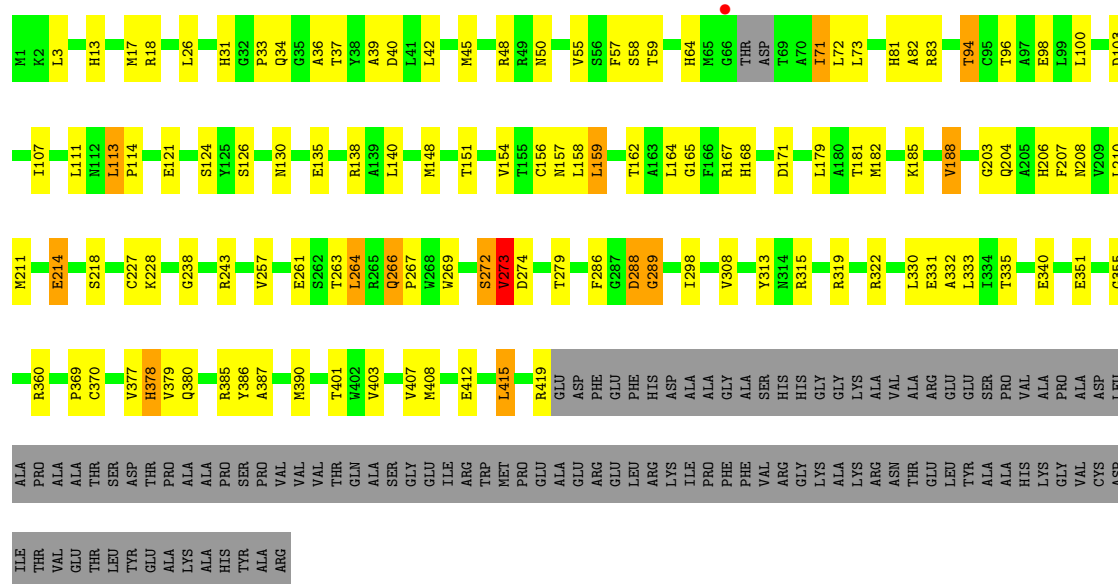


- Molecule 1: Light-independent protochlorophyllide reductase subunit N

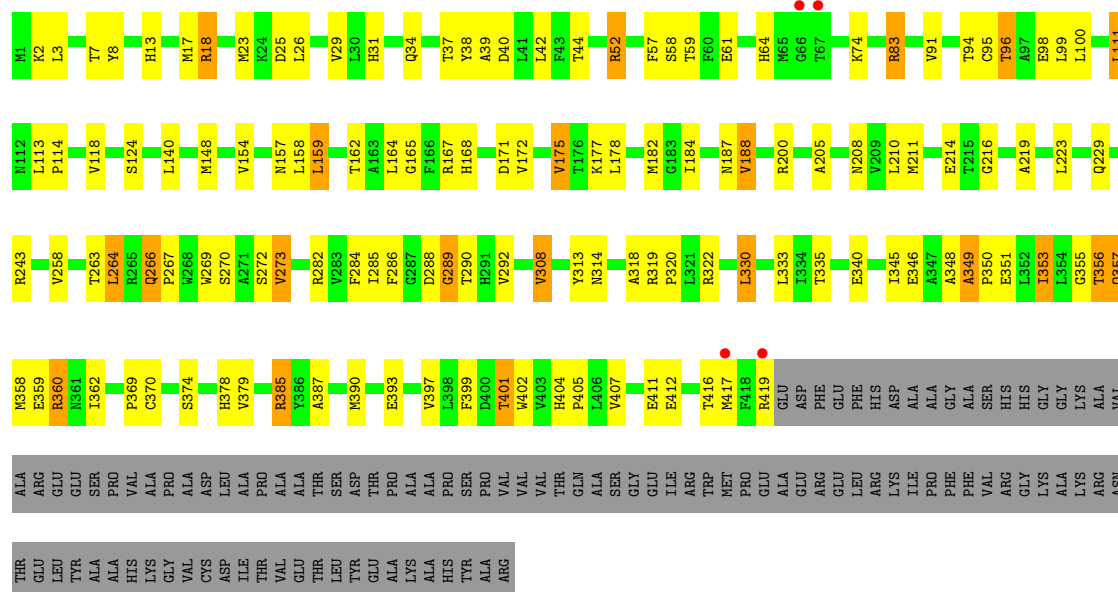


- Molecule 2: Light-independent protochlorophyllide reductase subunit B





• Molecule 2: Light-independent protochlorophyllide reductase subunit B



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	81.35Å 80.61Å 176.22Å 90.00° 101.17° 90.00°	Depositor
Resolution (Å)	39.90 – 2.90 39.90 – 2.90	Depositor EDS
% Data completeness (in resolution range)	97.8 (39.90-2.90) 97.8 (39.90-2.90)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.65 (at 2.90Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.205 , 0.257 0.208 , 0.258	Depositor DCC
R_{free} test set	2467 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	44.6	Xtriage
Anisotropy	0.173	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 38.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.011 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	12752	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.98% 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: SF4

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	2/3223 (0.1%)	1.07	6/4377 (0.1%)
1	C	0.74	0/3223	1.03	4/4377 (0.1%)
2	B	0.76	0/3263	1.01	3/4439 (0.1%)
2	D	0.75	0/3279	1.03	4/4463 (0.1%)
All	All	0.75	2/12988 (0.0%)	1.04	17/17656 (0.1%)

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
2	D	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	162	VAL	CA-CB	6.46	1.57	1.54
1	A	84	ASP	N-CA	-6.03	1.39	1.46

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	83	ALA	CA-C-N	-8.10	110.41	122.24
1	A	83	ALA	C-N-CA	-8.10	110.41	122.24
1	C	82	LEU	N-CA-C	8.10	122.83	113.19
1	A	84	ASP	CB-CA-C	7.56	122.10	111.74
2	D	314	ASN	N-CA-CB	-6.83	100.76	110.46
1	A	223	GLN	CA-C-N	5.99	125.67	119.56
1	A	223	GLN	C-N-CA	5.99	125.67	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	138	VAL	N-CA-C	5.79	116.28	108.17
2	B	273	VAL	N-CA-C	5.60	116.33	110.62
2	D	370	CYS	N-CA-C	5.57	117.57	108.55
1	C	71	THR	CB-CA-C	5.52	118.64	110.14
2	D	83	ARG	N-CA-C	5.46	117.04	111.14
2	B	83	ARG	N-CA-C	5.38	116.95	111.14
2	B	370	CYS	N-CA-C	5.38	117.26	108.55
1	C	84	ASP	N-CA-CB	-5.28	102.85	110.56
2	D	349	ALA	N-CA-C	-5.22	99.99	109.44
1	A	82	LEU	CA-CB-CG	5.05	133.97	116.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	D	348	ALA	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	3160	0	3196	85	0
1	C	3160	0	3196	77	0
2	B	3193	0	3228	79	0
2	D	3208	0	3240	94	0
3	A	8	0	0	0	0
3	C	8	0	0	1	0
4	A	1	0	0	0	0
4	B	5	0	0	0	0
4	C	2	0	0	0	0
4	D	7	0	0	0	0
All	All	12752	0	12860	313	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 12.

All (313) 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:84:ASP:HB3	1:A:87:LYS:HB2	1.25	1.16
1:A:322:THR:HG22	1:A:323:GLU:H	1.05	1.14
2:B:103:ASP:O	2:B:107:ILE:HG12	1.44	1.12
1:C:322:THR:HG22	1:C:323:GLU:H	0.93	1.04
2:D:171:ASP:HB3	2:D:390:MET:HE2	1.41	1.00
1:C:322:THR:CG2	1:C:323:GLU:H	1.74	1.00
1:C:322:THR:HG22	1:C:323:GLU:N	1.74	0.97
1:A:27:GLY:H	1:A:148:THR:HG22	1.34	0.92
1:A:27:GLY:HA3	1:A:148:THR:HG21	1.51	0.91
2:D:18:ARG:HG2	2:D:18:ARG:HH11	1.33	0.90
1:A:27:GLY:HA3	1:A:148:THR:CG2	2.02	0.89
1:C:86:HIS:CD2	1:C:127:ARG:HH22	1.90	0.89
1:A:322:THR:HG22	1:A:323:GLU:N	1.86	0.88
1:A:322:THR:CG2	1:A:323:GLU:H	1.85	0.88
1:A:148:THR:HA	1:A:152:GLN:HE21	1.38	0.87
1:A:84:ASP:CB	1:A:87:LYS:HB2	2.04	0.87
2:B:273:VAL:H	1:C:376:ASN:HD21	1.20	0.87
1:C:260:ALA:HB1	1:C:265:VAL:HG12	1.54	0.86
1:A:276:ALA:HB3	1:A:277:PRO:HD3	1.58	0.85
1:C:372:LEU:O	2:D:44:THR:HG21	1.76	0.84
2:D:162:THR:H	2:D:168:HIS:HD2	1.25	0.83
1:A:148:THR:HA	1:A:152:GLN:NE2	1.95	0.82
1:A:84:ASP:HB3	1:A:87:LYS:CB	2.08	0.81
1:C:253:THR:OG1	1:C:278:ARG:HD3	1.81	0.80
1:A:297:LEU:O	1:A:322:THR:HB	1.80	0.80
2:B:71:ILE:HD13	2:B:71:ILE:H	1.48	0.79
2:B:162:THR:H	2:B:168:HIS:HD2	1.30	0.79
1:A:341:LEU:HD23	1:A:342:PRO:HD2	1.65	0.78
2:B:378:HIS:HB3	2:B:380:GLN:OE1	1.83	0.78
2:B:18:ARG:HD2	2:B:164:LEU:HB2	1.66	0.77
1:C:322:THR:CG2	1:C:323:GLU:N	2.39	0.77
2:B:264:LEU:HD22	2:B:267:PRO:HD3	1.66	0.76
2:D:284:PHE:HB2	2:D:350:PRO:HG3	1.67	0.76
1:C:86:HIS:HD2	1:C:127:ARG:HH22	1.30	0.75
1:A:27:GLY:N	1:A:148:THR:HG22	2.02	0.75
1:A:299:MET:HE3	1:A:369:VAL:HG21	1.68	0.75
2:D:282:ARG:NH2	2:D:308:VAL:HG21	2.02	0.74
1:A:27:GLY:CA	1:A:148:THR:CG2	2.65	0.74
2:D:356:THR:HB	2:D:359:GLU:OE2	1.89	0.72
1:A:112:CYS:HB2	1:A:113:PRO:HD3	1.71	0.72
1:C:297:LEU:O	1:C:322:THR:HB	1.90	0.72
1:A:376:ASN:HD21	2:D:273:VAL:H	1.37	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:269:TRP:O	2:D:272:SER:HB3	1.92	0.70
2:D:356:THR:HG22	2:D:358:MET:H	1.56	0.70
1:A:306:GLU:HG3	1:A:325:ALA:O	1.92	0.69
2:B:313:TYR:HA	2:B:335:THR:O	1.92	0.69
2:B:273:VAL:H	1:C:376:ASN:ND2	1.91	0.69
2:B:360:ARG:HG3	2:B:360:ARG:HH11	1.58	0.69
1:A:322:THR:CG2	1:A:323:GLU:N	2.50	0.68
2:D:94:THR:HG22	2:D:96:THR:H	1.59	0.68
1:A:27:GLY:N	1:A:148:THR:CG2	2.58	0.67
1:A:84:ASP:HB3	1:A:87:LYS:H	1.59	0.66
2:D:172:VAL:HG22	2:D:211:MET:HE1	1.77	0.66
1:A:27:GLY:H	1:A:148:THR:CG2	2.06	0.65
2:B:264:LEU:HD22	2:B:267:PRO:CD	2.26	0.64
1:A:86:HIS:ND1	1:A:127:ARG:NH2	2.44	0.64
2:D:313:TYR:HA	2:D:335:THR:O	1.97	0.64
1:A:188:LEU:HD13	1:A:201:MET:CE	2.28	0.64
1:C:52:ALA:HA	1:C:71:THR:HG21	1.79	0.63
2:B:148:MET:HE1	2:B:204:GLN:HE21	1.64	0.63
1:A:333:ILE:HG22	1:A:334:MET:HE2	1.81	0.62
1:C:188:LEU:HD22	1:C:201:MET:CE	2.29	0.62
1:A:22:LYS:HD3	2:B:34:GLN:HE21	1.65	0.62
1:C:188:LEU:HD22	1:C:201:MET:HE1	1.82	0.61
2:D:270:SER:HB3	2:D:399:PHE:CE1	2.35	0.61
2:D:351:GLU:O	2:D:369:PRO:HD2	2.01	0.61
1:C:22:LYS:H	2:D:59:THR:HG21	1.65	0.61
1:A:22:LYS:CD	2:B:34:GLN:HE21	2.14	0.60
2:B:408:MET:HA	2:B:408:MET:HE2	1.83	0.60
2:D:59:THR:HG22	2:D:59:THR:O	2.01	0.60
2:B:64:HIS:CD2	2:B:72:LEU:HD11	2.36	0.60
1:A:384:ALA:HB2	1:A:416:ARG:HD2	1.84	0.59
2:B:130:ASN:HD22	2:B:214:GLU:HB2	1.68	0.59
1:A:147:ASP:OD1	1:A:147:ASP:N	2.32	0.59
1:C:35:HIS:O	1:C:68:ARG:NH2	2.36	0.59
2:D:18:ARG:HG2	2:D:18:ARG:NH1	2.11	0.59
2:B:17:MET:HE1	2:B:39:ALA:HB3	1.84	0.59
2:D:397:VAL:O	2:D:401:THR:OG1	2.20	0.59
2:D:148:MET:HE1	2:D:200:ARG:O	2.03	0.58
1:A:305:LEU:O	1:A:308:PRO:HD2	2.03	0.58
1:C:194:LEU:O	1:C:265:VAL:HG21	2.02	0.58
2:D:61:GLU:HG2	2:D:64:HIS:HD2	1.69	0.58
1:C:83:ALA:HB3	1:C:84:ASP:OD1	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:31:HIS:HD2	2:D:58:SER:OG	1.87	0.57
2:D:285:ILE:HG22	2:D:292:VAL:HG13	1.84	0.57
1:A:266:SER:OG	1:A:268:GLU:HB2	2.04	0.57
2:D:157:ASN:ND2	2:D:188:VAL:H	2.03	0.57
1:A:79:LEU:O	1:A:81:GLY:N	2.30	0.57
2:B:167:ARG:HD2	2:B:387:ALA:O	2.05	0.57
2:D:13:HIS:HD2	2:D:17:MET:HE2	1.70	0.57
1:C:28:LEU:HD22	3:C:425:SF4:S2	2.45	0.57
1:C:306:GLU:HG3	1:C:325:ALA:O	2.05	0.57
2:B:322:ARG:HG2	2:B:332:ALA:HB3	1.87	0.56
1:A:270:PHE:O	1:A:274:THR:HG22	2.05	0.56
2:B:103:ASP:O	2:B:107:ILE:CG1	2.37	0.56
2:D:243:ARG:HG3	2:D:243:ARG:HH11	1.70	0.56
2:D:356:THR:CG2	2:D:358:MET:H	2.19	0.56
1:C:112:CYS:HB2	1:C:113:PRO:HD3	1.88	0.55
1:C:315:ARG:HD2	1:C:340:LEU:O	2.06	0.55
2:D:345:ILE:O	2:D:349:ALA:HA	2.07	0.55
1:C:260:ALA:HB1	1:C:265:VAL:CG1	2.33	0.55
2:D:34:GLN:HA	2:D:59:THR:HG23	1.88	0.55
2:D:162:THR:H	2:D:168:HIS:CD2	2.14	0.55
2:D:412:GLU:O	2:D:416:THR:HG23	2.07	0.55
1:A:274:THR:O	1:A:278:ARG:HG3	2.07	0.54
2:D:288:ASP:O	2:D:288:ASP:OD2	2.25	0.54
2:D:167:ARG:HD2	2:D:387:ALA:O	2.06	0.54
1:C:117:LEU:HD13	2:D:99:LEU:HD13	1.89	0.54
1:C:22:LYS:HD2	2:D:34:GLN:HE21	1.72	0.54
2:D:282:ARG:HG3	2:D:351:GLU:OE1	2.06	0.54
1:C:204:ALA:HB1	1:C:209:ILE:HD12	1.89	0.54
1:A:169:GLU:HG2	1:A:169:GLU:O	2.08	0.53
1:C:386:LYS:NZ	1:C:390:GLU:OE1	2.36	0.52
1:C:359:ARG:O	1:C:363:ILE:HG12	2.09	0.52
2:B:33:PRO:HD2	2:B:36:ALA:HB2	1.91	0.52
2:D:157:ASN:HD22	2:D:188:VAL:H	1.55	0.52
1:C:22:LYS:HB2	2:D:59:THR:HG21	1.90	0.52
2:B:71:ILE:H	2:B:71:ILE:CD1	2.18	0.52
1:A:149:THR:H	1:A:152:GLN:NE2	2.07	0.52
2:D:8:TYR:HE2	2:D:356:THR:HG21	1.75	0.52
2:D:158:LEU:HB3	2:D:211:MET:HE2	1.91	0.52
2:D:288:ASP:O	2:D:288:ASP:CG	2.52	0.51
1:A:416:ARG:HH11	1:A:416:ARG:HB2	1.75	0.51
2:B:360:ARG:HG3	2:B:360:ARG:NH1	2.24	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:345:ILE:HD13	2:D:353:ILE:HD12	1.93	0.51
1:C:276:ALA:HB3	1:C:277:PRO:HD3	1.93	0.51
1:A:30:SER:O	1:A:34:LEU:HB2	2.11	0.51
2:B:13:HIS:HD2	2:B:17:MET:HE2	1.75	0.51
2:B:162:THR:H	2:B:168:HIS:CD2	2.20	0.51
2:B:94:THR:HG22	2:B:96:THR:H	1.75	0.51
1:C:225:PHE:HA	1:C:304:GLN:NE2	2.26	0.51
2:B:111:LEU:O	2:B:111:LEU:HD23	2.11	0.51
1:C:188:LEU:CD1	1:C:199:VAL:HG22	2.41	0.51
2:D:335:THR:HG21	2:D:340:GLU:HB2	1.93	0.50
2:B:238:GLY:CA	2:B:298:ILE:HD11	2.40	0.50
2:B:351:GLU:O	2:B:369:PRO:HD2	2.11	0.50
2:B:39:ALA:O	2:B:40:ASP:C	2.54	0.50
1:C:82:LEU:O	1:C:83:ALA:O	2.30	0.50
2:D:18:ARG:HG2	2:D:164:LEU:H	1.76	0.50
2:B:57:PHE:HB2	2:B:59:THR:HG23	1.94	0.50
1:C:360:HIS:HE1	1:C:368:THR:OG1	1.94	0.50
1:C:86:HIS:CD2	1:C:127:ARG:NH2	2.72	0.49
2:D:266:GLN:HE21	2:D:267:PRO:N	2.09	0.49
1:C:184:GLU:CD	1:C:205:ARG:HH21	2.19	0.49
2:D:13:HIS:CD2	2:D:17:MET:HE2	2.47	0.49
1:C:105:GLN:HE21	1:C:207:SER:HB2	1.78	0.49
1:A:158:LEU:HA	1:A:161:MET:HE3	1.94	0.49
1:C:21:GLN:HG3	2:D:57:PHE:O	2.13	0.49
2:D:13:HIS:CD2	2:D:17:MET:CE	2.96	0.49
2:D:288:ASP:O	2:D:290:THR:N	2.45	0.49
1:A:34:LEU:HG	1:A:38:MET:CE	2.42	0.49
2:D:187:ASN:HD22	2:D:205:ALA:HB2	1.77	0.49
1:A:286:ALA:HA	1:A:289:LEU:HD12	1.94	0.49
1:C:79:LEU:O	1:C:81:GLY:N	2.40	0.48
1:A:250:GLU:HG2	1:A:254:LEU:HD22	1.94	0.48
2:B:148:MET:CE	2:B:204:GLN:HE21	2.24	0.48
1:A:305:LEU:C	1:A:308:PRO:HD2	2.38	0.48
1:A:84:ASP:HB3	1:A:87:LYS:N	2.26	0.48
1:C:330:HIS:CD2	1:C:333:ILE:HD12	2.49	0.48
1:A:82:LEU:O	1:A:83:ALA:O	2.31	0.48
1:A:304:GLN:N	1:A:306:GLU:OE1	2.47	0.48
1:A:350:GLY:O	1:A:351:GLN:HB3	2.14	0.48
2:D:402:TRP:O	2:D:405:PRO:HD2	2.13	0.48
2:D:165:GLY:HA3	2:D:168:HIS:CD2	2.49	0.48
2:B:203:GLY:HA2	2:B:227:CYS:SG	2.54	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:165:GLY:HA3	2:D:168:HIS:CG	2.48	0.48
2:D:356:THR:HG22	2:D:358:MET:N	2.26	0.48
2:B:157:ASN:HD22	2:B:188:VAL:H	1.62	0.47
1:A:291:THR:HG21	1:A:414:ARG:HD3	1.96	0.47
2:B:157:ASN:ND2	2:B:188:VAL:H	2.11	0.47
2:D:286:PHE:O	2:D:355:GLY:HA2	2.14	0.47
2:D:393:GLU:O	2:D:397:VAL:HG23	2.14	0.47
1:A:276:ALA:HB3	1:A:277:PRO:CD	2.39	0.47
2:B:159:LEU:HD22	2:B:208:ASN:HB3	1.96	0.47
1:A:59:ALA:O	1:A:60:GLY:C	2.56	0.47
2:D:113:LEU:HB3	2:D:114:PRO:CD	2.45	0.47
1:A:224:PRO:HA	1:A:245:PHE:CZ	2.50	0.47
2:B:135:GLU:HA	2:B:135:GLU:OE1	2.14	0.47
2:D:270:SER:HB3	2:D:399:PHE:HE1	1.77	0.47
2:B:266:GLN:HE21	2:B:267:PRO:N	2.12	0.47
1:C:354:GLU:HB3	2:D:83:ARG:NH1	2.30	0.47
2:D:319:ARG:HB2	2:D:320:PRO:HD3	1.97	0.47
2:B:26:LEU:C	2:B:26:LEU:HD23	2.40	0.47
1:C:304:GLN:HA	1:C:326:THR:OG1	2.14	0.47
2:D:182:MET:HG3	2:D:258:VAL:H	1.80	0.47
2:D:23:MET:SD	2:D:26:LEU:HD13	2.55	0.46
2:D:157:ASN:HB2	2:D:208:ASN:OD1	2.15	0.46
2:B:18:ARG:HG3	2:B:164:LEU:H	1.81	0.46
1:C:176:VAL:HG12	1:C:226:LEU:HD13	1.97	0.46
1:C:411:ARG:HB3	1:C:412:PRO:HD3	1.95	0.46
1:A:98:GLU:C	1:A:100:ARG:H	2.23	0.46
1:A:155:ASP:OD2	1:A:228:GLU:HB2	2.16	0.46
2:D:318:ALA:O	2:D:322:ARG:HG3	2.15	0.46
2:B:17:MET:HG2	2:B:55:VAL:HG21	1.98	0.46
1:C:19:ARG:CZ	1:C:19:ARG:HB3	2.46	0.46
2:B:156:CYS:HB3	2:B:207:PHE:CE2	2.51	0.46
2:B:286:PHE:O	2:B:355:GLY:HA2	2.16	0.46
2:B:111:LEU:HD22	2:B:113:LEU:HD13	1.96	0.45
2:B:266:GLN:HE21	2:B:266:GLN:C	2.24	0.45
2:D:111:LEU:HD13	2:D:113:LEU:HD11	1.97	0.45
1:A:280:ARG:NH2	1:A:400:GLU:OE1	2.49	0.45
2:B:113:LEU:HB3	2:B:114:PRO:HD2	1.98	0.45
1:C:112:CYS:SG	1:C:146:LEU:HG	2.56	0.45
1:A:95:LYS:HE2	1:A:99:ARG:HH21	1.81	0.45
2:B:415:LEU:HD23	2:B:419:ARG:HH21	1.81	0.45
2:D:282:ARG:CZ	2:D:308:VAL:HG21	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:13:HIS:HD2	2:D:17:MET:CE	2.30	0.45
2:B:273:VAL:HG21	1:C:375:ALA:HB1	1.98	0.45
1:C:252:THR:HG23	1:C:398:PHE:CD2	2.51	0.45
1:A:360:HIS:HE1	1:A:368:THR:OG1	2.00	0.45
2:B:279:THR:OG1	1:C:415:ARG:HD2	2.15	0.45
2:D:404:HIS:HB3	2:D:405:PRO:HD3	1.97	0.45
1:A:128:LEU:HD12	1:A:128:LEU:HA	1.87	0.45
1:C:350:GLY:O	1:C:351:GLN:HB3	2.17	0.45
2:D:266:GLN:HE21	2:D:266:GLN:C	2.25	0.45
1:A:18:GLU:OE1	1:A:351:GLN:HA	2.17	0.45
2:B:165:GLY:HA3	2:B:168:HIS:CD2	2.52	0.45
1:C:322:THR:CG2	1:C:363:ILE:HG21	2.47	0.45
2:D:8:TYR:CE2	2:D:356:THR:HG21	2.52	0.45
1:C:59:ALA:O	1:C:60:GLY:C	2.59	0.44
1:A:252:THR:HG22	1:A:256:LEU:HD22	1.99	0.44
1:A:341:LEU:HD23	1:A:342:PRO:CD	2.43	0.44
1:C:297:LEU:HB2	1:C:319:MET:HE2	1.98	0.44
2:B:273:VAL:N	1:C:376:ASN:HD21	2.02	0.44
1:A:29:THR:HG21	1:A:150:PHE:CE1	2.52	0.44
2:D:357:GLN:HG2	2:D:360:ARG:NH2	2.32	0.44
1:A:329:LEU:HD12	1:A:329:LEU:C	2.43	0.44
1:C:274:THR:HG23	1:C:278:ARG:HE	1.83	0.44
1:A:298:PHE:CE1	1:A:323:GLU:HB3	2.53	0.43
1:A:219:PHE:O	1:A:240:ARG:HA	2.18	0.43
1:C:22:LYS:N	2:D:59:THR:HG21	2.30	0.43
1:C:104:ARG:NH1	1:C:135:HIS:CD2	2.85	0.43
2:D:175:VAL:HG22	2:D:178:LEU:HD11	1.99	0.43
1:A:173:LEU:HA	1:A:218:ARG:O	2.18	0.43
1:C:82:LEU:O	1:C:83:ALA:C	2.60	0.43
1:A:139:TYR:CD2	1:A:139:TYR:N	2.86	0.43
2:D:159:LEU:HD22	2:D:208:ASN:HB3	1.99	0.43
1:C:45:VAL:HB	1:C:71:THR:HB	1.99	0.43
1:C:82:LEU:O	1:C:82:LEU:HD12	2.19	0.43
2:D:95:CYS:HB3	2:D:124:SER:OG	2.19	0.43
2:B:37:THR:HG22	2:B:57:PHE:CD1	2.53	0.43
1:C:113:PRO:HG3	2:D:96:THR:HG22	2.01	0.43
1:A:82:LEU:HB2	1:A:83:ALA:H	1.31	0.43
1:A:19:ARG:NH2	2:B:64:HIS:HE1	2.17	0.43
1:C:112:CYS:HB2	2:D:96:THR:HG21	2.01	0.43
1:C:155:ASP:HB2	1:C:225:PHE:O	2.19	0.43
1:A:36:ARG:HG2	1:A:36:ARG:HH11	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:253:THR:OG1	1:A:278:ARG:HD3	2.18	0.42
1:C:84:ASP:O	1:C:85:ALA:C	2.60	0.42
2:D:39:ALA:O	2:D:40:ASP:C	2.62	0.42
2:B:269:TRP:O	2:B:272:SER:HB3	2.18	0.42
1:C:30:SER:HA	1:C:33:TRP:CH2	2.54	0.42
1:C:99:ARG:O	1:C:99:ARG:HG3	2.20	0.42
2:D:38:TYR:CD2	2:D:38:TYR:C	2.97	0.42
2:B:148:MET:HE1	2:B:204:GLN:NE2	2.33	0.42
2:D:345:ILE:CD1	2:D:353:ILE:HD12	2.49	0.42
1:C:125:ALA:HA	1:C:138:VAL:HG22	2.01	0.42
2:D:113:LEU:N	2:D:113:LEU:HD12	2.34	0.42
1:A:34:LEU:HG	1:A:38:MET:HE1	2.01	0.42
2:B:50:ASN:HD22	2:B:50:ASN:H	1.67	0.42
2:B:156:CYS:SG	2:B:179:LEU:HD13	2.60	0.42
2:B:157:ASN:HD21	2:B:188:VAL:HG13	1.84	0.42
2:B:181:THR:O	2:B:181:THR:CG2	2.68	0.42
1:C:158:LEU:HD23	1:C:158:LEU:HA	1.70	0.42
2:B:171:ASP:CG	2:B:390:MET:HG3	2.44	0.42
1:A:22:LYS:HD2	2:B:34:GLN:HE21	1.85	0.42
2:B:386:TYR:O	2:D:385:ARG:NH1	2.53	0.42
2:D:29:VAL:O	2:D:91:VAL:HA	2.19	0.42
2:D:42:LEU:HB3	2:D:164:LEU:HD11	2.01	0.42
2:B:17:MET:HE1	2:B:39:ALA:CB	2.50	0.42
2:B:182:MET:O	2:B:182:MET:HG2	2.19	0.42
1:C:77:GLN:HE21	1:C:77:GLN:HB2	1.76	0.42
2:D:171:ASP:CG	2:D:390:MET:HG3	2.44	0.42
1:A:144:SER:O	1:A:148:THR:HB	2.20	0.41
2:B:13:HIS:HD2	2:B:17:MET:CE	2.33	0.41
2:B:81:HIS:O	2:B:82:ALA:C	2.63	0.41
2:B:138:ARG:HG3	2:B:218:SER:HB3	2.02	0.41
2:D:219:ALA:O	2:D:223:LEU:HG	2.19	0.41
1:C:303:SER:O	1:C:304:GLN:HB2	2.20	0.41
2:D:17:MET:HE1	2:D:39:ALA:HB3	2.02	0.41
2:B:335:THR:HG21	2:B:340:GLU:HB3	2.02	0.41
1:A:43:PHE:CD1	1:A:43:PHE:N	2.88	0.41
2:B:31:HIS:HA	2:B:58:SER:OG	2.21	0.41
2:B:243:ARG:HH21	2:B:261:GLU:CD	2.26	0.41
1:A:155:ASP:CG	1:A:228:GLU:HB2	2.46	0.41
1:A:168:THR:O	1:A:214:GLY:HA3	2.20	0.41
2:B:31:HIS:CD2	2:B:73:LEU:HB2	2.56	0.41
2:B:158:LEU:HB3	2:B:211:MET:HE2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:50:ASN:H	2:B:50:ASN:ND2	2.18	0.41
2:B:151:THR:O	2:B:206:HIS:HE1	2.03	0.41
2:B:408:MET:O	2:B:412:GLU:HG2	2.21	0.41
1:A:104:ARG:HH11	1:A:104:ARG:HG2	1.85	0.41
2:B:264:LEU:CD2	2:B:267:PRO:HD3	2.45	0.41
1:C:62:MET:HE3	1:C:62:MET:HB2	1.89	0.41
1:C:274:THR:O	1:C:278:ARG:HG3	2.20	0.41
2:D:358:MET:HE3	2:D:362:ILE:HG13	2.03	0.41
1:A:248:GLY:HA3	1:A:312:PHE:CD1	2.55	0.41
1:A:307:ILE:HG23	1:A:341:LEU:HD12	2.03	0.41
2:B:288:ASP:O	2:B:289:GLY:C	2.63	0.41
2:D:264:LEU:HD13	2:D:267:PRO:HG2	2.02	0.41
1:A:401:GLN:CD	1:A:401:GLN:N	2.79	0.40
2:B:111:LEU:HD22	2:B:113:LEU:CD1	2.51	0.40
1:C:36:ARG:HH11	1:C:36:ARG:HG2	1.85	0.40
2:D:330:LEU:HD12	2:D:330:LEU:HA	1.98	0.40
1:A:84:ASP:CB	1:A:87:LYS:H	2.30	0.40
1:C:396:VAL:HB	1:C:405:LEU:HD13	2.04	0.40
2:D:52:ARG:H	2:D:52:ARG:HG2	1.74	0.40
2:D:288:ASP:O	2:D:289:GLY:C	2.63	0.40
1:A:276:ALA:CB	1:A:277:PRO:HD3	2.41	0.40
1:C:354:GLU:CD	2:D:52:ARG:HH22	2.30	0.40
1:C:387:TRP:CD1	1:C:387:TRP:H	2.39	0.40
1:A:112:CYS:HB2	1:A:113:PRO:CD	2.47	0.40
2:D:177:LYS:HE2	2:D:177:LYS:HB3	1.79	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	412/436 (94%)	381 (92%)	27 (7%)	4 (1%)	12 39

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	412/436 (94%)	394 (96%)	17 (4%)	1 (0%)	43	72
2	B	413/525 (79%)	384 (93%)	28 (7%)	1 (0%)	43	72
2	D	417/525 (79%)	393 (94%)	21 (5%)	3 (1%)	18	48
All	All	1654/1922 (86%)	1552 (94%)	93 (6%)	9 (0%)	24	54

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	82	LEU
1	A	83	ALA
2	B	289	GLY
1	C	83	ALA
2	D	289	GLY
1	A	80	ALA
1	A	268	GLU
2	D	216	GLY
2	D	379	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	329/344 (96%)	279 (85%)	50 (15%)	3	9
1	C	329/344 (96%)	289 (88%)	40 (12%)	5	16
2	B	334/416 (80%)	292 (87%)	42 (13%)	4	14
2	D	336/416 (81%)	294 (88%)	42 (12%)	4	15
All	All	1328/1520 (87%)	1154 (87%)	174 (13%)	4	13

All (174) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	SER
1	A	15	VAL

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Mol	Chain	Res	Type
1	A	19	ARG
1	A	21	GLN
1	A	37	LYS
1	A	54	LEU
1	A	55	LEU
1	A	61	VAL
1	A	66	GLU
1	A	74	LEU
1	A	79	LEU
1	A	82	LEU
1	A	97	LEU
1	A	100	ARG
1	A	104	ARG
1	A	118	LYS
1	A	121	LEU
1	A	123	ARG
1	A	128	LEU
1	A	137	ARG
1	A	138	VAL
1	A	147	ASP
1	A	148	THR
1	A	164	THR
1	A	173	LEU
1	A	182	VAL
1	A	188	LEU
1	A	196	VAL
1	A	199	VAL
1	A	200	ARG
1	A	213	VAL
1	A	240	ARG
1	A	254	LEU
1	A	256	LEU
1	A	269	LYS
1	A	282	LYS
1	A	292	LEU
1	A	306	GLU
1	A	322	THR
1	A	329	LEU
1	A	341	LEU
1	A	372	LEU
1	A	374	LEU
1	A	378	LEU

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Mol	Chain	Res	Type
1	A	381	LYS
1	A	389	ILE
1	A	392	VAL
1	A	396	VAL
1	A	408	LEU
1	A	414	ARG
2	B	3	LEU
2	B	42	LEU
2	B	45	MET
2	B	48	ARG
2	B	71	ILE
2	B	94	THR
2	B	98	GLU
2	B	100	LEU
2	B	113	LEU
2	B	121	GLU
2	B	124	SER
2	B	126	SER
2	B	140	LEU
2	B	154	VAL
2	B	159	LEU
2	B	185	LYS
2	B	188	VAL
2	B	210	LEU
2	B	214	GLU
2	B	228	LYS
2	B	257	VAL
2	B	263	THR
2	B	264	LEU
2	B	266	GLN
2	B	272	SER
2	B	273	VAL
2	B	274	ASP
2	B	288	ASP
2	B	308	VAL
2	B	315	ARG
2	B	319	ARG
2	B	330	LEU
2	B	331	GLU
2	B	333	LEU
2	B	377	VAL
2	B	378	HIS

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Mol	Chain	Res	Type
2	B	379	VAL
2	B	385	ARG
2	B	401	THR
2	B	403	VAL
2	B	407	VAL
2	B	415	LEU
1	C	11	THR
1	C	19	ARG
1	C	28	LEU
1	C	54	LEU
1	C	61	VAL
1	C	71	THR
1	C	73	VAL
1	C	74	LEU
1	C	77	GLN
1	C	79	LEU
1	C	84	ASP
1	C	95	LYS
1	C	117	LEU
1	C	121	LEU
1	C	128	LEU
1	C	131	LEU
1	C	137	ARG
1	C	138	VAL
1	C	167	THR
1	C	168	THR
1	C	173	LEU
1	C	188	LEU
1	C	199	VAL
1	C	209	ILE
1	C	239	LYS
1	C	254	LEU
1	C	274	THR
1	C	289	LEU
1	C	292	LEU
1	C	306	GLU
1	C	322	THR
1	C	334	MET
1	C	341	LEU
1	C	343	SER
1	C	372	LEU
1	C	378	LEU

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Mol	Chain	Res	Type
1	C	391	LEU
1	C	408	LEU
1	C	414	ARG
1	C	420	ASN
2	D	2	LYS
2	D	3	LEU
2	D	7	THR
2	D	18	ARG
2	D	25	ASP
2	D	37	THR
2	D	52	ARG
2	D	74	LYS
2	D	96	THR
2	D	98	GLU
2	D	100	LEU
2	D	111	LEU
2	D	118	VAL
2	D	140	LEU
2	D	154	VAL
2	D	159	LEU
2	D	175	VAL
2	D	184	ILE
2	D	188	VAL
2	D	210	LEU
2	D	214	GLU
2	D	229	GLN
2	D	263	THR
2	D	264	LEU
2	D	266	GLN
2	D	273	VAL
2	D	308	VAL
2	D	330	LEU
2	D	333	LEU
2	D	346	GLU
2	D	353	ILE
2	D	356	THR
2	D	357	GLN
2	D	360	ARG
2	D	374	SER
2	D	378	HIS
2	D	385	ARG
2	D	401	THR

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Mol	Chain	Res	Type
2	D	407	VAL
2	D	411	GLU
2	D	417	MET
2	D	419	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (46) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	21	GLN
1	A	105	GLN
1	A	132	HIS
1	A	152	GLN
1	A	216	ASN
1	A	351	GLN
1	A	360	HIS
1	A	376	ASN
2	B	13	HIS
2	B	31	HIS
2	B	34	GLN
2	B	50	ASN
2	B	64	HIS
2	B	105	ASN
2	B	130	ASN
2	B	157	ASN
2	B	168	HIS
2	B	187	ASN
2	B	204	GLN
2	B	206	HIS
2	B	229	GLN
2	B	266	GLN
1	C	39	GLN
1	C	77	GLN
1	C	86	HIS
1	C	135	HIS
1	C	152	GLN
1	C	193	GLN
1	C	288	HIS
1	C	304	GLN
1	C	351	GLN
1	C	360	HIS
1	C	376	ASN
1	C	420	ASN

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Mol	Chain	Res	Type
2	D	13	HIS
2	D	31	HIS
2	D	34	GLN
2	D	64	HIS
2	D	87	GLN
2	D	157	ASN
2	D	168	HIS
2	D	204	GLN
2	D	229	GLN
2	D	266	GLN
2	D	380	GLN
2	D	413	HIS

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](#)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	SF4	A	425	1	0,12,12	-	-	-		
3	SF4	C	425	1	0,12,12	-	-	-		

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	SF4	A	425	1	-	-	0/6/5/5
3	SF4	C	425	1	-	-	0/6/5/5

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	425	SF4	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	414/436 (94%)	-0.27	5 (1%) 76 69	3, 25, 39, 44	1 (0%)
1	C	414/436 (94%)	-0.22	6 (1%) 73 65	4, 25, 39, 44	1 (0%)
2	B	417/525 (79%)	-0.21	1 (0%) 91 89	12, 25, 40, 54	0
2	D	419/525 (79%)	-0.22	4 (0%) 79 73	12, 25, 40, 58	0
All	All	1664/1922 (86%)	-0.23	16 (0%) 79 73	3, 25, 40, 58	2 (0%)

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	33	TRP	6.7
1	A	82	LEU	6.2
1	C	80	ALA	5.8
2	B	66	GLY	5.8
1	A	33	TRP	5.7
1	C	83	ALA	5.6
1	C	82	LEU	5.3
1	A	83	ALA	4.0
2	D	67	THR	3.9
1	A	81	GLY	3.4
1	A	393	PHE	3.0
1	C	19	ARG	2.7
1	C	81	GLY	2.5
2	D	419	ARG	2.4
2	D	417	MET	2.3
2	D	66	GLY	2.3

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	SF4	A	425	8/8	0.99	0.03	14,19,22,27	0
3	SF4	C	425	8/8	0.99	0.03	17,19,21,29	0

6.5 Other polymers [i](#)

There are no such residues in this entry.