



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 07:57 PM GMT

PDB ID : 1HR8
Title : Yeast Mitochondrial Processing Peptidase beta-E73Q Mutant Complexed with Cytochrome C Oxidase IV Signal Peptide
Authors : Taylor, A.B.; Smith, B.S.; Kitada, S.; Kojima, K.; Miyaura, H.; Otwinowski, Z.; Ito, A.; Deisenhofer, J.
Deposited on : 2000-12-21
Resolution : 2.70 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

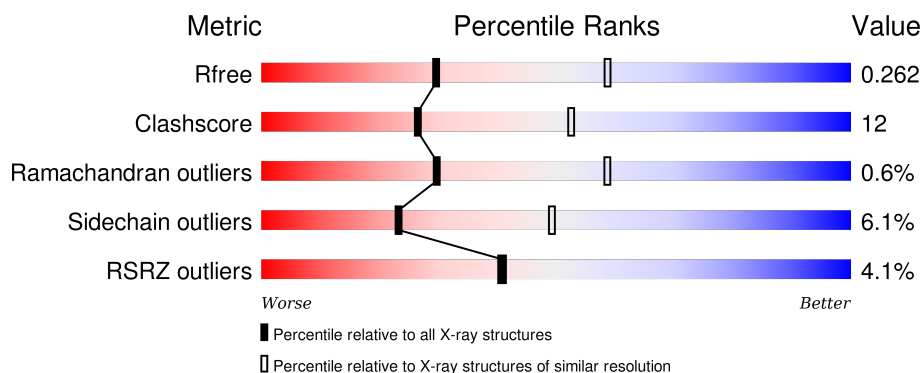
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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}	91344	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	475	<div> <div>3%</div> <div>73%</div> <div>19%</div> <div>• 5%</div> </div>
1	C	475	<div> <div>2%</div> <div>72%</div> <div>20%</div> <div>• 6%</div> </div>
1	E	475	<div> <div>3%</div> <div>70%</div> <div>21%</div> <div>• 6%</div> </div>
1	G	475	<div> <div>2%</div> <div>69%</div> <div>22%</div> <div>• 6%</div> </div>
2	B	443	<div> <div>71%</div> <div>24%</div> <div>• •</div> </div>

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Mol	Chain	Length	Quality of chain
2	D	443	
2	F	443	
2	H	443	
3	O	24	
3	P	24	
3	Q	24	
3	R	24	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	EPE	A	489	-	-	-	X
5	EPE	G	489	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 27990 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 MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	452	Total	C	N	O	S	0	0	0
			3499	2213	594	673	19			
1	C	448	Total	C	N	O	S	0	0	0
			3471	2198	587	667	19			
1	E	445	Total	C	N	O	S	0	0	0
			3459	2190	586	664	19			
1	G	448	Total	C	N	O	S	0	0	0
			3475	2198	589	669	19			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	177	GLY	GLU	SEE REMARK 999	UNP P11914
A	217	GLY	GLU	SEE REMARK 999	UNP P11914
A	483	HIS	-	EXPRESSION TAG	UNP P11914
A	484	HIS	-	EXPRESSION TAG	UNP P11914
A	485	HIS	-	EXPRESSION TAG	UNP P11914
A	486	HIS	-	EXPRESSION TAG	UNP P11914
A	487	HIS	-	EXPRESSION TAG	UNP P11914
A	488	HIS	-	EXPRESSION TAG	UNP P11914
C	177	GLY	GLU	SEE REMARK 999	UNP P11914
C	217	GLY	GLU	SEE REMARK 999	UNP P11914
C	483	HIS	-	EXPRESSION TAG	UNP P11914
C	484	HIS	-	EXPRESSION TAG	UNP P11914
C	485	HIS	-	EXPRESSION TAG	UNP P11914
C	486	HIS	-	EXPRESSION TAG	UNP P11914
C	487	HIS	-	EXPRESSION TAG	UNP P11914
C	488	HIS	-	EXPRESSION TAG	UNP P11914
E	177	GLY	GLU	SEE REMARK 999	UNP P11914
E	217	GLY	GLU	SEE REMARK 999	UNP P11914
E	483	HIS	-	EXPRESSION TAG	UNP P11914
E	484	HIS	-	EXPRESSION TAG	UNP P11914

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Chain	Residue	Modelled	Actual	Comment	Reference
E	485	HIS	-	EXPRESSION TAG	UNP P11914
E	486	HIS	-	EXPRESSION TAG	UNP P11914
E	487	HIS	-	EXPRESSION TAG	UNP P11914
E	488	HIS	-	EXPRESSION TAG	UNP P11914
G	177	GLY	GLU	SEE REMARK 999	UNP P11914
G	217	GLY	GLU	SEE REMARK 999	UNP P11914
G	483	HIS	-	EXPRESSION TAG	UNP P11914
G	484	HIS	-	EXPRESSION TAG	UNP P11914
G	485	HIS	-	EXPRESSION TAG	UNP P11914
G	486	HIS	-	EXPRESSION TAG	UNP P11914
G	487	HIS	-	EXPRESSION TAG	UNP P11914
G	488	HIS	-	EXPRESSION TAG	UNP P11914

- Molecule 2 is a protein called MITOCHONDRIAL PROCESSING PEPTIDASE BETA SUB-UNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	439	Total	C	N	O	S	0	0	0
			3414	2148	591	668	7			
2	D	443	Total	C	N	O	S	0	0	0
			3442	2165	596	674	7			
2	F	443	Total	C	N	O	S	0	0	0
			3442	2165	596	674	7			
2	H	441	Total	C	N	O	S	0	0	0
			3431	2159	594	671	7			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	20	ALA	-	CLONING ARTIFACT	UNP P10507
B	73	GLN	GLU	ENGINEERED	UNP P10507
B	84	PRO	SER	SEE REMARK 999	UNP P10507
B	350	ARG	GLN	SEE REMARK 999	UNP P10507
D	20	ALA	-	CLONING ARTIFACT	UNP P10507
D	73	GLN	GLU	ENGINEERED	UNP P10507
D	84	PRO	SER	SEE REMARK 999	UNP P10507
D	350	ARG	GLN	SEE REMARK 999	UNP P10507
F	20	ALA	-	CLONING ARTIFACT	UNP P10507
F	73	GLN	GLU	ENGINEERED	UNP P10507
F	84	PRO	SER	SEE REMARK 999	UNP P10507
F	350	ARG	GLN	SEE REMARK 999	UNP P10507
H	20	ALA	-	CLONING ARTIFACT	UNP P10507

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Chain	Residue	Modelled	Actual	Comment	Reference
H	73	GLN	GLU	ENGINEERED	UNP P10507
H	84	PRO	SER	SEE REMARK 999	UNP P10507
H	350	ARG	GLN	SEE REMARK 999	UNP P10507

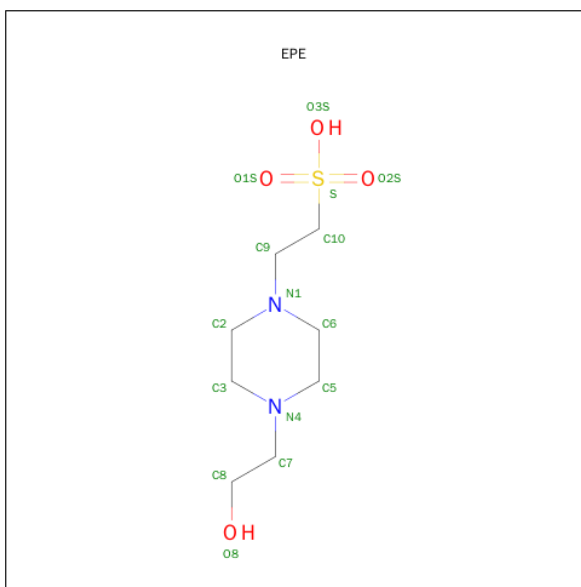
- Molecule 3 is a protein called CYTOCHROME C OXIDASE POLYPEPTIDE IV.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	O	13	Total	C	N	O	S	0	0	0
			107	70	20	16	1			
3	P	9	Total	C	N	O		0	0	0
			76	52	13	11				
3	Q	10	Total	C	N	O	S	0	0	0
			82	55	14	12	1			
3	R	7	Total	C	N	O		0	0	0
			54	34	11	9				

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	H	1	Total	Zn	0	0
			1	1		
4	B	1	Total	Zn	0	0
			1	1		
4	D	1	Total	Zn	0	0
			1	1		
4	F	1	Total	Zn	0	0
			1	1		

- Molecule 5 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: C₈H₁₈N₂O₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
5	G	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

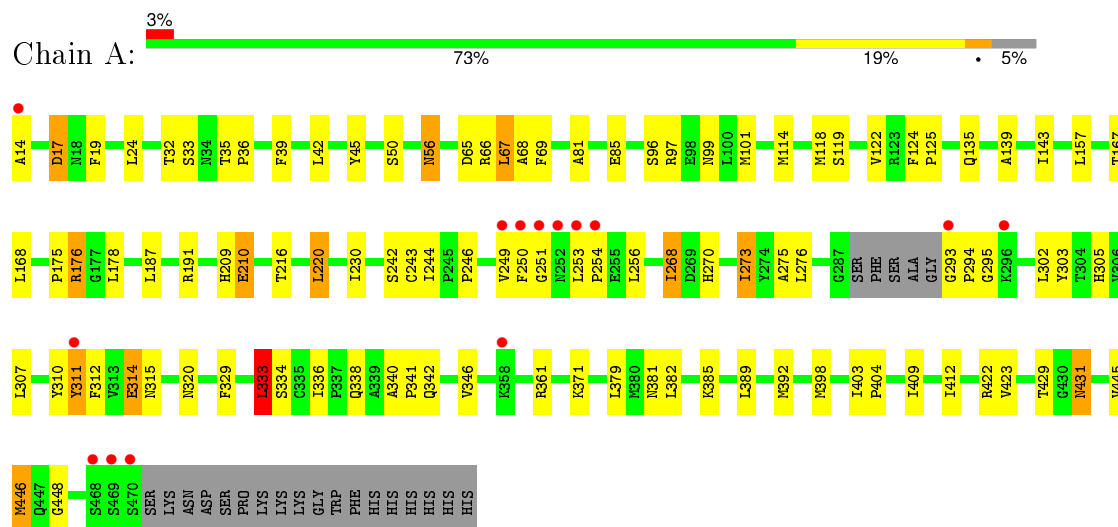
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	F	1	Total	O	0	0
			1	1		
6	H	1	Total	O	0	0
			1	1		
6	O	1	Total	O	0	0
			1	1		
6	P	1	Total	O	0	0
			1	1		

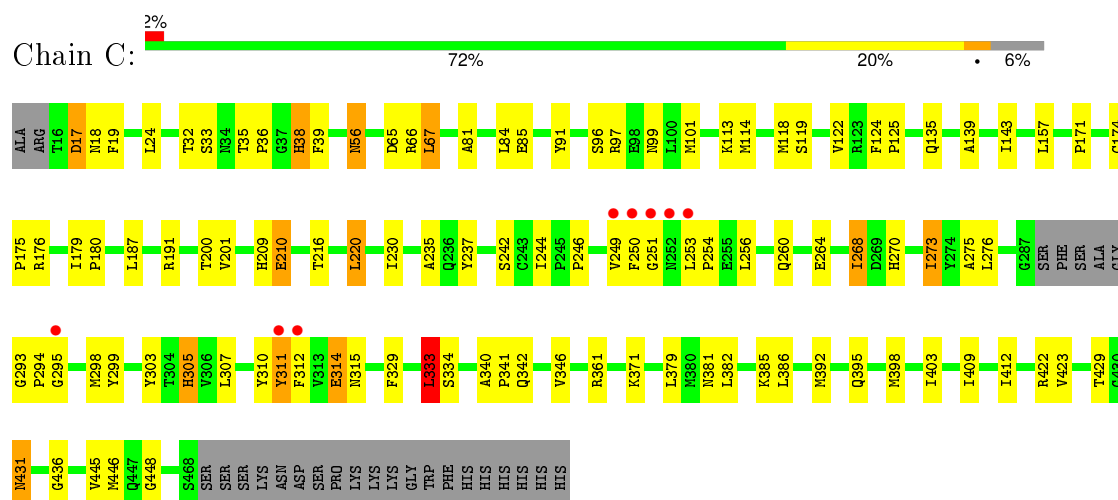
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT

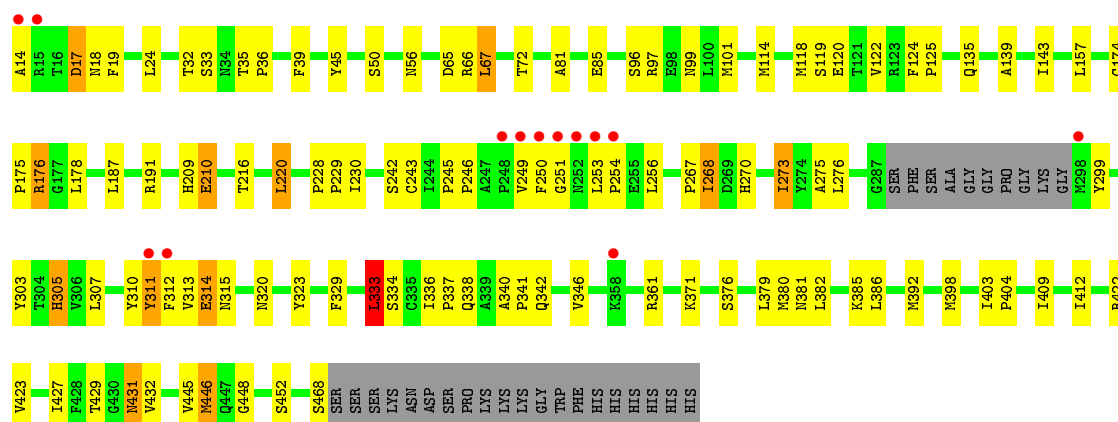


• Molecule 1: MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT

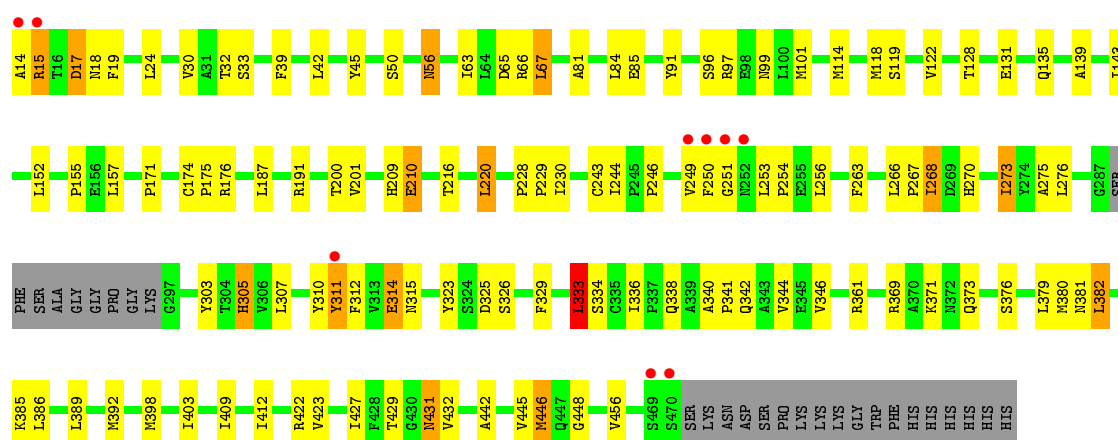


• Molecule 1: MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT

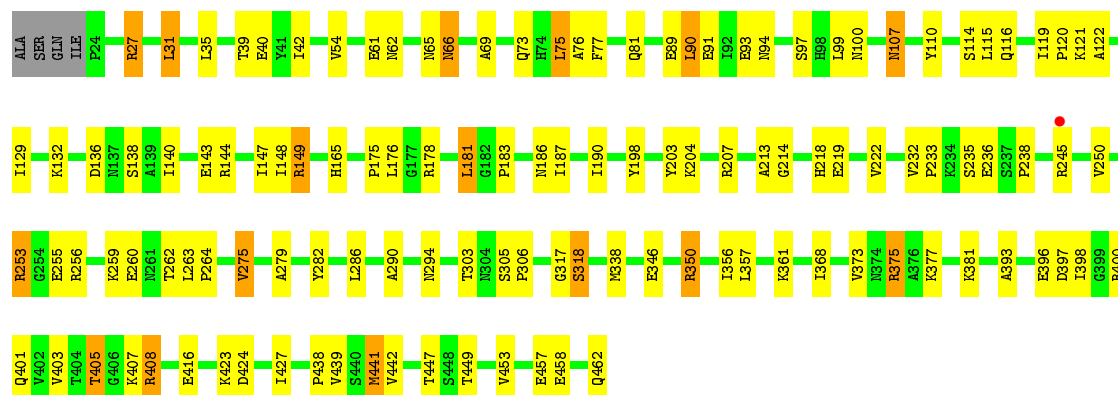




• Molecule 1: MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT

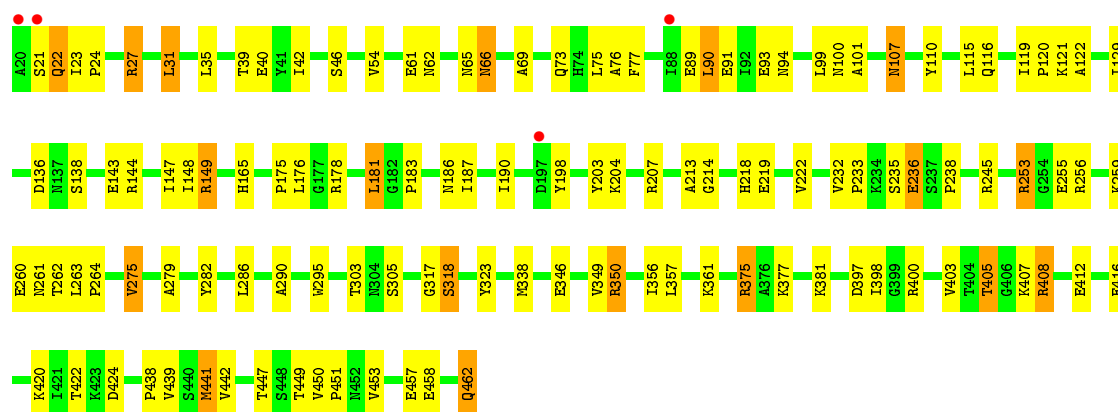


• Molecule 2: MITOCHONDRIAL PROCESSING PEPTIDASE BETA SUBUNIT

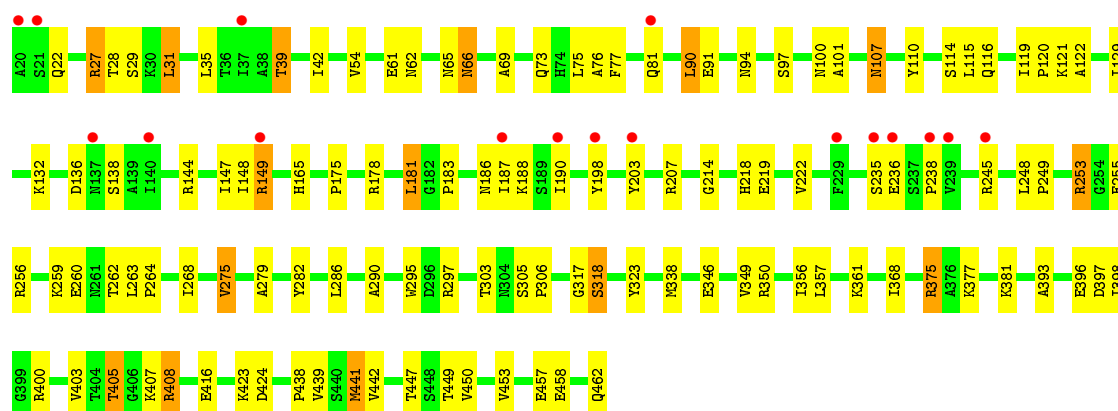
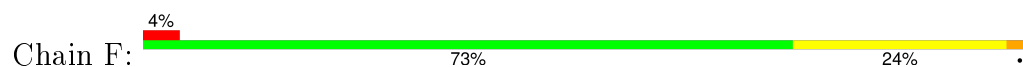


• Molecule 2: MITOCHONDRIAL PROCESSING PEPTIDASE BETA SUBUNIT

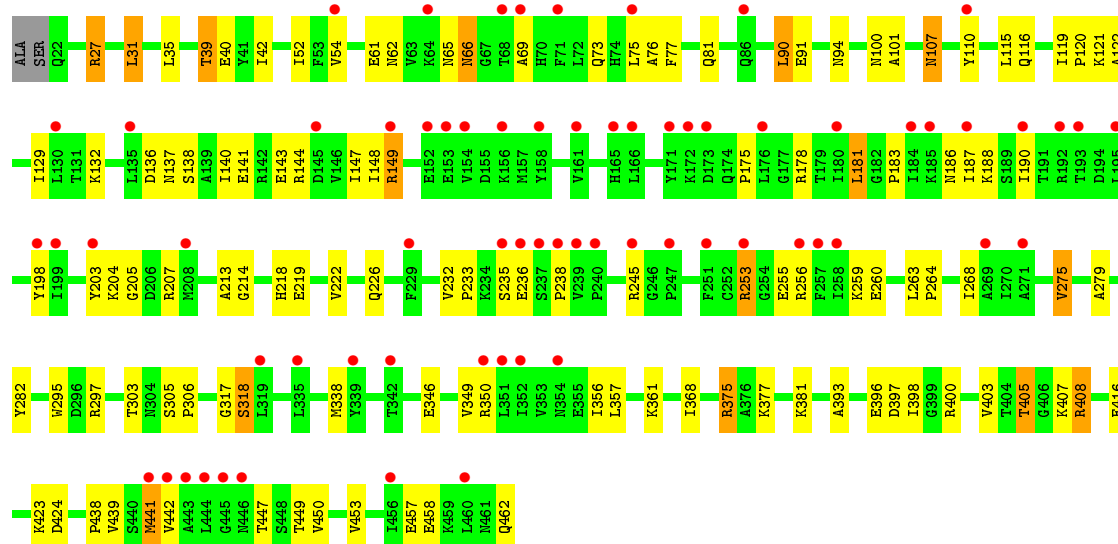




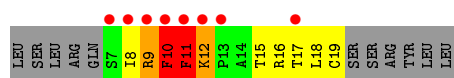
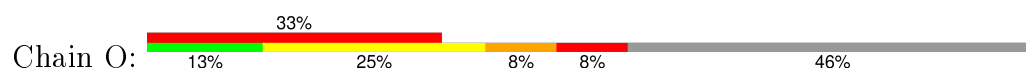
• Molecule 2: MITOCHONDRIAL PROCESSING PEPTIDASE BETA SUBUNIT



• Molecule 2: MITOCHONDRIAL PROCESSING PEPTIDASE BETA SUBUNIT



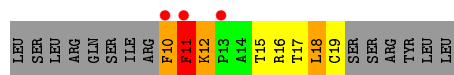
• Molecule 3: CYTOCHROME C OXIDASE POLYPEPTIDE IV



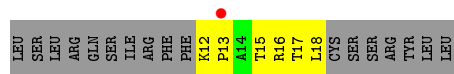
• Molecule 3: CYTOCHROME C OXIDASE POLYPEPTIDE IV



• Molecule 3: CYTOCHROME C OXIDASE POLYPEPTIDE IV



• Molecule 3: CYTOCHROME C OXIDASE POLYPEPTIDE IV



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	134.26Å 178.12Å 202.21Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.63 – 2.70 48.63 – 2.69	Depositor EDS
% Data completeness (in resolution range)	99.9 (48.63-2.70) 99.5 (48.63-2.69)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.61 (at 2.69Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.229 , 0.264 0.228 , 0.262	Depositor DCC
R_{free} test set	2016 reflections (1.51%)	DCC
Wilson B-factor (Å ²)	52.9	Xtriage
Anisotropy	0.269	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 52.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 134150 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	27990	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.35% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: ZN, EPE

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	0.67	2/3570 (0.1%)	0.77	3/4830 (0.1%)
1	C	0.65	2/3542 (0.1%)	0.76	4/4793 (0.1%)
1	E	0.60	2/3529 (0.1%)	0.85	4/4776 (0.1%)
1	G	0.62	3/3545 (0.1%)	0.74	3/4797 (0.1%)
2	B	0.62	0/3478	0.82	7/4720 (0.1%)
2	D	0.66	4/3506 (0.1%)	0.91	8/4759 (0.2%)
2	F	0.51	0/3506	0.87	10/4759 (0.2%)
2	H	0.47	0/3495	0.97	10/4744 (0.2%)
3	O	0.99	0/109	1.37	3/145 (2.1%)
3	P	1.11	0/78	0.96	0/104
3	Q	1.02	0/84	1.08	1/112 (0.9%)
3	R	0.86	0/54	0.86	0/72
All	All	0.61	13/28496 (0.0%)	0.84	53/38611 (0.1%)

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	462	GLN	CD-NE2	-10.01	1.07	1.32
2	D	261	ASN	CG-OD1	-9.49	1.03	1.24
2	D	462	GLN	CD-OE1	-9.15	1.03	1.24
2	D	261	ASN	CG-ND2	-9.05	1.10	1.32
1	A	431	ASN	CG-ND2	-6.59	1.16	1.32
1	G	431	ASN	CG-OD1	-6.47	1.09	1.24
1	E	431	ASN	CG-OD1	-6.45	1.09	1.24
1	C	431	ASN	CG-ND2	-6.36	1.17	1.32
1	A	431	ASN	CG-OD1	-6.29	1.10	1.24
1	E	431	ASN	CG-ND2	-6.22	1.17	1.32
1	G	431	ASN	CG-ND2	-6.11	1.17	1.32
1	C	431	ASN	CG-OD1	-6.02	1.10	1.24
1	G	311	TYR	CE2-CZ	5.72	1.46	1.38

All (53) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	149	ARG	NE-CZ-NH2	-21.41	109.60	120.30
2	D	253	ARG	NE-CZ-NH1	-21.33	109.63	120.30
2	D	253	ARG	NE-CZ-NH2	20.88	130.74	120.30
2	H	149	ARG	NE-CZ-NH1	20.82	130.71	120.30
1	E	422	ARG	NE-CZ-NH1	-20.01	110.30	120.30
2	H	207	ARG	NE-CZ-NH1	-19.93	110.34	120.30
2	H	207	ARG	NE-CZ-NH2	19.44	130.02	120.30
2	F	350	ARG	NE-CZ-NH2	19.14	129.87	120.30
1	E	422	ARG	NE-CZ-NH2	18.46	129.53	120.30
2	F	350	ARG	NE-CZ-NH1	-18.03	111.29	120.30
2	H	149	ARG	CD-NE-CZ	10.78	138.69	123.60
2	F	350	ARG	CD-NE-CZ	10.38	138.13	123.60
2	D	253	ARG	CD-NE-CZ	10.29	138.00	123.60
1	E	422	ARG	CD-NE-CZ	9.97	137.56	123.60
2	H	207	ARG	CD-NE-CZ	8.60	135.64	123.60
2	B	350	ARG	NE-CZ-NH1	8.49	124.54	120.30
2	B	350	ARG	NE-CZ-NH2	-8.33	116.14	120.30
1	G	422	ARG	NE-CZ-NH2	-7.89	116.35	120.30
2	D	149	ARG	NE-CZ-NH2	7.62	124.11	120.30
1	A	422	ARG	NE-CZ-NH2	-7.51	116.55	120.30
2	F	149	ARG	NE-CZ-NH2	7.51	124.05	120.30
1	C	422	ARG	NE-CZ-NH2	-7.34	116.63	120.30
2	F	149	ARG	NE-CZ-NH1	-7.29	116.66	120.30
1	A	422	ARG	NE-CZ-NH1	7.26	123.93	120.30
2	B	149	ARG	NE-CZ-NH2	7.21	123.91	120.30
3	O	9	ARG	N-CA-C	7.01	129.92	111.00
1	C	422	ARG	NE-CZ-NH1	7.00	123.80	120.30
2	D	149	ARG	NE-CZ-NH1	-6.94	116.83	120.30
2	D	350	ARG	NE-CZ-NH2	-6.79	116.90	120.30
2	B	149	ARG	NE-CZ-NH1	-6.77	116.92	120.30
2	B	207	ARG	NE-CZ-NH1	6.74	123.67	120.30
2	H	350	ARG	NE-CZ-NH2	-6.56	117.02	120.30
1	G	422	ARG	NE-CZ-NH1	6.42	123.51	120.30
2	D	207	ARG	NE-CZ-NH2	-6.29	117.15	120.30
2	B	253	ARG	NE-CZ-NH1	6.08	123.34	120.30
2	H	207	ARG	CB-CG-CD	-6.04	95.90	111.60
2	D	207	ARG	NE-CZ-NH1	6.01	123.30	120.30
2	F	207	ARG	NE-CZ-NH2	-5.89	117.36	120.30
2	F	253	ARG	NE-CZ-NH1	5.86	123.23	120.30
2	H	253	ARG	NE-CZ-NH1	5.77	123.18	120.30
2	B	207	ARG	NE-CZ-NH2	-5.75	117.42	120.30
2	H	253	ARG	NE-CZ-NH2	-5.73	117.44	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	207	ARG	NE-CZ-NH1	5.60	123.10	120.30
1	G	333	LEU	CA-CB-CG	5.59	128.17	115.30
2	F	253	ARG	NE-CZ-NH2	-5.54	117.53	120.30
3	O	10	PHE	N-CA-C	5.54	125.95	111.00
1	A	333	LEU	CA-CB-CG	5.31	127.50	115.30
3	O	12	LYS	N-CA-C	5.28	125.25	111.00
1	C	333	LEU	CA-CB-CG	5.27	127.42	115.30
1	E	333	LEU	CA-CB-CG	5.22	127.30	115.30
3	Q	12	LYS	N-CA-C	5.21	125.07	111.00
2	F	350	ARG	CG-CD-NE	5.18	122.69	111.80
1	C	38	HIS	CG-ND1-CE1	5.17	115.43	108.20

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	3499	0	3460	77	0
1	C	3471	0	3432	77	0
1	E	3459	0	3421	76	0
1	G	3475	0	3434	86	0
2	B	3414	0	3414	97	0
2	D	3442	0	3442	101	0
2	F	3442	0	3442	92	0
2	H	3431	0	3432	87	0
3	O	107	0	114	14	0
3	P	76	0	80	10	0
3	Q	82	0	85	13	0
3	R	54	0	62	7	0
4	B	1	0	0	0	0
4	D	1	0	0	0	0
4	F	1	0	0	0	0
4	H	1	0	0	0	0
5	A	15	0	17	0	0
5	G	15	0	17	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	F	1	0	0	0	0
6	H	1	0	0	0	0
6	O	1	0	0	0	0
6	P	1	0	0	0	0
All	All	27990	0	27852	683	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 (683) 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:G:33:SER:HB3	1:G:392:MET:HE3	1.18	1.12
1:G:14:ALA:N	1:G:19:PHE:HB3	1.64	1.11
1:C:33:SER:HB3	1:C:392:MET:HE1	1.28	1.10
1:A:33:SER:HB3	1:A:392:MET:HE1	1.27	1.10
1:E:33:SER:HB3	1:E:392:MET:HE1	1.42	1.02
2:D:256:ARG:HH11	2:D:256:ARG:HG3	1.33	0.93
2:F:256:ARG:HG3	2:F:256:ARG:HH11	1.34	0.91
2:B:256:ARG:HG3	2:B:256:ARG:HH11	1.34	0.91
1:C:295:GLY:HA2	2:D:93:GLU:HG2	1.52	0.90
2:H:256:ARG:HH11	2:H:256:ARG:HG3	1.37	0.84
1:G:33:SER:CB	1:G:392:MET:HE3	2.04	0.82
1:E:268:ILE:HD11	1:E:398:MET:SD	2.19	0.82
1:A:268:ILE:HD11	1:A:398:MET:SD	2.19	0.82
1:A:295:GLY:HA2	2:B:93:GLU:HG2	1.61	0.81
1:C:230:ILE:H	1:C:230:ILE:HD12	1.46	0.80
1:C:268:ILE:HD11	1:C:398:MET:SD	2.21	0.80
1:G:230:ILE:HD12	1:G:230:ILE:H	1.48	0.79
1:E:33:SER:HB3	1:E:392:MET:CE	2.13	0.79
2:H:186:ASN:O	2:H:190:ILE:HG12	1.83	0.78
1:A:33:SER:CB	1:A:392:MET:HE1	2.10	0.78
1:G:268:ILE:HD11	1:G:398:MET:SD	2.24	0.78
1:G:157:LEU:HB3	1:G:445:VAL:HG21	1.65	0.78
2:B:115:LEU:HD12	2:B:115:LEU:H	1.49	0.77
1:C:33:SER:CB	1:C:392:MET:HE1	2.12	0.76
2:B:144:ARG:O	2:B:148:ILE:HG12	1.86	0.76
2:H:144:ARG:O	2:H:148:ILE:HG12	1.85	0.76
2:B:62:ASN:H	2:B:65:ASN:HB3	1.51	0.76
2:F:186:ASN:O	2:F:190:ILE:HG12	1.85	0.76
2:F:375:ARG:HB3	2:F:375:ARG:NH1	2.01	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:230:ILE:HD12	1:A:230:ILE:H	1.49	0.75
2:H:115:LEU:H	2:H:115:LEU:HD12	1.51	0.75
2:D:338:MET:HG2	2:D:356:ILE:HD13	1.67	0.75
2:H:62:ASN:H	2:H:65:ASN:HB3	1.52	0.75
2:B:186:ASN:O	2:B:190:ILE:HG12	1.87	0.74
2:H:338:MET:HG2	2:H:356:ILE:HD13	1.68	0.74
2:F:144:ARG:O	2:F:148:ILE:HG12	1.87	0.74
2:D:186:ASN:O	2:D:190:ILE:HG12	1.88	0.74
2:B:405:THR:HG22	2:B:407:LYS:H	1.52	0.74
2:H:181:LEU:HD13	3:R:16:ARG:HG3	1.70	0.73
1:E:230:ILE:HD12	1:E:230:ILE:H	1.51	0.73
2:F:62:ASN:H	2:F:65:ASN:HB3	1.54	0.73
2:D:375:ARG:HB3	2:D:375:ARG:NH1	2.04	0.73
2:B:338:MET:HG2	2:B:356:ILE:HD13	1.69	0.72
2:F:405:THR:HG22	2:F:407:LYS:H	1.54	0.72
2:D:62:ASN:H	2:D:65:ASN:HB3	1.53	0.72
2:H:375:ARG:NH1	2:H:375:ARG:HB3	2.04	0.72
1:C:230:ILE:N	1:C:230:ILE:HD12	2.05	0.72
2:D:144:ARG:O	2:D:148:ILE:HG12	1.89	0.72
2:F:256:ARG:HG3	2:F:256:ARG:NH1	2.05	0.71
2:H:136:ASP:OD2	2:H:138:SER:HB3	1.90	0.71
2:F:338:MET:HG2	2:F:356:ILE:HD13	1.71	0.70
2:H:76:ALA:HB1	2:H:129:ILE:CG2	2.22	0.70
2:B:375:ARG:NH1	2:B:375:ARG:HB3	2.06	0.70
2:D:77:PHE:CD1	3:P:18:LEU:HD22	2.27	0.70
2:F:136:ASP:OD2	2:F:138:SER:HB3	1.91	0.70
2:H:303:THR:HG22	2:H:305:SER:H	1.57	0.70
2:B:303:THR:HG22	2:B:305:SER:H	1.57	0.69
2:H:405:THR:HG22	2:H:407:LYS:H	1.57	0.69
1:E:33:SER:CB	1:E:392:MET:HE1	2.20	0.69
2:D:136:ASP:OD2	2:D:138:SER:HB3	1.92	0.68
1:E:246:PRO:HG3	1:E:448:GLY:HA2	1.74	0.68
2:D:303:THR:HG22	2:D:305:SER:H	1.57	0.68
2:H:90:LEU:HD13	2:H:94:ASN:ND2	2.08	0.68
1:G:230:ILE:HD12	1:G:230:ILE:N	2.08	0.68
2:F:115:LEU:H	2:F:115:LEU:HD12	1.59	0.68
2:F:76:ALA:HB1	2:F:129:ILE:CG2	2.22	0.68
1:A:175:PRO:HB3	1:E:175:PRO:HB3	1.75	0.67
2:D:115:LEU:HD12	2:D:115:LEU:H	1.57	0.67
1:A:230:ILE:N	1:A:230:ILE:HD12	2.09	0.67
2:B:350:ARG:HH11	2:D:420:LYS:HB3	1.58	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:230:ILE:N	1:E:230:ILE:HD12	2.09	0.67
1:E:157:LEU:HB3	1:E:445:VAL:HG21	1.75	0.67
1:C:38:HIS:HD2	2:D:412:GLU:OE2	1.78	0.67
2:F:303:THR:HG22	2:F:305:SER:H	1.60	0.66
2:B:136:ASP:OD2	2:B:138:SER:HB3	1.95	0.66
2:D:175:PRO:HA	2:D:178:ARG:NH1	2.11	0.66
2:D:405:THR:HG22	2:D:407:LYS:H	1.59	0.66
2:H:275:VAL:HG22	2:H:279:ALA:CB	2.25	0.66
1:C:295:GLY:CA	2:D:93:GLU:HG2	2.26	0.66
2:B:76:ALA:HB1	2:B:129:ILE:CG2	2.26	0.66
2:D:76:ALA:HB1	2:D:129:ILE:CG2	2.27	0.65
2:B:77:PHE:CD1	3:O:18:LEU:HD22	2.30	0.65
2:B:256:ARG:HG3	2:B:256:ARG:NH1	2.07	0.65
2:H:275:VAL:HG11	2:H:282:TYR:HA	1.78	0.65
1:G:24:LEU:HD11	1:G:216:THR:HG22	1.78	0.65
2:H:256:ARG:NH1	2:H:256:ARG:HG3	2.10	0.65
2:D:165:HIS:HD2	2:D:256:ARG:HE	1.44	0.65
2:H:458:GLU:O	2:H:462:GLN:HB2	1.96	0.65
1:C:122:VAL:O	1:C:191:ARG:NH2	2.30	0.65
2:H:39:THR:HB	2:H:218:HIS:HD2	1.62	0.64
1:G:14:ALA:N	1:G:17:ASP:OD2	2.30	0.64
1:C:157:LEU:HB3	1:C:445:VAL:HG21	1.79	0.64
1:A:19:PHE:HD1	1:A:392:MET:CE	2.11	0.64
1:G:246:PRO:HG3	1:G:448:GLY:HA2	1.80	0.64
2:B:458:GLU:O	2:B:462:GLN:HB2	1.97	0.64
2:H:77:PHE:CE1	3:R:18:LEU:HD22	2.31	0.64
2:H:175:PRO:HA	2:H:178:ARG:NH1	2.13	0.63
2:D:181:LEU:HD13	3:P:16:ARG:HG3	1.79	0.63
2:H:181:LEU:CD1	3:R:16:ARG:HG3	2.28	0.63
1:E:243:CYS:HA	1:E:446:MET:O	1.97	0.63
1:E:210:GLU:OE1	1:E:210:GLU:HA	1.98	0.63
1:G:19:PHE:HD1	1:G:392:MET:CE	2.12	0.63
1:A:157:LEU:HB3	1:A:445:VAL:HG21	1.80	0.63
2:B:290:ALA:HB2	3:O:10:PHE:CZ	2.34	0.62
1:A:210:GLU:HA	1:A:210:GLU:OE1	1.99	0.62
2:D:458:GLU:O	2:D:462:GLN:HB2	1.99	0.62
2:F:458:GLU:O	2:F:462:GLN:HB2	1.99	0.62
1:C:210:GLU:HA	1:C:210:GLU:OE1	1.99	0.62
2:H:76:ALA:O	2:H:129:ILE:HG23	2.00	0.62
2:F:275:VAL:HG11	2:F:282:TYR:HA	1.82	0.62
2:B:245:ARG:HA	2:B:245:ARG:HE	1.65	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:90:LEU:HD13	2:B:94:ASN:ND2	2.15	0.62
2:H:27:ARG:HH11	2:H:27:ARG:HB3	1.64	0.62
1:A:242:SER:OG	1:E:176:ARG:NH2	2.33	0.62
2:F:90:LEU:HD13	2:F:94:ASN:ND2	2.14	0.62
1:G:210:GLU:OE1	1:G:210:GLU:HA	2.00	0.61
3:O:17:THR:HG22	3:O:19:CYS:N	2.15	0.61
2:F:375:ARG:HB3	2:F:375:ARG:CZ	2.31	0.61
2:D:90:LEU:HD13	2:D:94:ASN:ND2	2.16	0.61
2:B:54:VAL:O	2:B:107:ASN:HB3	2.00	0.61
1:C:24:LEU:HD11	1:C:216:THR:HG22	1.82	0.61
2:F:175:PRO:HA	2:F:178:ARG:NH1	2.16	0.61
1:C:246:PRO:HG3	1:C:448:GLY:HA2	1.81	0.61
1:C:19:PHE:HD1	1:C:392:MET:CE	2.13	0.60
2:D:275:VAL:HG11	2:D:282:TYR:HA	1.83	0.60
2:D:116:GLN:O	2:D:119:ILE:HG12	2.01	0.60
1:C:298:MET:HG2	2:D:93:GLU:OE2	2.01	0.60
2:F:76:ALA:O	2:F:129:ILE:HG23	2.02	0.60
2:F:101:ALA:O	3:Q:17:THR:HG23	2.02	0.60
1:A:19:PHE:CD1	1:A:392:MET:CE	2.86	0.59
2:B:175:PRO:HA	2:B:178:ARG:NH1	2.17	0.59
2:D:375:ARG:HB3	2:D:375:ARG:CZ	2.32	0.59
1:G:15:ARG:HG3	1:G:15:ARG:HH11	1.66	0.59
2:H:375:ARG:HB3	2:H:375:ARG:CZ	2.33	0.59
2:B:275:VAL:HG11	2:B:282:TYR:HA	1.83	0.59
2:H:90:LEU:CD1	2:H:94:ASN:HD21	2.15	0.59
3:P:10:PHE:O	3:P:12:LYS:HE2	2.03	0.59
2:F:27:ARG:HH11	2:F:27:ARG:HB3	1.66	0.59
2:D:256:ARG:HG3	2:D:256:ARG:NH1	2.06	0.58
2:F:275:VAL:HG22	2:F:279:ALA:CB	2.32	0.58
2:H:236:GLU:C	2:H:238:PRO:HD3	2.23	0.58
1:E:187:LEU:O	1:E:191:ARG:HG3	2.03	0.58
1:G:275:ALA:HB3	1:G:423:VAL:HG21	1.85	0.58
2:F:116:GLN:O	2:F:119:ILE:HG12	2.03	0.58
1:G:157:LEU:CB	1:G:445:VAL:HG21	2.33	0.58
2:D:290:ALA:HB2	3:P:10:PHE:CZ	2.39	0.58
2:B:181:LEU:HD13	3:O:16:ARG:HG3	1.86	0.58
2:H:116:GLN:O	2:H:119:ILE:HG12	2.02	0.58
2:H:54:VAL:O	2:H:107:ASN:HB3	2.04	0.58
1:A:294:PRO:HB3	2:B:89:GLU:HA	1.86	0.58
2:F:181:LEU:HD13	3:Q:16:ARG:HG3	1.85	0.58
3:Q:17:THR:C	3:Q:19:CYS:H	2.07	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:230:ILE:H	1:C:230:ILE:CD1	2.16	0.58
2:H:76:ALA:HB1	2:H:129:ILE:HG22	1.86	0.58
1:C:38:HIS:CD2	2:D:412:GLU:OE2	2.56	0.58
2:H:101:ALA:O	3:R:17:THR:HG23	2.02	0.57
1:G:187:LEU:O	1:G:191:ARG:HG3	2.04	0.57
1:G:122:VAL:O	1:G:191:ARG:NH2	2.36	0.57
1:C:429:THR:CG2	1:C:431:ASN:HD22	2.16	0.57
2:D:181:LEU:CD1	3:P:16:ARG:HG3	2.34	0.57
2:F:39:THR:HB	2:F:218:HIS:HD2	1.70	0.57
2:H:39:THR:HB	2:H:218:HIS:CD2	2.38	0.57
1:G:119:SER:HB3	1:G:220:LEU:HD11	1.86	0.57
2:D:165:HIS:HD2	2:D:256:ARG:NE	2.02	0.57
2:B:439:VAL:HG13	2:B:457:GLU:HG2	1.86	0.57
2:F:76:ALA:HB1	2:F:129:ILE:HG22	1.86	0.57
2:H:218:HIS:O	2:H:222:VAL:HG23	2.05	0.57
2:F:218:HIS:O	2:F:222:VAL:HG23	2.05	0.56
2:B:375:ARG:HB3	2:B:375:ARG:CZ	2.35	0.56
1:G:33:SER:HB3	1:G:392:MET:CE	2.12	0.56
1:G:19:PHE:CD1	1:G:392:MET:CE	2.88	0.56
2:B:115:LEU:N	2:B:115:LEU:HD12	2.20	0.56
1:G:15:ARG:HG3	1:G:15:ARG:NH1	2.20	0.56
2:B:275:VAL:HG22	2:B:279:ALA:CB	2.36	0.56
1:C:119:SER:HB3	1:C:220:LEU:HD11	1.88	0.56
2:D:286:LEU:HD21	3:P:11:PHE:CE1	2.40	0.56
2:D:275:VAL:HG22	2:D:279:ALA:CB	2.35	0.56
2:F:377:LYS:O	2:F:381:LYS:HG3	2.05	0.56
2:F:290:ALA:HB2	3:Q:10:PHE:CE1	2.39	0.56
1:A:114:MET:HE3	1:A:118:MET:HG3	1.86	0.56
2:D:27:ARG:HB3	2:D:27:ARG:HH11	1.71	0.56
1:C:19:PHE:CD1	1:C:392:MET:CE	2.89	0.56
2:B:62:ASN:OD1	2:B:65:ASN:HB2	2.04	0.56
2:F:290:ALA:HB2	3:Q:10:PHE:CZ	2.41	0.56
2:D:439:VAL:HG13	2:D:457:GLU:HG2	1.87	0.56
1:G:268:ILE:HD13	1:G:268:ILE:N	2.20	0.56
1:A:187:LEU:O	1:A:191:ARG:HG3	2.06	0.56
2:D:62:ASN:OD1	2:D:65:ASN:HB2	2.05	0.56
2:F:245:ARG:HE	2:F:245:ARG:HA	1.70	0.56
2:D:290:ALA:HB2	3:P:10:PHE:CE1	2.41	0.55
2:D:218:HIS:O	2:D:222:VAL:HG23	2.06	0.55
1:E:139:ALA:O	1:E:143:ILE:HD13	2.07	0.55
1:C:187:LEU:O	1:C:191:ARG:HG3	2.05	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:236:GLU:C	2:D:238:PRO:HD3	2.27	0.55
2:H:115:LEU:N	2:H:115:LEU:HD12	2.22	0.55
1:E:122:VAL:O	1:E:191:ARG:NH2	2.40	0.55
1:C:429:THR:HG22	1:C:431:ASN:HD22	1.70	0.55
2:D:441:MET:HG2	2:D:442:VAL:N	2.22	0.55
1:E:14:ALA:HB3	1:E:404:PRO:HB3	1.87	0.55
1:C:157:LEU:CB	1:C:445:VAL:HG21	2.36	0.55
2:D:204:LYS:HG3	2:D:235:SER:OG	2.07	0.55
2:B:116:GLN:O	2:B:119:ILE:HG12	2.07	0.55
2:F:236:GLU:C	2:F:238:PRO:HD3	2.26	0.55
2:B:76:ALA:O	2:B:129:ILE:HG23	2.08	0.54
2:B:90:LEU:CD1	2:B:94:ASN:HD21	2.20	0.54
1:C:299:TYR:CZ	2:D:90:LEU:HD23	2.43	0.54
2:H:439:VAL:HG13	2:H:457:GLU:HG2	1.89	0.54
2:B:27:ARG:HH11	2:B:27:ARG:HB3	1.71	0.54
2:B:181:LEU:CD1	3:O:16:ARG:HG3	2.37	0.54
1:C:379:LEU:HD13	2:D:46:SER:HB2	1.90	0.54
2:D:245:ARG:HA	2:D:245:ARG:HE	1.73	0.54
1:G:96:SER:HB3	1:G:99:ASN:OD1	2.07	0.54
2:H:62:ASN:OD1	2:H:65:ASN:HB2	2.08	0.54
2:D:76:ALA:O	2:D:129:ILE:HG23	2.07	0.54
2:B:218:HIS:O	2:B:222:VAL:HG23	2.08	0.54
2:F:90:LEU:CD1	2:F:94:ASN:HD21	2.21	0.54
2:F:181:LEU:CD1	3:Q:16:ARG:HG3	2.37	0.54
2:B:236:GLU:C	2:B:238:PRO:HD3	2.28	0.54
2:B:77:PHE:CE1	3:O:18:LEU:HD22	2.42	0.54
1:C:96:SER:HB3	1:C:99:ASN:OD1	2.08	0.54
1:E:157:LEU:CB	1:E:445:VAL:HG21	2.38	0.53
2:H:397:ASP:OD2	2:H:408:ARG:NH1	2.41	0.53
1:E:270:HIS:O	1:E:273:ILE:HB	2.08	0.53
2:B:441:MET:HG2	2:B:442:VAL:N	2.24	0.53
2:B:40:GLU:OE1	2:B:408:ARG:NH2	2.41	0.53
1:C:268:ILE:HD13	1:C:268:ILE:N	2.23	0.53
2:F:119:ILE:O	2:F:122:ALA:HB3	2.08	0.53
2:F:54:VAL:O	2:F:107:ASN:HB3	2.09	0.53
1:A:230:ILE:CD1	1:A:230:ILE:H	2.18	0.53
1:G:114:MET:HE3	1:G:118:MET:HG3	1.91	0.53
2:B:290:ALA:HB2	3:O:10:PHE:HZ	1.73	0.53
1:A:24:LEU:HD11	1:A:216:THR:HG22	1.91	0.53
1:A:268:ILE:N	1:A:268:ILE:HD13	2.24	0.53
1:A:333:LEU:HD13	1:A:334:SER:N	2.24	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:31:LEU:HD22	2:B:35:LEU:HD23	1.91	0.53
1:E:39:PHE:CE1	1:E:385:LYS:HD2	2.44	0.52
1:E:119:SER:HB3	1:E:220:LEU:HD11	1.90	0.52
2:F:31:LEU:HD22	2:F:35:LEU:HD23	1.92	0.52
1:A:429:THR:O	1:A:429:THR:HG22	2.09	0.52
1:E:24:LEU:HD11	1:E:216:THR:HG22	1.90	0.52
1:A:122:VAL:O	1:A:191:ARG:NH2	2.42	0.52
2:B:377:LYS:O	2:B:381:LYS:HG3	2.08	0.52
1:A:99:ASN:HB2	1:A:101:MET:HE3	1.90	0.52
2:D:253:ARG:HB3	2:D:438:PRO:HB2	1.92	0.52
1:A:429:THR:CG2	1:A:431:ASN:HD22	2.22	0.52
2:F:439:VAL:HG13	2:F:457:GLU:HG2	1.90	0.52
2:H:90:LEU:CD1	2:H:94:ASN:ND2	2.71	0.52
1:A:403:ILE:O	1:A:403:ILE:HG23	2.10	0.52
1:E:19:PHE:CD1	1:E:392:MET:HE2	2.45	0.52
1:G:379:LEU:HD11	1:G:409:ILE:HD11	1.91	0.52
1:A:139:ALA:O	1:A:143:ILE:HD13	2.09	0.52
1:E:268:ILE:N	1:E:268:ILE:HD13	2.25	0.52
1:A:176:ARG:NH2	1:E:242:SER:OG	2.43	0.52
1:E:32:THR:HG21	1:E:209:HIS:HA	1.92	0.52
1:C:403:ILE:HG23	1:C:403:ILE:O	2.10	0.52
1:E:19:PHE:HD1	1:E:392:MET:CE	2.23	0.51
1:G:230:ILE:CD1	1:G:230:ILE:H	2.18	0.51
1:G:157:LEU:HB3	1:G:445:VAL:CG2	2.38	0.51
1:C:429:THR:O	1:C:429:THR:HG22	2.09	0.51
1:C:249:VAL:HG23	1:C:249:VAL:O	2.10	0.51
1:E:299:TYR:CZ	2:F:90:LEU:HD23	2.44	0.51
2:H:441:MET:HG2	2:H:442:VAL:N	2.25	0.51
2:F:62:ASN:OD1	2:F:65:ASN:HB2	2.10	0.51
1:A:371:LYS:HE3	1:A:412:ILE:O	2.11	0.51
2:F:441:MET:HG2	2:F:442:VAL:N	2.25	0.51
2:H:69:ALA:HB2	2:H:198:TYR:CZ	2.45	0.51
2:B:76:ALA:HB1	2:B:129:ILE:HG22	1.93	0.51
1:A:119:SER:HB3	1:A:220:LEU:HD11	1.91	0.51
1:G:333:LEU:HD13	1:G:334:SER:N	2.26	0.51
1:E:96:SER:HB3	1:E:99:ASN:OD1	2.11	0.51
2:B:350:ARG:NH1	2:D:420:LYS:HB3	2.25	0.51
2:B:286:LEU:HD21	3:O:11:PHE:CE1	2.46	0.51
1:C:81:ALA:O	1:C:85:GLU:HG3	2.10	0.51
2:D:76:ALA:HB1	2:D:129:ILE:HG22	1.93	0.51
1:E:81:ALA:O	1:E:85:GLU:HG3	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:R:12:LYS:N	3:R:13:PRO:HD3	2.27	0.50
2:D:42:ILE:HG13	2:D:214:GLY:HA2	1.92	0.50
1:A:157:LEU:CB	1:A:445:VAL:HG21	2.42	0.50
2:F:39:THR:HB	2:F:218:HIS:CD2	2.45	0.50
2:D:441:MET:HE3	2:D:453:VAL:HG23	1.93	0.50
1:A:379:LEU:HD11	1:A:409:ILE:HD11	1.93	0.50
1:A:19:PHE:CD1	1:A:392:MET:HE2	2.46	0.50
3:O:17:THR:C	3:O:19:CYS:H	2.15	0.50
2:F:397:ASP:OD2	2:F:408:ARG:NH1	2.43	0.50
2:B:245:ARG:NE	2:B:245:ARG:HA	2.26	0.50
1:A:342:GLN:O	1:A:346:VAL:HG23	2.11	0.50
2:F:255:GLU:HB3	2:F:453:VAL:HG23	1.94	0.50
1:E:230:ILE:CD1	1:E:230:ILE:H	2.21	0.50
2:H:453:VAL:O	2:H:457:GLU:HG3	2.11	0.50
2:H:119:ILE:O	2:H:122:ALA:HB3	2.12	0.50
2:B:119:ILE:O	2:B:122:ALA:HB3	2.12	0.50
1:C:314:GLU:OE2	1:C:315:ASN:HB2	2.12	0.50
2:B:416:GLU:HA	2:B:416:GLU:OE1	2.11	0.50
1:G:310:TYR:HB3	1:G:312:PHE:CZ	2.46	0.50
1:G:276:LEU:HD11	1:G:329:PHE:CD2	2.47	0.50
3:Q:10:PHE:O	3:Q:11:PHE:O	2.30	0.50
1:G:243:CYS:HA	1:G:446:MET:O	2.11	0.50
2:F:61:GLU:OE1	2:F:66:ASN:HA	2.12	0.50
1:G:371:LYS:HE3	1:G:412:ILE:O	2.12	0.50
1:G:139:ALA:O	1:G:143:ILE:HD13	2.11	0.50
2:B:42:ILE:HG13	2:B:214:GLY:HA2	1.93	0.49
1:G:270:HIS:O	1:G:273:ILE:HB	2.13	0.49
1:E:340:ALA:HB3	1:E:341:PRO:HD3	1.94	0.49
1:A:314:GLU:OE2	1:A:315:ASN:HB2	2.12	0.49
2:D:115:LEU:HD12	2:D:115:LEU:N	2.26	0.49
1:A:270:HIS:O	1:A:273:ILE:HB	2.12	0.49
3:O:11:PHE:O	3:O:12:LYS:HG2	2.11	0.49
2:H:255:GLU:HB3	2:H:453:VAL:HG23	1.94	0.49
1:C:114:MET:HE3	1:C:118:MET:HG3	1.95	0.49
2:H:317:GLY:O	2:H:318:SER:CB	2.60	0.49
1:E:67:LEU:HD13	1:E:135:GLN:HG3	1.95	0.49
2:F:253:ARG:HB3	2:F:438:PRO:HB2	1.95	0.49
3:Q:11:PHE:O	3:Q:12:LYS:HG2	2.13	0.49
2:F:69:ALA:HB2	2:F:198:TYR:CZ	2.48	0.49
1:A:19:PHE:HD1	1:A:392:MET:HE2	1.78	0.49
2:D:77:PHE:CE1	3:P:18:LEU:HD22	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:81:ALA:O	1:G:85:GLU:HG3	2.13	0.49
1:A:429:THR:HG22	1:A:431:ASN:HD22	1.78	0.48
1:A:32:THR:HG21	1:A:209:HIS:HA	1.94	0.48
2:H:31:LEU:HD22	2:H:35:LEU:HD23	1.95	0.48
1:G:249:VAL:O	1:G:249:VAL:HG23	2.13	0.48
2:B:69:ALA:HB2	2:B:198:TYR:CZ	2.48	0.48
2:D:119:ILE:O	2:D:122:ALA:HB3	2.13	0.48
1:G:67:LEU:HD13	1:G:135:GLN:HG3	1.94	0.48
1:E:114:MET:HE3	1:E:118:MET:HG3	1.95	0.48
1:E:249:VAL:O	1:E:249:VAL:HG23	2.13	0.48
2:F:90:LEU:CD1	2:F:94:ASN:ND2	2.76	0.48
1:A:96:SER:HB3	1:A:99:ASN:OD1	2.13	0.48
1:A:81:ALA:O	1:A:85:GLU:HG3	2.14	0.48
2:H:253:ARG:HB3	2:H:438:PRO:HB2	1.95	0.48
1:G:32:THR:HG21	1:G:209:HIS:HA	1.94	0.48
1:C:371:LYS:HE3	1:C:412:ILE:O	2.13	0.48
2:B:76:ALA:HB1	2:B:129:ILE:HG23	1.95	0.48
2:B:90:LEU:CD1	2:B:94:ASN:ND2	2.77	0.48
1:A:340:ALA:HB3	1:A:341:PRO:HD3	1.95	0.48
2:D:377:LYS:O	2:D:381:LYS:HG3	2.14	0.48
2:D:235:SER:O	2:D:238:PRO:HG3	2.13	0.48
1:C:340:ALA:HB3	1:C:341:PRO:HD3	1.95	0.48
2:B:368:ILE:O	2:B:423:LYS:HE3	2.13	0.48
2:H:42:ILE:HG13	2:H:214:GLY:HA2	1.95	0.48
2:D:90:LEU:CD1	2:D:94:ASN:HD21	2.27	0.48
2:H:119:ILE:N	2:H:120:PRO:HD2	2.29	0.48
2:H:398:ILE:HA	2:H:408:ARG:HG3	1.96	0.48
1:E:371:LYS:HE3	1:E:412:ILE:O	2.14	0.48
1:C:294:PRO:HB3	2:D:89:GLU:HA	1.96	0.48
1:E:314:GLU:OE2	1:E:315:ASN:HB2	2.14	0.48
2:F:375:ARG:HB3	2:F:375:ARG:HH11	1.78	0.47
2:B:183:PRO:HD2	2:B:186:ASN:HB2	1.96	0.47
2:D:54:VAL:O	2:D:107:ASN:HB3	2.14	0.47
2:H:91:GLU:OE2	2:H:121:LYS:HD2	2.14	0.47
1:A:99:ASN:HB2	1:A:101:MET:CE	2.44	0.47
1:C:275:ALA:HB3	1:C:423:VAL:HG21	1.96	0.47
1:A:293:GLY:HA3	2:B:99:LEU:O	2.14	0.47
1:E:333:LEU:HD13	1:E:334:SER:N	2.28	0.47
2:H:245:ARG:HA	2:H:245:ARG:HE	1.79	0.47
2:D:143:GLU:O	2:D:147:ILE:HG12	2.13	0.47
1:G:19:PHE:CD1	1:G:392:MET:HE1	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:R:16:ARG:HD3	3:R:16:ARG:HA	1.67	0.47
1:C:276:LEU:HD11	1:C:329:PHE:CD2	2.49	0.47
2:D:232:VAL:HA	2:D:233:PRO:HD3	1.67	0.47
2:F:115:LEU:HD12	2:F:115:LEU:N	2.28	0.47
1:G:275:ALA:CB	1:G:423:VAL:HG21	2.44	0.47
1:A:45:TYR:N	1:A:45:TYR:CD1	2.83	0.47
1:C:19:PHE:CD1	1:C:392:MET:HE3	2.48	0.47
2:D:62:ASN:CG	2:D:65:ASN:HB2	2.35	0.47
2:D:91:GLU:OE2	2:D:121:LYS:HD2	2.15	0.47
2:H:77:PHE:CD1	3:R:18:LEU:HD22	2.50	0.47
2:F:73:GLN:HA	2:F:110:TYR:OH	2.15	0.47
1:G:429:THR:O	1:G:429:THR:HG22	2.15	0.47
2:F:255:GLU:HB3	2:F:453:VAL:CG2	2.45	0.47
1:E:99:ASN:HB2	1:E:101:MET:CE	2.44	0.47
1:C:235:ALA:O	1:C:436:GLY:HA3	2.14	0.47
2:D:101:ALA:O	3:P:17:THR:HG23	2.15	0.47
2:H:368:ILE:O	2:H:423:LYS:HE3	2.15	0.47
2:H:377:LYS:O	2:H:381:LYS:HG3	2.14	0.47
2:F:22:GLN:OE1	2:F:22:GLN:HA	2.14	0.47
2:B:61:GLU:OE1	2:B:66:ASN:HA	2.14	0.47
2:F:183:PRO:HD2	2:F:186:ASN:HB2	1.97	0.47
3:Q:17:THR:C	3:Q:19:CYS:N	2.68	0.47
1:E:99:ASN:HB2	1:E:101:MET:HE3	1.96	0.47
1:C:342:GLN:O	1:C:346:VAL:HG23	2.15	0.47
1:A:249:VAL:HG23	1:A:249:VAL:O	2.15	0.47
1:C:32:THR:HG21	1:C:209:HIS:HA	1.96	0.47
1:A:67:LEU:HD13	1:A:135:GLN:HG3	1.97	0.47
2:D:439:VAL:CG1	2:D:457:GLU:HG2	2.45	0.47
2:F:263:LEU:HA	2:F:264:PRO:HD3	1.69	0.47
1:G:403:ILE:HG23	1:G:403:ILE:O	2.13	0.46
2:B:439:VAL:HG22	2:B:453:VAL:HG13	1.96	0.46
1:A:35:THR:HB	1:A:36:PRO:CD	2.44	0.46
2:F:42:ILE:HG13	2:F:214:GLY:HA2	1.97	0.46
1:A:42:LEU:HD23	1:A:42:LEU:N	2.30	0.46
2:F:245:ARG:NE	2:F:245:ARG:HA	2.31	0.46
2:H:439:VAL:CG1	2:H:457:GLU:HG2	2.46	0.46
2:D:317:GLY:O	2:D:318:SER:CB	2.64	0.46
1:G:39:PHE:CE1	1:G:385:LYS:HD2	2.51	0.46
1:C:270:HIS:O	1:C:273:ILE:HB	2.14	0.46
2:H:357:LEU:O	2:H:361:LYS:HG3	2.16	0.46
2:D:349:VAL:HG11	2:D:450:VAL:HG22	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:76:ALA:HB1	2:H:129:ILE:HG23	1.97	0.46
1:C:429:THR:CG2	1:C:429:THR:O	2.63	0.46
2:H:255:GLU:HB3	2:H:453:VAL:CG2	2.46	0.46
1:A:275:ALA:HB3	1:A:423:VAL:HG21	1.97	0.46
2:H:62:ASN:CG	2:H:65:ASN:HB2	2.35	0.46
2:B:439:VAL:CG1	2:B:457:GLU:HG2	2.45	0.46
2:B:253:ARG:HB3	2:B:438:PRO:HB2	1.98	0.46
2:D:398:ILE:HA	2:D:408:ARG:HG3	1.97	0.46
2:H:349:VAL:HG11	2:H:450:VAL:HG22	1.97	0.46
2:F:349:VAL:HG11	2:F:450:VAL:HG22	1.98	0.46
1:G:268:ILE:N	1:G:268:ILE:CD1	2.79	0.46
2:B:453:VAL:O	2:B:457:GLU:HG3	2.16	0.46
1:C:333:LEU:HD13	1:C:334:SER:N	2.31	0.46
2:H:61:GLU:OE1	2:H:66:ASN:HA	2.16	0.46
2:B:62:ASN:CG	2:B:65:ASN:HB2	2.36	0.46
1:A:178:LEU:HD11	1:E:178:LEU:HD11	1.97	0.46
2:H:81:GLN:HG3	2:H:132:LYS:O	2.16	0.46
2:F:76:ALA:HB1	2:F:129:ILE:HG23	1.97	0.46
2:D:40:GLU:O	2:D:213:ALA:HA	2.16	0.46
1:A:33:SER:HB3	1:A:392:MET:CE	2.20	0.45
1:A:114:MET:CE	1:A:118:MET:HG3	2.46	0.45
2:F:91:GLU:OE2	2:F:121:LYS:HD2	2.16	0.45
1:G:256:LEU:CD1	1:G:314:GLU:HG2	2.46	0.45
1:A:253:LEU:HA	1:A:254:PRO:HD3	1.80	0.45
2:D:31:LEU:HD22	2:D:35:LEU:HD23	1.98	0.45
2:D:263:LEU:HA	2:D:264:PRO:HD3	1.67	0.45
1:G:340:ALA:HB3	1:G:341:PRO:HD3	1.97	0.45
2:F:119:ILE:N	2:F:120:PRO:HD2	2.32	0.45
2:F:235:SER:O	2:F:238:PRO:HG3	2.16	0.45
2:B:397:ASP:OD2	2:B:408:ARG:NH1	2.47	0.45
2:D:73:GLN:HA	2:D:110:TYR:OH	2.17	0.45
1:E:429:THR:O	1:E:429:THR:HG22	2.16	0.45
1:E:19:PHE:HD1	1:E:392:MET:HE2	1.82	0.45
2:B:357:LEU:O	2:B:361:LYS:HG3	2.16	0.45
2:B:263:LEU:HA	2:B:264:PRO:HD3	1.67	0.45
2:D:119:ILE:N	2:D:120:PRO:HD2	2.32	0.45
2:F:286:LEU:HD21	3:Q:11:PHE:CE1	2.51	0.45
2:B:97:SER:OG	2:B:114:SER:HB3	2.17	0.45
2:H:143:GLU:O	2:H:147:ILE:HG12	2.17	0.45
1:C:139:ALA:O	1:C:143:ILE:HD13	2.17	0.45
1:E:342:GLN:O	1:E:346:VAL:HG23	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:403:ILE:O	1:E:403:ILE:HG23	2.16	0.45
2:F:165:HIS:HD2	2:F:256:ARG:HE	1.65	0.45
2:B:260:GLU:HG3	2:B:263:LEU:HG	1.98	0.45
2:F:368:ILE:O	2:F:423:LYS:HE3	2.15	0.45
2:F:295:TRP:CZ2	2:F:297:ARG:HA	2.52	0.45
2:D:260:GLU:HG3	2:D:263:LEU:HG	1.98	0.45
1:A:19:PHE:CD1	1:A:392:MET:HE3	2.52	0.45
2:D:255:GLU:HB3	2:D:453:VAL:HG23	1.98	0.45
2:B:203:TYR:CD1	2:B:203:TYR:N	2.85	0.45
2:F:441:MET:HE3	2:F:453:VAL:HG23	1.99	0.45
1:C:17:ASP:O	1:C:18:ASN:HB3	2.17	0.45
2:B:73:GLN:HA	2:B:110:TYR:OH	2.16	0.45
2:H:40:GLU:O	2:H:213:ALA:HA	2.17	0.45
2:D:76:ALA:HB1	2:D:129:ILE:HG23	1.99	0.45
2:B:290:ALA:HB2	3:O:10:PHE:CE1	2.52	0.45
1:G:99:ASN:HB2	1:G:101:MET:HE3	1.98	0.45
2:D:397:ASP:OD2	2:D:408:ARG:NH1	2.49	0.45
1:E:379:LEU:HD11	1:E:409:ILE:HD11	1.99	0.45
2:F:357:LEU:O	2:F:361:LYS:HG3	2.17	0.45
1:C:157:LEU:HD11	1:C:244:ILE:HD13	1.98	0.44
2:F:398:ILE:HA	2:F:408:ARG:HG3	1.99	0.44
1:E:67:LEU:HD13	1:E:135:GLN:CG	2.47	0.44
2:D:260:GLU:CG	2:D:263:LEU:HG	2.47	0.44
2:B:147:ILE:HG22	2:B:187:ILE:HD13	2.00	0.44
2:H:144:ARG:HH21	2:H:188:LYS:C	2.21	0.44
1:E:256:LEU:CD1	1:E:314:GLU:HG2	2.47	0.44
1:G:314:GLU:OE2	1:G:315:ASN:HB2	2.16	0.44
2:B:260:GLU:CG	2:B:263:LEU:HG	2.48	0.44
1:A:243:CYS:HA	1:A:446:MET:O	2.17	0.44
1:E:157:LEU:HB3	1:E:445:VAL:CG2	2.44	0.44
1:A:35:THR:HB	1:A:36:PRO:HD2	1.98	0.44
1:E:310:TYR:HB3	1:E:312:PHE:CZ	2.53	0.44
1:A:429:THR:O	1:A:429:THR:CG2	2.66	0.44
2:D:61:GLU:OE1	2:D:66:ASN:HA	2.17	0.44
1:C:310:TYR:CD1	1:C:312:PHE:CZ	3.06	0.44
2:D:90:LEU:CD1	2:D:94:ASN:ND2	2.80	0.44
1:G:96:SER:OG	1:G:97:ARG:N	2.50	0.44
2:F:77:PHE:CE1	3:Q:18:LEU:HD22	2.53	0.44
1:G:50:SER:OG	1:G:97:ARG:HA	2.17	0.44
2:B:317:GLY:O	2:B:318:SER:CB	2.65	0.44
1:G:344:VAL:HG21	1:G:456:VAL:HG22	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:124:PHE:N	1:E:125:PRO:CD	2.80	0.44
2:H:73:GLN:HA	2:H:110:TYR:OH	2.17	0.44
2:F:62:ASN:CG	2:F:65:ASN:HB2	2.38	0.44
2:H:90:LEU:HD13	2:H:94:ASN:HD21	1.77	0.44
1:G:63:ILE:HG22	1:G:67:LEU:HD22	2.00	0.44
2:D:23:ILE:HA	2:D:24:PRO:HD3	1.82	0.44
2:D:349:VAL:HG23	2:D:449:THR:HG23	2.00	0.44
1:E:427:ILE:HD13	1:E:432:VAL:CG2	2.47	0.44
2:H:295:TRP:CZ2	2:H:297:ARG:HA	2.53	0.44
1:A:295:GLY:CA	2:B:93:GLU:HG2	2.41	0.43
1:E:336:ILE:HG22	1:E:338:GLN:OE1	2.18	0.43
2:H:259:LYS:HG3	2:H:447:THR:HG22	2.00	0.43
1:A:56:ASN:HA	1:A:56:ASN:HD22	1.62	0.43
1:E:256:LEU:HD23	1:E:336:ILE:HD13	2.01	0.43
2:F:97:SER:OG	2:F:114:SER:HB3	2.18	0.43
3:O:8:ILE:O	3:O:9:ARG:HG3	2.18	0.43
1:A:157:LEU:HD11	1:A:244:ILE:HD13	2.00	0.43
1:G:310:TYR:CD1	1:G:312:PHE:CZ	3.06	0.43
1:G:266:LEU:HA	1:G:267:PRO:HD3	1.85	0.43
2:H:260:GLU:CG	2:H:263:LEU:HG	2.49	0.43
2:D:203:TYR:CD1	2:D:203:TYR:N	2.85	0.43
1:E:275:ALA:HB3	1:E:423:VAL:HG21	2.00	0.43
2:F:144:ARG:HH21	2:F:188:LYS:C	2.21	0.43
2:B:350:ARG:HD2	2:D:420:LYS:HB2	1.99	0.43
2:D:453:VAL:O	2:D:457:GLU:HG3	2.18	0.43
2:D:21:SER:OG	2:D:22:GLN:N	2.51	0.43
1:G:17:ASP:O	1:G:18:ASN:HB3	2.18	0.43
3:Q:16:ARG:HD3	3:Q:16:ARG:HA	1.74	0.43
1:C:119:SER:HB3	1:C:220:LEU:CD1	2.49	0.43
1:C:256:LEU:CD1	1:C:314:GLU:HG2	2.49	0.43
1:C:294:PRO:HD2	2:D:99:LEU:HB3	1.99	0.43
2:F:77:PHE:CD1	3:Q:18:LEU:HD22	2.54	0.43
2:F:393:ALA:O	2:F:396:GLU:HB3	2.19	0.43
2:F:416:GLU:HA	2:F:416:GLU:OE1	2.19	0.43
2:H:183:PRO:HD2	2:H:186:ASN:HB2	2.01	0.43
2:F:305:SER:HA	2:F:306:PRO:HD3	1.81	0.43
2:H:416:GLU:HA	2:H:416:GLU:OE1	2.19	0.43
1:C:311:TYR:CD2	1:C:311:TYR:N	2.84	0.43
2:H:204:LYS:HG3	2:H:235:SER:OG	2.18	0.43
1:E:19:PHE:CD1	1:E:392:MET:CE	3.01	0.43
2:B:305:SER:HA	2:B:306:PRO:HD3	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:350:ARG:NH1	2:D:416:GLU:OE2	2.52	0.43
3:O:10:PHE:O	3:O:11:PHE:O	2.37	0.43
1:C:99:ASN:HB2	1:C:101:MET:HE3	2.00	0.43
1:A:276:LEU:HD11	1:A:329:PHE:CD2	2.53	0.43
1:E:305:HIS:N	1:E:305:HIS:ND1	2.67	0.43
2:B:458:GLU:CD	2:D:422:THR:HB	2.39	0.43
2:F:439:VAL:CG1	2:F:457:GLU:HG2	2.49	0.43
1:E:35:THR:HB	1:E:36:PRO:CD	2.49	0.43
1:G:152:LEU:O	1:G:155:PRO:HD2	2.18	0.43
2:F:259:LYS:HG3	2:F:447:THR:HG22	2.01	0.43
1:C:84:LEU:HD13	1:C:91:TYR:CZ	2.54	0.43
1:C:253:LEU:HA	1:C:254:PRO:HD3	1.80	0.43
1:G:305:HIS:N	1:G:305:HIS:ND1	2.67	0.43
1:G:310:TYR:HB3	1:G:312:PHE:CE2	2.54	0.43
1:G:67:LEU:HD13	1:G:135:GLN:CG	2.49	0.43
2:D:69:ALA:HB2	2:D:198:TYR:CZ	2.53	0.43
1:E:228:PRO:HA	1:E:229:PRO:HD3	1.86	0.43
1:E:276:LEU:HD11	1:E:329:PHE:CD2	2.52	0.43
1:G:84:LEU:HD13	1:G:91:TYR:CZ	2.54	0.43
3:P:16:ARG:HD3	3:P:16:ARG:HA	1.92	0.43
2:B:31:LEU:HD12	2:B:31:LEU:HA	1.80	0.43
1:E:376:SER:O	1:E:380:MET:HG3	2.19	0.43
1:G:99:ASN:HB2	1:G:101:MET:CE	2.49	0.42
1:A:256:LEU:CD1	1:A:314:GLU:HG2	2.49	0.42
2:H:260:GLU:HG3	2:H:263:LEU:HG	2.00	0.42
2:B:232:VAL:HA	2:B:233:PRO:HD3	1.73	0.42
1:G:174:CYS:HA	1:G:175:PRO:HD3	1.94	0.42
2:B:393:ALA:O	2:B:396:GLU:HB3	2.19	0.42
2:F:317:GLY:O	2:F:318:SER:CB	2.66	0.42
1:A:311:TYR:CD2	1:A:311:TYR:N	2.83	0.42
1:G:325:ASP:O	1:G:326:SER:HB2	2.18	0.42
1:A:50:SER:OG	1:A:97:ARG:HA	2.18	0.42
2:D:183:PRO:HD2	2:D:186:ASN:HB2	2.01	0.42
2:D:255:GLU:HB3	2:D:453:VAL:CG2	2.49	0.42
1:E:50:SER:OG	1:E:97:ARG:HA	2.19	0.42
2:F:260:GLU:HG3	2:F:263:LEU:HG	2.01	0.42
1:A:124:PHE:N	1:A:125:PRO:CD	2.82	0.42
2:F:165:HIS:HD2	2:F:256:ARG:NE	2.16	0.42
2:F:260:GLU:CG	2:F:263:LEU:HG	2.50	0.42
2:H:137:ASN:O	2:H:141:GLU:HG2	2.19	0.42
2:F:147:ILE:HG22	2:F:187:ILE:HD13	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:45:TYR:CD1	1:E:45:TYR:N	2.87	0.42
1:G:157:LEU:HD11	1:G:244:ILE:HD13	2.01	0.42
2:H:136:ASP:O	2:H:140:ILE:HG13	2.19	0.42
2:B:91:GLU:OE2	2:B:121:LYS:HD2	2.19	0.42
1:C:67:LEU:HD13	1:C:135:GLN:HG3	2.01	0.42
2:B:398:ILE:HA	2:B:408:ARG:HG3	2.02	0.42
2:H:147:ILE:HG22	2:H:187:ILE:HD13	2.02	0.42
2:H:268:ILE:HD12	2:H:268:ILE:N	2.35	0.42
2:D:147:ILE:HG22	2:D:187:ILE:HD13	2.02	0.42
2:B:259:LYS:HG3	2:B:447:THR:HG22	2.00	0.42
2:B:255:GLU:HB3	2:B:453:VAL:HG23	2.00	0.42
2:D:350:ARG:HG3	2:D:451:PRO:HB3	2.02	0.42
1:G:45:TYR:OH	1:G:389:LEU:HG	2.20	0.42
2:D:165:HIS:CD2	2:D:256:ARG:HE	2.31	0.42
2:B:165:HIS:HD2	2:B:256:ARG:NE	2.18	0.42
2:B:401:GLN:O	2:B:405:THR:HB	2.20	0.42
2:F:453:VAL:O	2:F:457:GLU:HG3	2.20	0.42
1:C:395:GLN:OE1	1:C:403:ILE:HG22	2.20	0.42
2:F:81:GLN:HG3	2:F:132:LYS:O	2.19	0.42
1:G:119:SER:HB3	1:G:220:LEU:CD1	2.48	0.42
1:C:96:SER:OG	1:C:97:ARG:N	2.53	0.42
1:C:310:TYR:HB3	1:C:312:PHE:CZ	2.54	0.42
1:C:124:PHE:N	1:C:125:PRO:CD	2.83	0.42
1:A:14:ALA:N	1:A:17:ASP:OD2	2.52	0.42
1:A:39:PHE:O	1:A:385:LYS:HE3	2.19	0.42
1:C:237:TYR:CG	1:C:264:GLU:HB2	2.54	0.42
1:C:56:ASN:HA	1:C:56:ASN:HD22	1.56	0.42
2:F:203:TYR:CD1	2:F:203:TYR:N	2.88	0.42
2:D:245:ARG:HA	2:D:245:ARG:NE	2.33	0.42
1:E:311:TYR:N	1:E:311:TYR:CD2	2.81	0.42
2:H:305:SER:HA	2:H:306:PRO:HD3	1.83	0.41
1:C:157:LEU:HB3	1:C:445:VAL:CG2	2.48	0.41
2:H:439:VAL:HG22	2:H:453:VAL:HG13	2.02	0.41
2:B:40:GLU:O	2:B:213:ALA:HA	2.20	0.41
1:E:267:PRO:HA	1:E:323:TYR:O	2.20	0.41
1:E:245:PRO:HA	1:E:246:PRO:HD3	1.87	0.41
1:E:96:SER:OG	1:E:97:ARG:N	2.51	0.41
2:H:349:VAL:HG23	2:H:449:THR:HG23	2.03	0.41
1:E:174:CYS:HA	1:E:175:PRO:HD3	1.97	0.41
1:G:267:PRO:HA	1:G:323:TYR:O	2.20	0.41
2:H:232:VAL:HA	2:H:233:PRO:HD3	1.70	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:167:THR:OG1	1:A:168:LEU:N	2.52	0.41
1:G:200:THR:HG22	1:G:201:VAL:N	2.34	0.41
1:A:68:ALA:O	1:A:69:PHE:HB2	2.20	0.41
1:G:268:ILE:CD1	1:G:268:ILE:H	2.33	0.41
1:G:30:VAL:HG22	1:G:216:THR:HG21	2.03	0.41
1:C:260:GLN:HB2	1:C:445:VAL:HG12	2.03	0.41
1:C:379:LEU:HD11	1:C:409:ILE:HD11	2.03	0.41
2:D:31:LEU:HA	2:D:31:LEU:HD12	1.90	0.41
1:E:310:TYR:CD1	1:E:312:PHE:CZ	3.08	0.41
1:G:427:ILE:HD13	1:G:432:VAL:CG2	2.50	0.41
1:G:19:PHE:CD1	1:G:392:MET:HE2	2.55	0.41
1:C:99:ASN:HB2	1:C:101:MET:CE	2.51	0.41
2:B:203:TYR:HD1	2:B:203:TYR:N	2.19	0.41
1:G:128:THR:OG1	1:G:131:GLU:HG3	2.21	0.41
2:B:204:LYS:HG3	2:B:235:SER:OG	2.21	0.41
1:G:228:PRO:HA	1:G:229:PRO:HD3	1.83	0.41
1:C:268:ILE:CD1	1:C:268:ILE:N	2.83	0.41
1:A:99:ASN:HD22	1:A:101:MET:HE3	1.85	0.41
1:A:14:ALA:N	1:A:404:PRO:HB3	2.36	0.41
1:G:263:PHE:CE2	1:G:442:ALA:HB2	2.55	0.41
1:E:72:THR:HG21	1:E:120:GLU:HB3	2.02	0.41
1:G:369:ARG:O	1:G:373:GLN:HG3	2.20	0.41
2:D:295:TRP:HB3	2:D:323:TYR:CE2	2.54	0.41
1:G:42:LEU:N	1:G:42:LEU:HD23	2.34	0.41
2:B:375:ARG:HB3	2:B:375:ARG:HH11	1.82	0.41
2:D:286:LEU:HA	2:D:286:LEU:HD23	1.88	0.41
1:C:293:GLY:HA3	2:D:99:LEU:O	2.20	0.41
1:C:273:ILE:HD13	1:C:273:ILE:HA	1.88	0.41
1:G:45:TYR:N	1:G:45:TYR:CD1	2.88	0.41
1:E:311:TYR:CD2	1:E:311:TYR:C	2.94	0.41
1:G:376:SER:O	1:G:380:MET:HG3	2.21	0.41
1:C:305:HIS:ND1	1:C:305:HIS:N	2.68	0.41
1:G:119:SER:CB	1:G:220:LEU:HD11	2.50	0.41
2:B:75:LEU:HD21	2:B:140:ILE:HG12	2.02	0.41
2:H:203:TYR:N	2:H:203:TYR:CD1	2.89	0.41
1:A:268:ILE:N	1:A:268:ILE:CD1	2.83	0.41
2:H:35:LEU:HA	2:H:205:GLY:O	2.20	0.41
2:F:295:TRP:HB3	2:F:323:TYR:CE2	2.56	0.41
2:B:143:GLU:O	2:B:147:ILE:HG12	2.20	0.41
1:C:200:THR:HG22	1:C:201:VAL:N	2.36	0.41
2:F:28:THR:HG22	2:F:29:SER:N	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:17:ASP:O	1:E:18:ASN:HB3	2.21	0.41
2:F:248:LEU:HA	2:F:249:PRO:HD3	1.92	0.41
2:B:423:LYS:O	2:B:427:ILE:HG13	2.20	0.41
1:G:429:THR:O	1:G:429:THR:CG2	2.69	0.41
2:H:263:LEU:HA	2:H:264:PRO:HD3	1.67	0.41
2:D:203:TYR:N	2:D:203:TYR:HD1	2.19	0.41
1:E:311:TYR:C	1:E:313:VAL:H	2.24	0.41
1:E:253:LEU:HA	1:E:254:PRO:HD3	1.81	0.41
1:G:382:LEU:HA	1:G:382:LEU:HD12	1.91	0.41
1:G:253:LEU:HA	1:G:254:PRO:HD3	1.82	0.40
1:C:113:LYS:HA	1:C:113:LYS:HD2	1.92	0.40
1:G:56:ASN:HA	1:G:56:ASN:HD22	1.58	0.40
1:E:268:ILE:CD1	1:E:268:ILE:N	2.84	0.40
2:B:119:ILE:N	2:B:120:PRO:HD2	2.36	0.40
1:A:311:TYR:CD2	1:A:311:TYR:C	2.95	0.40
2:D:357:LEU:O	2:D:361:LYS:HG3	2.21	0.40
2:H:31:LEU:HD21	2:H:226:GLN:HA	2.03	0.40
2:B:294:ASN:ND2	3:O:9:ARG:HA	2.36	0.40
1:G:342:GLN:O	1:G:346:VAL:HG23	2.22	0.40
1:C:179:ILE:N	1:C:180:PRO:CD	2.84	0.40
1:C:35:THR:HB	1:C:36:PRO:CD	2.51	0.40
2:D:259:LYS:HG3	2:D:447:THR:HG22	2.03	0.40
2:F:268:ILE:HD12	2:F:268:ILE:N	2.36	0.40
2:H:52:ILE:O	2:H:52:ILE:HG23	2.21	0.40
1:A:310:TYR:HB3	1:A:312:PHE:CZ	2.56	0.40
2:B:373:VAL:O	2:B:377:LYS:HG3	2.22	0.40
1:E:114:MET:CE	1:E:118:MET:HG3	2.51	0.40
1:C:174:CYS:HA	1:C:175:PRO:HD3	1.90	0.40
1:A:302:LEU:HA	1:A:302:LEU:HD23	1.85	0.40
2:F:256:ARG:CG	2:F:256:ARG:NH1	2.78	0.40
1:E:336:ILE:HG23	1:E:337:PRO:HD2	2.04	0.40
1:A:45:TYR:OH	1:A:389:LEU:HG	2.21	0.40
2:F:349:VAL:HG23	2:F:449:THR:HG23	2.03	0.40
1:G:336:ILE:HG22	1:G:338:GLN:OE1	2.22	0.40
2:B:81:GLN:HG3	2:B:132:LYS:O	2.21	0.40
1:A:336:ILE:HG22	1:A:338:GLN:OE1	2.21	0.40
2:H:393:ALA:O	2:H:396:GLU:HB3	2.21	0.40
1:A:246:PRO:HG3	1:A:448:GLY:HA2	2.02	0.40
1:C:39:PHE:CE1	1:C:385:LYS:HD2	2.57	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	448/475 (94%)	427 (95%)	19 (4%)	2 (0%)	39	69
1	C	444/475 (94%)	426 (96%)	15 (3%)	3 (1%)	26	55
1	E	441/475 (93%)	423 (96%)	15 (3%)	3 (1%)	26	55
1	G	444/475 (94%)	424 (96%)	16 (4%)	4 (1%)	21	49
2	B	437/443 (99%)	420 (96%)	16 (4%)	1 (0%)	52	80
2	D	441/443 (100%)	420 (95%)	19 (4%)	2 (0%)	34	63
2	F	441/443 (100%)	425 (96%)	15 (3%)	1 (0%)	52	80
2	H	439/443 (99%)	422 (96%)	16 (4%)	1 (0%)	52	80
3	O	11/24 (46%)	6 (54%)	4 (36%)	1 (9%)	1	1
3	P	7/24 (29%)	5 (71%)	1 (14%)	1 (14%)	0	0
3	Q	8/24 (33%)	3 (38%)	4 (50%)	1 (12%)	0	0
3	R	5/24 (21%)	4 (80%)	1 (20%)	0	100	100
All	All	3566/3768 (95%)	3405 (96%)	141 (4%)	20 (1%)	30	59

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	O	11	PHE
3	P	11	PHE
3	Q	11	PHE
1	C	250	PHE
1	G	15	ARG
1	G	250	PHE
1	A	250	PHE
2	B	318	SER
2	D	318	SER
1	E	250	PHE
1	E	251	GLY
2	F	318	SER

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Mol	Chain	Res	Type
2	H	318	SER
1	A	251	GLY
2	D	22	GLN
1	E	452	SER
1	G	251	GLY
1	C	251	GLY
1	C	171	PRO
1	G	171	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	381/401 (95%)	360 (94%)	21 (6%)	27	55
1	C	378/401 (94%)	356 (94%)	22 (6%)	25	52
1	E	377/401 (94%)	353 (94%)	24 (6%)	22	47
1	G	379/401 (94%)	357 (94%)	22 (6%)	25	52
2	B	376/379 (99%)	352 (94%)	24 (6%)	22	47
2	D	379/379 (100%)	356 (94%)	23 (6%)	23	49
2	F	379/379 (100%)	358 (94%)	21 (6%)	27	55
2	H	378/379 (100%)	358 (95%)	20 (5%)	28	57
3	O	12/23 (52%)	9 (75%)	3 (25%)	1	2
3	P	8/23 (35%)	5 (62%)	3 (38%)	0	0
3	Q	9/23 (39%)	5 (56%)	4 (44%)	0	0
3	R	6/23 (26%)	5 (83%)	1 (17%)	3	7
All	All	3062/3212 (95%)	2874 (94%)	188 (6%)	23	49

All (188) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	ASP
1	A	56	ASN

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Mol	Chain	Res	Type
1	A	65	ASP
1	A	66	ARG
1	A	67	LEU
1	A	176	ARG
1	A	210	GLU
1	A	220	LEU
1	A	268	ILE
1	A	273	ILE
1	A	303	TYR
1	A	305	HIS
1	A	307	LEU
1	A	311	TYR
1	A	314	GLU
1	A	320	ASN
1	A	333	LEU
1	A	361	ARG
1	A	381	ASN
1	A	382	LEU
1	A	446	MET
2	B	27	ARG
2	B	31	LEU
2	B	39	THR
2	B	66	ASN
2	B	75	LEU
2	B	90	LEU
2	B	100	ASN
2	B	107	ASN
2	B	149	ARG
2	B	176	LEU
2	B	181	LEU
2	B	219	GLU
2	B	250	VAL
2	B	262	THR
2	B	275	VAL
2	B	346	GLU
2	B	375	ARG
2	B	400	ARG
2	B	403	VAL
2	B	405	THR
2	B	408	ARG
2	B	424	ASP
2	B	441	MET

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Mol	Chain	Res	Type
2	B	449	THR
1	C	17	ASP
1	C	56	ASN
1	C	65	ASP
1	C	66	ARG
1	C	67	LEU
1	C	176	ARG
1	C	210	GLU
1	C	220	LEU
1	C	242	SER
1	C	268	ILE
1	C	273	ILE
1	C	303	TYR
1	C	305	HIS
1	C	307	LEU
1	C	311	TYR
1	C	314	GLU
1	C	333	LEU
1	C	361	ARG
1	C	381	ASN
1	C	382	LEU
1	C	386	LEU
1	C	446	MET
2	D	27	ARG
2	D	31	LEU
2	D	39	THR
2	D	66	ASN
2	D	75	LEU
2	D	90	LEU
2	D	100	ASN
2	D	107	ASN
2	D	149	ARG
2	D	176	LEU
2	D	181	LEU
2	D	219	GLU
2	D	236	GLU
2	D	262	THR
2	D	275	VAL
2	D	346	GLU
2	D	375	ARG
2	D	400	ARG
2	D	403	VAL

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Mol	Chain	Res	Type
2	D	405	THR
2	D	408	ARG
2	D	424	ASP
2	D	441	MET
1	E	17	ASP
1	E	56	ASN
1	E	65	ASP
1	E	66	ARG
1	E	67	LEU
1	E	176	ARG
1	E	210	GLU
1	E	220	LEU
1	E	268	ILE
1	E	273	ILE
1	E	303	TYR
1	E	305	HIS
1	E	307	LEU
1	E	311	TYR
1	E	314	GLU
1	E	320	ASN
1	E	333	LEU
1	E	361	ARG
1	E	381	ASN
1	E	382	LEU
1	E	386	LEU
1	E	431	ASN
1	E	446	MET
1	E	468	SER
2	F	27	ARG
2	F	31	LEU
2	F	39	THR
2	F	66	ASN
2	F	75	LEU
2	F	90	LEU
2	F	100	ASN
2	F	107	ASN
2	F	149	ARG
2	F	181	LEU
2	F	219	GLU
2	F	262	THR
2	F	275	VAL
2	F	346	GLU

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Mol	Chain	Res	Type
2	F	375	ARG
2	F	400	ARG
2	F	403	VAL
2	F	405	THR
2	F	408	ARG
2	F	424	ASP
2	F	441	MET
1	G	17	ASP
1	G	56	ASN
1	G	65	ASP
1	G	66	ARG
1	G	67	LEU
1	G	176	ARG
1	G	210	GLU
1	G	220	LEU
1	G	268	ILE
1	G	273	ILE
1	G	303	TYR
1	G	305	HIS
1	G	307	LEU
1	G	311	TYR
1	G	314	GLU
1	G	333	LEU
1	G	361	ARG
1	G	381	ASN
1	G	382	LEU
1	G	386	LEU
1	G	431	ASN
1	G	446	MET
2	H	27	ARG
2	H	31	LEU
2	H	39	THR
2	H	66	ASN
2	H	75	LEU
2	H	90	LEU
2	H	100	ASN
2	H	107	ASN
2	H	149	ARG
2	H	181	LEU
2	H	219	GLU
2	H	275	VAL
2	H	346	GLU

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Mol	Chain	Res	Type
2	H	375	ARG
2	H	400	ARG
2	H	403	VAL
2	H	405	THR
2	H	408	ARG
2	H	424	ASP
2	H	441	MET
3	O	10	PHE
3	O	11	PHE
3	O	15	THR
3	P	10	PHE
3	P	11	PHE
3	P	15	THR
3	Q	10	PHE
3	Q	11	PHE
3	Q	15	THR
3	Q	18	LEU
3	R	15	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (62) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	56	ASN
1	A	99	ASN
1	A	320	ASN
1	A	349	GLN
1	A	406	ASN
1	A	431	ASN
2	B	44	ASN
2	B	137	ASN
2	B	165	HIS
2	B	186	ASN
2	B	223	GLN
2	B	354	ASN
2	B	374	ASN
1	C	38	HIS
1	C	56	ASN
1	C	99	ASN
1	C	320	ASN
1	C	349	GLN
1	C	406	ASN
1	C	431	ASN

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Mol	Chain	Res	Type
2	D	44	ASN
2	D	66	ASN
2	D	107	ASN
2	D	137	ASN
2	D	165	HIS
2	D	186	ASN
2	D	223	GLN
2	D	261	ASN
2	D	354	ASN
2	D	374	ASN
1	E	56	ASN
1	E	99	ASN
1	E	236	GLN
1	E	320	ASN
1	E	349	GLN
1	E	406	ASN
2	F	44	ASN
2	F	66	ASN
2	F	107	ASN
2	F	137	ASN
2	F	165	HIS
2	F	186	ASN
2	F	218	HIS
2	F	223	GLN
2	F	354	ASN
2	F	374	ASN
1	G	56	ASN
1	G	99	ASN
1	G	320	ASN
1	G	349	GLN
1	G	381	ASN
1	G	406	ASN
2	H	44	ASN
2	H	66	ASN
2	H	107	ASN
2	H	137	ASN
2	H	165	HIS
2	H	186	ASN
2	H	218	HIS
2	H	223	GLN
2	H	354	ASN
2	H	374	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 6 ligands modelled in this entry, 4 are monoatomic - leaving 2 for Mogul analysis.

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	$\# Z > 2$
5	EPE	A	489	-	14,15,15	1.26	2 (14%)	18,20,20	0.97	1 (5%)
5	EPE	G	489	-	14,15,15	1.13	0	18,20,20	1.16	3 (16%)

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
5	EPE	A	489	-	-	0/9/19/19	0/1/1/1
5	EPE	G	489	-	-	0/9/19/19	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	489	EPE	C2-N1	2.05	1.52	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	489	EPE	C6-N1	2.51	1.53	1.46

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	G	489	EPE	O1S-S-C10	-2.17	105.05	106.91
5	A	489	EPE	C7-N4-C5	-2.16	105.73	111.27
5	G	489	EPE	C7-N4-C5	-2.11	105.85	111.27
5	G	489	EPE	O2S-S-C10	-2.10	105.11	106.91

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	452/475 (95%)	-0.00	14 (3%) 52 52	22, 43, 88, 101	0
1	C	448/475 (94%)	-0.08	8 (1%) 71 72	25, 43, 80, 101	0
1	E	445/475 (93%)	0.09	13 (2%) 55 55	27, 51, 88, 101	0
1	G	448/475 (94%)	-0.00	9 (2%) 68 69	29, 49, 86, 101	0
2	B	439/443 (99%)	-0.11	1 (0%) 95 96	22, 43, 76, 101	0
2	D	443/443 (100%)	-0.04	4 (0%) 85 86	27, 52, 84, 101	0
2	F	443/443 (100%)	0.18	17 (3%) 44 44	33, 68, 98, 101	0
2	H	441/443 (99%)	0.81	68 (15%) 3 2	43, 91, 101, 101	0
3	O	13/24 (54%)	2.71	8 (61%) 0 0	52, 95, 101, 101	0
3	P	9/24 (37%)	1.41	2 (22%) 1 1	61, 77, 99, 101	0
3	Q	10/24 (41%)	2.02	3 (30%) 1 0	64, 101, 101, 101	0
3	R	7/24 (29%)	0.89	1 (14%) 4 3	89, 96, 101, 101	0
All	All	3598/3768 (95%)	0.13	148 (4%) 41 41	22, 53, 100, 101	0

All (148) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	250	PHE	7.2
3	Q	11	PHE	7.1
3	O	11	PHE	6.5
1	G	250	PHE	6.4
3	O	8	ILE	6.0
3	O	7	SER	6.0
2	D	20	ALA	5.9
1	C	252	ASN	5.9
1	E	14	ALA	5.7
1	E	249	VAL	5.5
3	Q	10	PHE	5.5

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Mol	Chain	Res	Type	RSRZ
1	C	250	PHE	5.4
3	P	11	PHE	5.3
2	H	171	TYR	5.3
2	H	456	ILE	5.2
1	E	252	ASN	5.2
2	H	198	TYR	5.2
1	E	311	TYR	5.2
2	D	21	SER	5.1
1	A	14	ALA	5.0
1	G	311	TYR	5.0
2	H	443	ALA	5.0
2	H	258	ILE	5.0
1	G	252	ASN	4.9
1	A	252	ASN	4.9
1	A	250	PHE	4.9
2	H	444	LEU	4.9
2	H	445	GLY	4.8
1	A	469	SER	4.7
2	H	64	LYS	4.6
2	H	176	LEU	4.5
2	F	21	SER	4.5
1	A	311	TYR	4.5
2	F	190	ILE	4.4
1	E	253	LEU	4.1
2	H	245	ARG	3.9
1	A	253	LEU	3.8
2	H	195	LEU	3.8
1	G	469	SER	3.8
2	H	71	PHE	3.7
1	A	249	VAL	3.7
2	F	236	GLU	3.7
2	H	238	PRO	3.7
2	H	193	THR	3.7
1	A	470	SER	3.6
2	F	245	ARG	3.6
1	E	251	GLY	3.6
2	H	185	LYS	3.6
3	O	10	PHE	3.5
1	G	470	SER	3.5
2	B	245	ARG	3.5
2	H	69	ALA	3.4
2	D	88	ILE	3.3

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Mol	Chain	Res	Type	RSRZ
2	F	20	ALA	3.2
1	G	249	VAL	3.2
2	H	256	ARG	3.2
1	C	312	PHE	3.2
1	C	311	TYR	3.1
2	F	149	ARG	3.1
2	H	237	SER	3.1
2	H	173	ASP	3.1
2	H	149	ARG	3.1
2	H	161	VAL	3.0
2	F	235	SER	3.0
1	G	14	ALA	3.0
1	G	251	GLY	3.0
2	H	184	ILE	2.9
1	E	312	PHE	2.9
1	C	249	VAL	2.9
3	O	9	ARG	2.9
2	H	145	ASP	2.9
2	H	86	GLN	2.8
1	E	298	MET	2.8
2	H	269	ALA	2.8
2	F	229	PHE	2.8
2	H	342	THR	2.8
2	H	352	ILE	2.8
2	H	158	TYR	2.8
3	R	13	PRO	2.8
2	D	197	ASP	2.8
1	A	296	LYS	2.7
2	H	187	ILE	2.7
1	A	251	GLY	2.7
2	H	335	LEU	2.7
2	H	180	ILE	2.7
2	H	235	SER	2.7
2	H	166	LEU	2.7
1	E	248	PRO	2.6
3	O	13	PRO	2.6
2	H	110	TYR	2.5
3	P	10	PHE	2.5
3	O	12	LYS	2.5
2	F	137	ASN	2.5
2	H	199	ILE	2.5
2	H	203	TYR	2.5

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Mol	Chain	Res	Type	RSRZ
2	H	319	LEU	2.5
2	F	198	TYR	2.5
2	H	247	PRO	2.5
1	C	251	GLY	2.5
2	H	208	MET	2.5
3	Q	13	PRO	2.4
2	H	135	LEU	2.4
3	O	17	THR	2.4
1	A	358	LYS	2.4
2	H	165	HIS	2.4
2	H	152	GLU	2.4
2	H	75	LEU	2.4
2	H	130	LEU	2.4
2	H	192	ARG	2.4
2	F	81	GLN	2.4
2	H	251	PHE	2.4
2	H	54	VAL	2.3
1	C	253	LEU	2.3
1	C	295	GLY	2.3
2	H	271	ALA	2.3
2	H	190	ILE	2.3
1	A	254	PRO	2.3
2	F	140	ILE	2.3
1	A	293	GLY	2.3
2	F	238	PRO	2.3
2	H	257	PHE	2.3
1	A	468	SER	2.2
2	H	354	ASN	2.2
2	H	441	MET	2.2
1	E	15	ARG	2.2
2	F	187	ILE	2.2
2	H	339	TYR	2.2
2	H	460	LEU	2.2
2	H	156	LYS	2.2
2	H	239	VAL	2.2
2	F	239	VAL	2.2
2	H	446	ASN	2.2
2	F	37	ILE	2.1
2	H	236	GLU	2.1
2	H	154	VAL	2.1
2	H	229	PHE	2.1
2	H	68	THR	2.1

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Mol	Chain	Res	Type	RSRZ
2	H	351	LEU	2.1
2	H	172	LYS	2.1
1	G	15	ARG	2.1
2	H	153	GLU	2.1
1	E	358	LYS	2.1
2	H	350	ARG	2.1
2	F	203	TYR	2.1
2	H	253	ARG	2.0
2	H	442	VAL	2.0
1	E	254	PRO	2.0
2	H	240	PRO	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
5	EPE	G	489	15/15	0.88	0.33	9.45	87,87,87,87	0
5	EPE	A	489	15/15	0.91	0.23	3.16	81,81,81,81	0
4	ZN	B	501	1/1	0.91	0.07	-2.18	72,72,72,72	0
4	ZN	D	502	1/1	0.95	0.07	-2.50	91,91,91,91	0
4	ZN	H	504	1/1	0.96	0.07	-2.78	101,101,101,101	0
4	ZN	F	503	1/1	0.93	0.08	-2.89	101,101,101,101	0

6.5 Other polymers [i](#)

There are no such residues in this entry.