



# Full wwPDB/EMDatabank EM Map/Model Validation Report ⓘ

Mar 2, 2017 – 11:21 am GMT

PDB ID : 3FOI  
EMDB ID: : EMD-1086  
Title : Fitting of gp18M crystal structure into 3D cryo-EM reconstruction of bacteriophage T4 contracted tail  
Authors : Aksyuk, A.A.; Leiman, P.G.; Kurochkina, L.P.; Shneider, M.M.; Kostyuchenko, V.A.; Mesyanzhinov, V.V.; Rossmann, M.G.  
Deposited on : 2008-12-30  
Resolution : 16.00 Å(reported)  
Based on PDB ID : 3FOA

This is a Full wwPDB/EMDatabank EM Map/Model Validation Report  
for a publicly released PDB/EMDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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MolProbity : 4.02b-467  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc29047

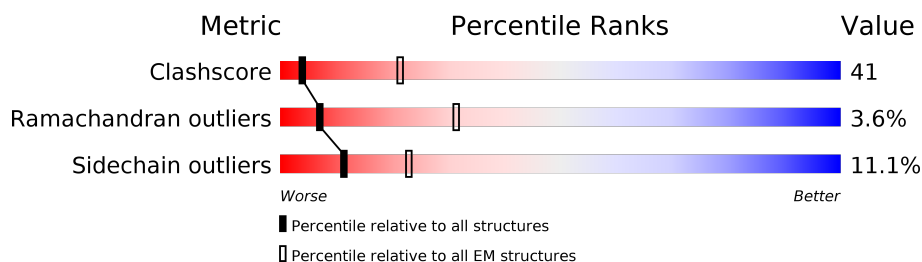
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 16.00 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)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	510	
1	B	510	
1	C	510	
1	D	510	
1	E	510	
1	F	510	

## 2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 21678 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 Tail sheath protein Gp18.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	479	Total	C	N	O	S	0	0
			3613	2279	600	726	8		
1	B	479	Total	C	N	O	S	0	0
			3613	2279	600	726	8		
1	C	479	Total	C	N	O	S	0	0
			3613	2279	600	726	8		
1	D	479	Total	C	N	O	S	0	0
			3613	2279	600	726	8		
1	E	479	Total	C	N	O	S	0	0
			3613	2279	600	726	8		
1	F	479	Total	C	N	O	S	0	0
			3613	2279	600	726	8		

There are 48 discrepancies between the modelled and reference sequences:

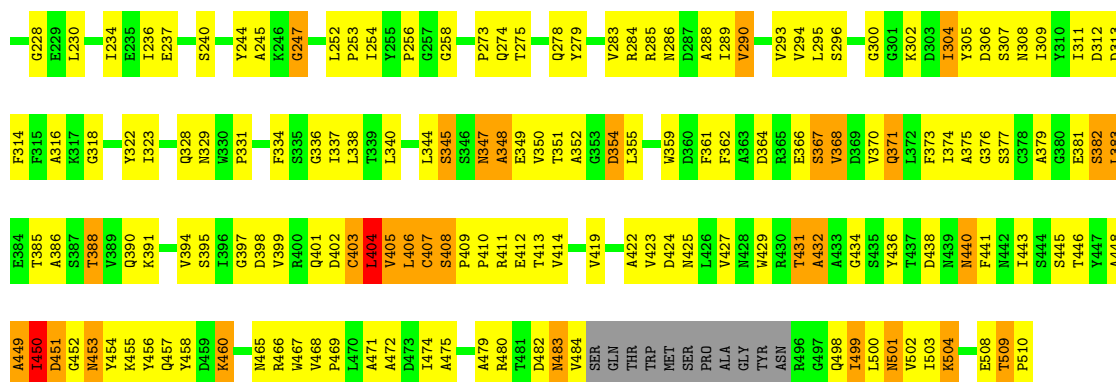
Chain	Residue	Modelled	Actual	Comment	Reference
A	100	GLU	ASP	SEE REMARK 999	UNP P13332
A	148	ALA	GLY	SEE REMARK 999	UNP P13332
A	150	ILE	ASN	SEE REMARK 999	UNP P13332
A	151	ILE	TYR	SEE REMARK 999	UNP P13332
A	301	GLY	GLU	SEE REMARK 999	UNP P13332
A	399	VAL	ALA	SEE REMARK 999	UNP P13332
A	454	TYR	HIS	SEE REMARK 999	UNP P13332
A	510	PRO	ARG	ENGINEERED	UNP P13332
B	100	GLU	ASP	SEE REMARK 999	UNP P13332
B	148	ALA	GLY	SEE REMARK 999	UNP P13332
B	150	ILE	ASN	SEE REMARK 999	UNP P13332
B	151	ILE	TYR	SEE REMARK 999	UNP P13332
B	301	GLY	GLU	SEE REMARK 999	UNP P13332
B	399	VAL	ALA	SEE REMARK 999	UNP P13332
B	454	TYR	HIS	SEE REMARK 999	UNP P13332
B	510	PRO	ARG	ENGINEERED	UNP P13332
C	100	GLU	ASP	SEE REMARK 999	UNP P13332
C	148	ALA	GLY	SEE REMARK 999	UNP P13332

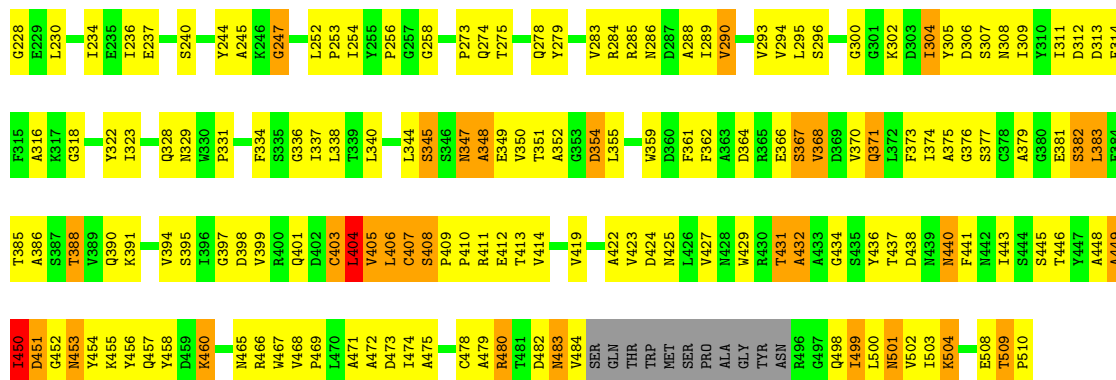
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Chain	Residue	Modelled	Actual	Comment	Reference
C	150	ILE	ASN	SEE REMARK 999	UNP P13332
C	151	ILE	TYR	SEE REMARK 999	UNP P13332
C	301	GLY	GLU	SEE REMARK 999	UNP P13332
C	399	VAL	ALA	SEE REMARK 999	UNP P13332
C	454	TYR	HIS	SEE REMARK 999	UNP P13332
C	510	PRO	ARG	ENGINEERED	UNP P13332
D	100	GLU	ASP	SEE REMARK 999	UNP P13332
D	148	ALA	GLY	SEE REMARK 999	UNP P13332
D	150	ILE	ASN	SEE REMARK 999	UNP P13332
D	151	ILE	TYR	SEE REMARK 999	UNP P13332
D	301	GLY	GLU	SEE REMARK 999	UNP P13332
D	399	VAL	ALA	SEE REMARK 999	UNP P13332
D	454	TYR	HIS	SEE REMARK 999	UNP P13332
D	510	PRO	ARG	ENGINEERED	UNP P13332
E	100	GLU	ASP	SEE REMARK 999	UNP P13332
E	148	ALA	GLY	SEE REMARK 999	UNP P13332
E	150	ILE	ASN	SEE REMARK 999	UNP P13332
E	151	ILE	TYR	SEE REMARK 999	UNP P13332
E	301	GLY	GLU	SEE REMARK 999	UNP P13332
E	399	VAL	ALA	SEE REMARK 999	UNP P13332
E	454	TYR	HIS	SEE REMARK 999	UNP P13332
E	510	PRO	ARG	ENGINEERED	UNP P13332
F	100	GLU	ASP	SEE REMARK 999	UNP P13332
F	148	ALA	GLY	SEE REMARK 999	UNP P13332
F	150	ILE	ASN	SEE REMARK 999	UNP P13332
F	151	ILE	TYR	SEE REMARK 999	UNP P13332
F	301	GLY	GLU	SEE REMARK 999	UNP P13332
F	399	VAL	ALA	SEE REMARK 999	UNP P13332
F	454	TYR	HIS	SEE REMARK 999	UNP P13332
F	510	PRO	ARG	ENGINEERED	UNP P13332

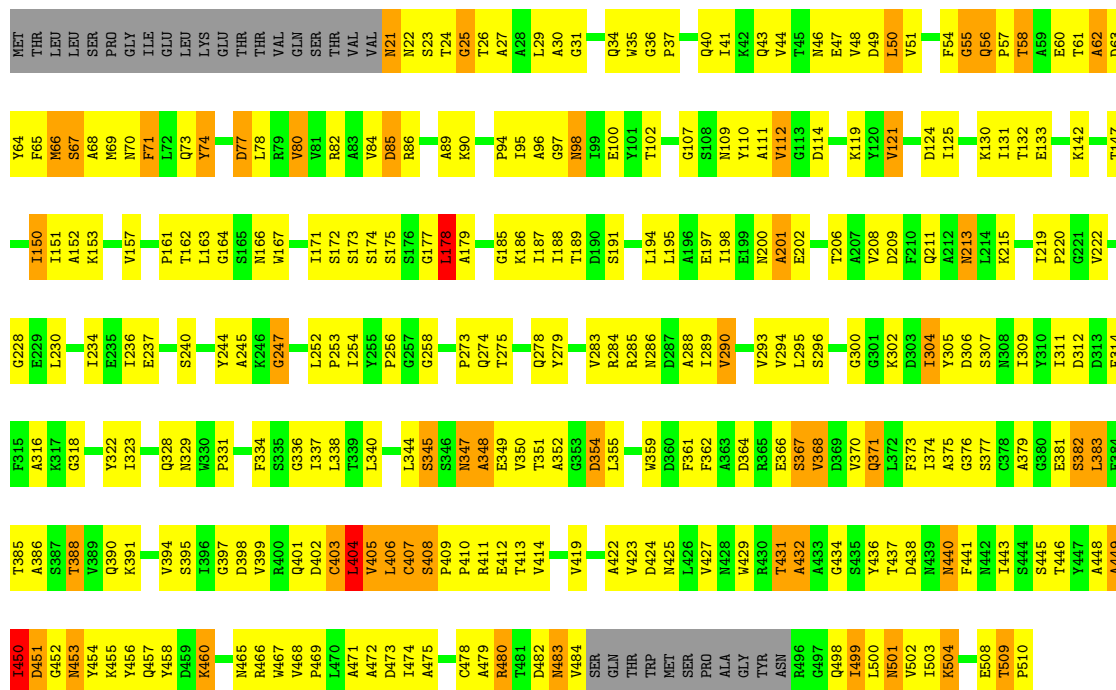






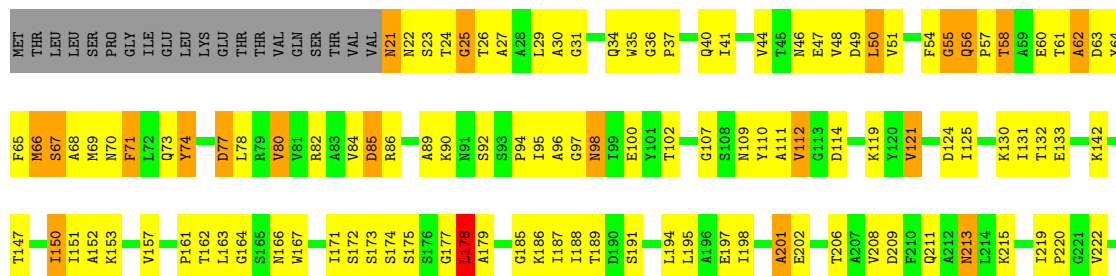
• Molecule 1: Tail sheath protein Gp18

Chain E: 40% 44% 10% 6%



• Molecule 1: Tail sheath protein Gp18

Chain F: 40% 43% 10% 6%



I450	D451	C452	N453	I454	K455	Y456	Q457	Y458	D459	K460	N465	R466	W467	V468	P469	I470	A471	A472	D473	I474	A475	C478	A479	R480	T481	D482	N483	V484	SER	GLN	THR	TRP	MET	SER	PRO	PRO	ALA	ALA	GLY	TYR	ASN	R496	G497	Q498	I499	L500	N501	V502	I503	K504	E508	T509	P510		
E384	T385	A386	S387	T388	V389	Q390	K391	V394	S395	S396	G397	D398	V399	R400	Q401	D402	C403	L404	V405	L406	C407	S408	P409	P410	R411	E412	T413	V414	V419	A422	N425	L426	V427	R428	W429	R430	T431	A432	A433	G434	S435	Y436	T437	D438	N439	N440	F441	N442	I443	S444	S445	T446	Y447	A448	A449
F315	A316	K317	G318	Y322	Y323	Q328	N329	W330	P331	F334	S335	G336	I337	L338	T339	L340	G343	L344	S345	S346	N347	A348	E349	V350	T351	A352	G353	D354	L355	W359	D360	F361	F362	A363	D364	R365	E366	S367	V368	D369	V370	Q371	L372	D373	F374	I375	G376	S377	C378	A379	V310	G380	E381	S382	L383
G228	E229	L230	I234	E235	I236	E237	S240	Y244	A245	K246	G247	L252	P253	I254	T255	P256	G257	G258	P273	Q274	T275	Q278	Y279	V283	R284	R285	N286	D287	A288	I289	V293	V294	L295	S296	G300	G301	K302	D303	I304	Y305	D306	S307	N308	I309	V310	I311	D312	D313	F314						



## 4 Experimental information

Property	Value	Source
Reconstruction method	Not provided	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images used	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	Not provided	Depositor
Microscope	Not provided	Depositor
Voltage (kV)	Not provided	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	Not provided	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	Not provided	Depositor

## 5 Model quality

### 5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 2$	RMSZ	$\# Z  > 2$
1	A	0.35	0/3677	0.78	21/5001 (0.4%)
1	B	0.35	0/3677	0.78	21/5001 (0.4%)
1	C	0.35	0/3677	0.78	21/5001 (0.4%)
1	D	0.35	0/3677	0.78	21/5001 (0.4%)
1	E	0.35	0/3677	0.78	21/5001 (0.4%)
1	F	0.35	0/3677	0.78	21/5001 (0.4%)
All	All	0.35	0/22062	0.78	126/30006 (0.4%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	4
1	B	0	4
1	C	0	4
1	D	0	4
1	E	0	4
1	F	0	4
All	All	0	24

There are no bond length outliers.

All (126) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	55	GLY	N-CA-C	18.03	158.17	113.10
1	A	55	GLY	N-CA-C	18.00	158.10	113.10
1	C	55	GLY	N-CA-C	18.00	158.10	113.10
1	D	55	GLY	N-CA-C	17.99	158.08	113.10
1	B	55	GLY	N-CA-C	17.99	158.07	113.10
1	F	55	GLY	N-CA-C	17.99	158.07	113.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	56	GLN	N-CA-CB	-11.37	90.13	110.60
1	B	56	GLN	N-CA-CB	-11.36	90.15	110.60
1	E	56	GLN	N-CA-CB	-11.36	90.15	110.60
1	A	56	GLN	N-CA-CB	-11.35	90.17	110.60
1	C	56	GLN	N-CA-CB	-11.35	90.17	110.60
1	F	56	GLN	N-CA-CB	-11.34	90.19	110.60
1	D	367	SER	N-CA-CB	-10.66	94.52	110.50
1	C	367	SER	N-CA-CB	-10.65	94.53	110.50
1	B	367	SER	N-CA-CB	-10.64	94.54	110.50
1	A	367	SER	N-CA-CB	-10.62	94.57	110.50
1	E	367	SER	N-CA-CB	-10.62	94.57	110.50
1	F	367	SER	N-CA-CB	-10.61	94.58	110.50
1	C	405	VAL	N-CA-C	-9.60	85.07	111.00
1	D	405	VAL	N-CA-C	-9.60	85.08	111.00
1	B	405	VAL	N-CA-C	-9.59	85.10	111.00
1	A	405	VAL	N-CA-C	-9.59	85.11	111.00
1	C	111	ALA	CB-CA-C	9.59	124.48	110.10
1	E	405	VAL	N-CA-C	-9.59	85.12	111.00
1	F	405	VAL	N-CA-C	-9.59	85.12	111.00
1	D	111	ALA	CB-CA-C	9.58	124.47	110.10
1	E	111	ALA	CB-CA-C	9.56	124.44	110.10
1	B	111	ALA	CB-CA-C	9.55	124.42	110.10
1	F	111	ALA	CB-CA-C	9.53	124.40	110.10
1	A	111	ALA	CB-CA-C	9.53	124.39	110.10
1	F	407	CYS	CB-CA-C	-9.52	91.37	110.40
1	A	112	VAL	N-CA-C	9.51	136.68	111.00
1	B	112	VAL	N-CA-C	9.50	136.66	111.00
1	D	112	VAL	N-CA-C	9.50	136.66	111.00
1	D	407	CYS	CB-CA-C	-9.50	91.39	110.40
1	B	407	CYS	CB-CA-C	-9.50	91.40	110.40
1	F	112	VAL	N-CA-C	9.50	136.64	111.00
1	E	112	VAL	N-CA-C	9.49	136.63	111.00
1	A	407	CYS	CB-CA-C	-9.49	91.42	110.40
1	C	112	VAL	N-CA-C	9.49	136.62	111.00
1	C	407	CYS	CB-CA-C	-9.48	91.43	110.40
1	E	407	CYS	CB-CA-C	-9.48	91.44	110.40
1	B	408	SER	N-CA-CB	-8.88	97.19	110.50
1	E	408	SER	N-CA-CB	-8.88	97.19	110.50
1	D	408	SER	N-CA-CB	-8.86	97.20	110.50
1	F	408	SER	N-CA-CB	-8.86	97.21	110.50
1	C	408	SER	N-CA-CB	-8.86	97.22	110.50
1	A	408	SER	N-CA-CB	-8.85	97.23	110.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	112	VAL	CB-CA-C	-7.62	96.93	111.40
1	A	112	VAL	CB-CA-C	-7.62	96.93	111.40
1	B	112	VAL	CB-CA-C	-7.60	96.95	111.40
1	C	112	VAL	CB-CA-C	-7.60	96.96	111.40
1	D	112	VAL	CB-CA-C	-7.60	96.97	111.40
1	E	112	VAL	CB-CA-C	-7.59	96.98	111.40
1	C	404	LEU	N-CA-C	-7.54	90.65	111.00
1	E	404	LEU	N-CA-C	-7.53	90.66	111.00
1	A	404	LEU	N-CA-C	-7.53	90.67	111.00
1	B	404	LEU	N-CA-C	-7.53	90.67	111.00
1	D	404	LEU	N-CA-C	-7.52	90.71	111.00
1	F	404	LEU	N-CA-C	-7.51	90.72	111.00
1	C	366	GLU	CB-CA-C	7.43	125.25	110.40
1	B	366	GLU	CB-CA-C	7.42	125.25	110.40
1	A	366	GLU	CB-CA-C	7.42	125.24	110.40
1	F	366	GLU	CB-CA-C	7.42	125.23	110.40
1	E	366	GLU	CB-CA-C	7.41	125.23	110.40
1	D	366	GLU	CB-CA-C	7.41	125.21	110.40
1	C	404	LEU	CB-CA-C	6.85	123.21	110.20
1	E	404	LEU	CB-CA-C	6.84	123.20	110.20
1	D	404	LEU	CB-CA-C	6.84	123.19	110.20
1	B	404	LEU	CB-CA-C	6.83	123.19	110.20
1	F	404	LEU	CB-CA-C	6.83	123.18	110.20
1	A	404	LEU	CB-CA-C	6.83	123.17	110.20
1	B	449	ALA	CB-CA-C	6.76	120.23	110.10
1	A	449	ALA	CB-CA-C	6.73	120.19	110.10
1	E	449	ALA	CB-CA-C	6.72	120.19	110.10
1	F	449	ALA	CB-CA-C	6.72	120.18	110.10
1	D	449	ALA	CB-CA-C	6.70	120.15	110.10
1	C	449	ALA	CB-CA-C	6.70	120.14	110.10
1	C	85	ASP	N-CA-C	-6.55	93.33	111.00
1	D	85	ASP	N-CA-C	-6.54	93.34	111.00
1	E	85	ASP	N-CA-C	-6.54	93.35	111.00
1	A	85	ASP	N-CA-C	-6.53	93.36	111.00
1	F	85	ASP	N-CA-C	-6.53	93.36	111.00
1	B	85	ASP	N-CA-C	-6.53	93.37	111.00
1	A	406	LEU	CB-CA-C	6.17	121.93	110.20
1	F	406	LEU	CB-CA-C	6.17	121.93	110.20
1	B	406	LEU	CB-CA-C	6.17	121.93	110.20
1	C	406	LEU	CB-CA-C	6.17	121.93	110.20
1	D	406	LEU	CB-CA-C	6.17	121.92	110.20
1	E	406	LEU	CB-CA-C	6.16	121.91	110.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	85	ASP	CB-CA-C	5.73	121.86	110.40
1	B	85	ASP	CB-CA-C	5.72	121.85	110.40
1	D	85	ASP	CB-CA-C	5.72	121.84	110.40
1	E	85	ASP	CB-CA-C	5.71	121.83	110.40
1	C	85	ASP	CB-CA-C	5.71	121.83	110.40
1	A	85	ASP	CB-CA-C	5.70	121.80	110.40
1	F	406	LEU	N-CA-C	-5.37	96.51	111.00
1	A	406	LEU	N-CA-C	-5.37	96.51	111.00
1	B	406	LEU	N-CA-C	-5.37	96.51	111.00
1	E	406	LEU	N-CA-C	-5.37	96.52	111.00
1	C	406	LEU	N-CA-C	-5.35	96.55	111.00
1	D	406	LEU	N-CA-C	-5.34	96.58	111.00
1	C	179	ALA	N-CA-C	5.25	125.18	111.00
1	E	179	ALA	N-CA-C	5.25	125.17	111.00
1	F	179	ALA	N-CA-C	5.24	125.16	111.00
1	D	179	ALA	N-CA-C	5.24	125.15	111.00
1	B	179	ALA	N-CA-C	5.24	125.15	111.00
1	A	179	ALA	N-CA-C	5.23	125.13	111.00
1	E	178	LEU	N-CA-CB	-5.19	100.03	110.40
1	F	178	LEU	N-CA-CB	-5.18	100.04	110.40
1	A	178	LEU	N-CA-CB	-5.18	100.04	110.40
1	B	178	LEU	N-CA-CB	-5.17	100.06	110.40
1	C	178	LEU	N-CA-CB	-5.17	100.06	110.40
1	D	178	LEU	N-CA-CB	-5.16	100.08	110.40
1	E	21	ASN	C-N-CA	5.07	134.36	121.70
1	C	21	ASN	C-N-CA	5.06	134.36	121.70
1	F	449	ALA	N-CA-C	-5.06	97.33	111.00
1	A	21	ASN	C-N-CA	5.05	134.31	121.70
1	C	449	ALA	N-CA-C	-5.05	97.37	111.00
1	A	449	ALA	N-CA-C	-5.04	97.38	111.00
1	B	21	ASN	C-N-CA	5.04	134.30	121.70
1	B	449	ALA	N-CA-C	-5.04	97.39	111.00
1	E	449	ALA	N-CA-C	-5.04	97.39	111.00
1	F	21	ASN	C-N-CA	5.04	134.30	121.70
1	D	21	ASN	C-N-CA	5.04	134.30	121.70
1	D	449	ALA	N-CA-C	-5.04	97.40	111.00

There are no chirality outliers.

All (24) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	21	ASN	Peptide

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Mol	Chain	Res	Type	Group
1	A	450	ILE	Peptide
1	A	451	ASP	Peptide
1	A	452	GLY	Peptide
1	B	21	ASN	Peptide
1	B	450	ILE	Peptide
1	B	451	ASP	Peptide
1	B	452	GLY	Peptide
1	C	21	ASN	Peptide
1	C	450	ILE	Peptide
1	C	451	ASP	Peptide
1	C	452	GLY	Peptide
1	D	21	ASN	Peptide
1	D	450	ILE	Peptide
1	D	451	ASP	Peptide
1	D	452	GLY	Peptide
1	E	21	ASN	Peptide
1	E	450	ILE	Peptide
1	E	451	ASP	Peptide
1	E	452	GLY	Peptide
1	F	21	ASN	Peptide
1	F	450	ILE	Peptide
1	F	451	ASP	Peptide
1	F	452	GLY	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	3613	0	3554	294	0
1	B	3613	0	3554	297	0
1	C	3613	0	3554	297	0
1	D	3613	0	3554	295	0
1	E	3613	0	3554	296	0
1	F	3613	0	3554	296	0
All	All	21678	0	21324	1775	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 41.

All (1775) 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:409:PRO:O	1:A:454:TYR:CE1	1.65	1.49
1:B:409:PRO:O	1:B:454:TYR:CE1	1.65	1.49
1:F:409:PRO:O	1:F:454:TYR:CE1	1.65	1.49
1:C:409:PRO:O	1:C:454:TYR:CE1	1.65	1.48
1:D:409:PRO:O	1:D:454:TYR:CE1	1.65	1.47
1:E:409:PRO:O	1:E:454:TYR:CE1	1.65	1.47
1:C:409:PRO:CD	1:C:451:ASP:O	1.75	1.34
1:B:409:PRO:CD	1:B:451:ASP:O	1.75	1.33
1:E:409:PRO:CD	1:E:451:ASP:O	1.75	1.33
1:F:409:PRO:CD	1:F:451:ASP:O	1.75	1.32
1:A:409:PRO:CD	1:A:451:ASP:O	1.75	1.32
1:D:409:PRO:CD	1:D:451:ASP:O	1.75	1.31
1:D:379:ALA:CB	1:D:454:TYR:OH	1.84	1.25
1:E:379:ALA:CB	1:E:454:TYR:OH	1.84	1.25
1:B:379:ALA:HB2	1:B:454:TYR:OH	1.37	1.25
1:B:379:ALA:CB	1:B:454:TYR:OH	1.84	1.25
1:C:379:ALA:CB	1:C:454:TYR:OH	1.84	1.24
1:A:379:ALA:CB	1:A:454:TYR:OH	1.84	1.24
1:F:379:ALA:CB	1:F:454:TYR:OH	1.84	1.24
1:A:379:ALA:HB2	1:A:454:TYR:OH	1.37	1.24
1:F:379:ALA:HB2	1:F:454:TYR:OH	1.37	1.21
1:E:379:ALA:HB2	1:E:454:TYR:OH	1.37	1.17
1:F:409:PRO:HD3	1:F:451:ASP:O	0.99	1.17
1:D:409:PRO:HD3	1:D:451:ASP:O	0.98	1.16
1:C:409:PRO:HD3	1:C:451:ASP:O	0.99	1.16
1:D:379:ALA:HB2	1:D:454:TYR:OH	1.37	1.16
1:A:409:PRO:HD3	1:A:451:ASP:O	0.98	1.15
1:C:379:ALA:HB2	1:C:454:TYR:OH	1.37	1.14
1:E:409:PRO:HD3	1:E:451:ASP:O	0.99	1.14
1:D:379:ALA:HB1	1:D:454:TYR:CZ	1.83	1.14
1:C:379:ALA:HB1	1:C:454:TYR:CZ	1.83	1.13
1:B:409:PRO:HD3	1:B:451:ASP:O	0.98	1.13
1:B:379:ALA:HB1	1:B:454:TYR:CZ	1.83	1.13
1:E:379:ALA:HB1	1:E:454:TYR:CZ	1.83	1.13
1:D:454:TYR:CE2	1:D:469:PRO:HA	1.84	1.12
1:A:379:ALA:HB1	1:A:454:TYR:CZ	1.83	1.12
1:C:454:TYR:CE2	1:C:469:PRO:HA	1.84	1.12
1:F:379:ALA:HB1	1:F:454:TYR:CZ	1.83	1.12
1:E:454:TYR:CE2	1:E:469:PRO:HA	1.84	1.11
1:F:454:TYR:CE2	1:F:469:PRO:HA	1.84	1.11

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:454:TYR:CE2	1:A:469:PRO:HA	1.84	1.11
1:B:454:TYR:CE2	1:B:469:PRO:HA	1.84	1.11
1:E:450:ILE:HG12	1:E:451:ASP:H	0.94	1.11
1:D:450:ILE:HG12	1:D:451:ASP:H	0.94	1.11
1:C:450:ILE:HG12	1:C:451:ASP:H	0.94	1.10
1:F:450:ILE:HG12	1:F:451:ASP:H	0.94	1.10
1:B:379:ALA:CB	1:B:454:TYR:CZ	2.35	1.09
1:D:379:ALA:CB	1:D:454:TYR:CZ	2.35	1.09
1:C:379:ALA:CB	1:C:454:TYR:CZ	2.35	1.09
1:E:379:ALA:CB	1:E:454:TYR:CZ	2.35	1.09
1:B:450:ILE:HG12	1:B:451:ASP:H	0.94	1.09
1:A:450:ILE:HG12	1:A:451:ASP:H	0.94	1.09
1:E:409:PRO:O	1:E:454:TYR:CZ	2.06	1.08
1:D:409:PRO:O	1:D:454:TYR:CZ	2.06	1.08
1:A:409:PRO:O	1:A:454:TYR:CZ	2.06	1.08
1:C:409:PRO:O	1:C:454:TYR:CZ	2.06	1.08
1:A:454:TYR:CD2	1:A:469:PRO:HA	1.89	1.07
1:D:51:VAL:HA	1:D:55:GLY:HA2	1.36	1.07
1:F:379:ALA:CB	1:F:454:TYR:CZ	2.35	1.07
1:F:454:TYR:CD2	1:F:469:PRO:HA	1.89	1.07
1:B:409:PRO:O	1:B:454:TYR:CZ	2.06	1.07
1:D:454:TYR:CD2	1:D:469:PRO:HA	1.89	1.07
1:C:454:TYR:CD2	1:C:469:PRO:HA	1.89	1.07
1:B:454:TYR:CD2	1:B:469:PRO:HA	1.89	1.07
1:E:51:VAL:HA	1:E:55:GLY:HA2	1.36	1.07
1:F:51:VAL:HA	1:F:55:GLY:HA2	1.36	1.07
1:F:409:PRO:O	1:F:454:TYR:CZ	2.06	1.06
1:A:51:VAL:HA	1:A:55:GLY:HA2	1.36	1.06
1:A:379:ALA:CB	1:A:454:TYR:CZ	2.35	1.06
1:B:450:ILE:HG12	1:B:451:ASP:N	1.67	1.06
1:C:51:VAL:HA	1:C:55:GLY:HA2	1.36	1.06
1:E:454:TYR:CD2	1:E:469:PRO:HA	1.89	1.05
1:B:51:VAL:HA	1:B:55:GLY:HA2	1.36	1.05
1:C:450:ILE:HG12	1:C:451:ASP:N	1.67	1.05
1:A:450:ILE:HG12	1:A:451:ASP:N	1.67	1.05
1:F:450:ILE:HG12	1:F:451:ASP:N	1.67	1.03
1:D:450:ILE:HG12	1:D:451:ASP:N	1.67	1.02
1:E:450:ILE:HG12	1:E:451:ASP:N	1.67	0.99
1:A:228:GLY:HA2	1:A:345:SER:HB3	1.47	0.97
1:B:228:GLY:HA2	1:B:345:SER:HB3	1.47	0.97
1:E:409:PRO:O	1:E:454:TYR:HE1	1.16	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:228:GLY:HA2	1:E:345:SER:HB3	1.47	0.96
1:F:228:GLY:HA2	1:F:345:SER:HB3	1.47	0.96
1:C:228:GLY:HA2	1:C:345:SER:HB3	1.47	0.96
1:A:112:VAL:O	1:A:112:VAL:CG1	2.14	0.96
1:D:228:GLY:HA2	1:D:345:SER:HB3	1.47	0.96
1:D:409:PRO:O	1:D:454:TYR:HE1	1.16	0.95
1:B:112:VAL:O	1:B:112:VAL:CG1	2.14	0.95
1:D:112:VAL:O	1:D:112:VAL:CG1	2.14	0.95
1:F:112:VAL:CG1	1:F:112:VAL:O	2.14	0.94
1:C:112:VAL:O	1:C:112:VAL:CG1	2.14	0.94
1:E:112:VAL:O	1:E:112:VAL:CG1	2.14	0.93
1:C:409:PRO:O	1:C:454:TYR:HE1	1.16	0.91
1:E:408:SER:CA	1:E:451:ASP:HB3	2.00	0.91
1:F:409:PRO:O	1:F:454:TYR:HE1	1.15	0.91
1:F:408:SER:CA	1:F:451:ASP:HB3	2.00	0.91
1:C:23:SER:OG	1:C:483:ASN:CB	2.19	0.91
1:D:408:SER:CA	1:D:451:ASP:HB3	2.00	0.91
1:C:408:SER:CA	1:C:451:ASP:HB3	2.00	0.91
1:E:23:SER:OG	1:E:483:ASN:CB	2.19	0.91
1:A:408:SER:CA	1:A:451:ASP:HB3	2.00	0.91
1:A:23:SER:OG	1:A:483:ASN:CB	2.19	0.91
1:B:408:SER:CA	1:B:451:ASP:HB3	2.00	0.90
1:F:23:SER:OG	1:F:483:ASN:CB	2.19	0.90
1:B:23:SER:OG	1:B:483:ASN:CB	2.19	0.90
1:E:408:SER:HA	1:E:451:ASP:HB3	1.54	0.89
1:D:23:SER:OG	1:D:483:ASN:CB	2.19	0.89
1:D:408:SER:HA	1:D:451:ASP:HB3	1.54	0.89
1:B:409:PRO:O	1:B:454:TYR:HE1	1.16	0.88
1:F:408:SER:HA	1:F:451:ASP:HB3	1.54	0.88
1:B:408:SER:HA	1:B:451:ASP:HB3	1.54	0.88
1:A:409:PRO:O	1:A:454:TYR:HE1	1.16	0.88
1:E:508:GLU:HG2	1:E:509:THR:HG22	1.55	0.88
1:D:23:SER:CB	1:D:483:ASN:HB3	2.04	0.88
1:E:23:SER:CB	1:E:483:ASN:HB3	2.04	0.88
1:C:408:SER:HA	1:C:451:ASP:HB3	1.54	0.88
1:A:23:SER:CB	1:A:483:ASN:HB3	2.04	0.87
1:A:508:GLU:HG2	1:A:509:THR:HG22	1.55	0.87
1:C:23:SER:CB	1:C:483:ASN:HB3	2.04	0.87
1:D:41:ILE:HD11	1:D:361:PHE:HB3	1.57	0.87
1:B:23:SER:CB	1:B:483:ASN:HB3	2.04	0.87
1:A:41:ILE:HD11	1:A:361:PHE:HB3	1.57	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:408:SER:HA	1:A:451:ASP:HB3	1.54	0.87
1:C:41:ILE:HD11	1:C:361:PHE:HB3	1.57	0.87
1:E:41:ILE:HD11	1:E:361:PHE:HB3	1.57	0.87
1:F:41:ILE:HD11	1:F:361:PHE:HB3	1.57	0.87
1:F:23:SER:CB	1:F:483:ASN:HB3	2.04	0.87
1:F:509:THR:OG1	1:F:510:PRO:OXT	1.93	0.87
1:C:391:LYS:NZ	1:C:440:ASN:ND2	2.23	0.86
1:D:508:GLU:HG2	1:D:509:THR:HG22	1.55	0.86
1:B:41:ILE:HD11	1:B:361:PHE:HB3	1.57	0.86
1:B:391:LYS:HE3	1:B:440:ASN:O	1.76	0.86
1:E:509:THR:OG1	1:E:510:PRO:OXT	1.93	0.86
1:C:508:GLU:HG2	1:C:509:THR:HG22	1.55	0.86
1:D:391:LYS:NZ	1:D:440:ASN:ND2	2.23	0.86
1:F:508:GLU:HG2	1:F:509:THR:HG22	1.55	0.86
1:B:508:GLU:HG2	1:B:509:THR:HG22	1.55	0.86
1:A:391:LYS:HE3	1:A:440:ASN:O	1.76	0.86
1:B:391:LYS:NZ	1:B:440:ASN:ND2	2.23	0.86
1:E:391:LYS:HE3	1:E:440:ASN:O	1.75	0.86
1:D:391:LYS:HE3	1:D:440:ASN:O	1.75	0.85
1:F:391:LYS:HE3	1:F:440:ASN:O	1.76	0.85
1:F:391:LYS:NZ	1:F:440:ASN:ND2	2.23	0.85
1:B:509:THR:OG1	1:B:510:PRO:OXT	1.93	0.85
1:E:391:LYS:NZ	1:E:440:ASN:ND2	2.23	0.85
1:A:509:THR:OG1	1:A:510:PRO:OXT	1.93	0.85
1:C:23:SER:OG	1:C:483:ASN:HB3	1.76	0.85
1:C:23:SER:CB	1:C:483:ASN:CB	2.55	0.85
1:A:391:LYS:NZ	1:A:440:ASN:ND2	2.23	0.85
1:C:509:THR:OG1	1:C:510:PRO:OXT	1.93	0.85
1:D:23:SER:CB	1:D:483:ASN:CB	2.55	0.85
1:D:509:THR:OG1	1:D:510:PRO:OXT	1.93	0.84
1:B:23:SER:CB	1:B:483:ASN:CB	2.55	0.84
1:D:23:SER:OG	1:D:483:ASN:HB3	1.76	0.84
1:E:23:SER:CB	1:E:483:ASN:CB	2.55	0.84
1:C:391:LYS:HE3	1:C:440:ASN:O	1.76	0.84
1:C:454:TYR:HE2	1:C:469:PRO:HA	1.43	0.84
1:F:23:SER:OG	1:F:483:ASN:HB3	1.76	0.84
1:B:454:TYR:HE2	1:B:469:PRO:HA	1.43	0.84
1:B:23:SER:OG	1:B:483:ASN:HB3	1.76	0.83
1:A:23:SER:OG	1:A:483:ASN:HB3	1.76	0.83
1:E:331:PRO:HB2	1:E:334:PHE:HB2	1.60	0.83
1:F:23:SER:CB	1:F:483:ASN:CB	2.55	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:23:SER:CB	1:A:483:ASN:CB	2.55	0.83
1:E:23:SER:OG	1:E:483:ASN:HB3	1.76	0.83
1:F:94:PRO:HB2	1:F:219:ILE:HD12	1.60	0.83
1:D:454:TYR:HE2	1:D:469:PRO:HA	1.43	0.83
1:D:331:PRO:HB2	1:D:334:PHE:HB2	1.60	0.83
1:B:94:PRO:HB2	1:B:219:ILE:HD12	1.61	0.83
1:C:94:PRO:HB2	1:C:219:ILE:HD12	1.61	0.83
1:E:94:PRO:HB2	1:E:219:ILE:HD12	1.61	0.82
1:F:331:PRO:HB2	1:F:334:PHE:HB2	1.60	0.82
1:D:94:PRO:HB2	1:D:219:ILE:HD12	1.61	0.82
1:C:379:ALA:HB2	1:C:454:TYR:CZ	2.11	0.82
1:B:110:TYR:CE1	1:B:178:LEU:O	2.33	0.82
1:A:110:TYR:CE1	1:A:178:LEU:O	2.33	0.81
1:C:110:TYR:CE1	1:C:178:LEU:O	2.33	0.81
1:C:331:PRO:HB2	1:C:334:PHE:HB2	1.60	0.81
1:D:110:TYR:CE1	1:D:178:LEU:O	2.33	0.81
1:A:94:PRO:HB2	1:A:219:ILE:HD12	1.61	0.81
1:E:454:TYR:HE2	1:E:469:PRO:HA	1.43	0.81
1:A:331:PRO:HB2	1:A:334:PHE:HB2	1.60	0.81
1:F:454:TYR:HE2	1:F:469:PRO:HA	1.43	0.81
1:E:110:TYR:CE1	1:E:178:LEU:O	2.33	0.81
1:D:379:ALA:HB2	1:D:454:TYR:CZ	2.11	0.81
1:B:331:PRO:HB2	1:B:334:PHE:HB2	1.60	0.81
1:F:112:VAL:HG12	1:F:112:VAL:O	1.82	0.80
1:F:110:TYR:CE1	1:F:178:LEU:O	2.33	0.80
1:B:379:ALA:HB1	1:B:454:TYR:OH	1.73	0.80
1:E:112:VAL:O	1:E:112:VAL:HG12	1.82	0.80
1:D:112:VAL:O	1:D:112:VAL:HG12	1.82	0.80
1:C:23:SER:HB3	1:C:483:ASN:HB3	1.64	0.80
1:D:391:LYS:HZ3	1:D:440:ASN:HD21	1.31	0.80
1:A:112:VAL:O	1:A:112:VAL:HG12	1.82	0.79
1:C:112:VAL:O	1:C:112:VAL:HG12	1.82	0.79
1:E:379:ALA:HB2	1:E:454:TYR:CZ	2.11	0.79
1:E:178:LEU:H	1:E:178:LEU:HD23	1.48	0.79
1:B:391:LYS:HZ3	1:B:440:ASN:HD21	1.31	0.79
1:D:23:SER:HB3	1:D:483:ASN:HB3	1.64	0.79
1:A:479:ALA:HA	1:A:484:VAL:HG11	1.65	0.79
1:F:479:ALA:HA	1:F:484:VAL:HG11	1.65	0.79
1:A:391:LYS:HZ1	1:A:440:ASN:ND2	1.77	0.78
1:A:509:THR:OG1	1:A:510:PRO:CA	2.32	0.78
1:B:509:THR:OG1	1:B:510:PRO:CA	2.32	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:178:LEU:H	1:D:178:LEU:HD23	1.48	0.78
1:D:509:THR:OG1	1:D:510:PRO:CA	2.31	0.78
1:E:509:THR:OG1	1:E:510:PRO:CA	2.32	0.78
1:F:178:LEU:HD23	1:F:178:LEU:H	1.47	0.78
1:B:479:ALA:HA	1:B:484:VAL:HG11	1.65	0.78
1:E:23:SER:HB3	1:E:483:ASN:HB3	1.64	0.78
1:E:479:ALA:HA	1:E:484:VAL:HG11	1.65	0.78
1:D:450:ILE:CG1	1:D:451:ASP:H	1.89	0.78
1:E:391:LYS:HZ3	1:E:440:ASN:HD21	1.32	0.78
1:B:112:VAL:HG12	1:B:112:VAL:O	1.82	0.78
1:D:479:ALA:HA	1:D:484:VAL:HG11	1.65	0.78
1:F:509:THR:OG1	1:F:510:PRO:CA	2.32	0.78
1:D:407:CYS:O	1:D:451:ASP:CB	2.32	0.78
1:E:407:CYS:O	1:E:451:ASP:CB	2.32	0.77
1:B:23:SER:HB3	1:B:483:ASN:HB3	1.64	0.77
1:C:407:CYS:O	1:C:451:ASP:HB2	1.85	0.77
1:D:407:CYS:O	1:D:451:ASP:HB2	1.85	0.77
1:F:407:CYS:O	1:F:451:ASP:CB	2.32	0.77
1:C:479:ALA:HA	1:C:484:VAL:HG11	1.65	0.77
1:F:23:SER:HB3	1:F:483:ASN:HB3	1.64	0.77
1:C:509:THR:OG1	1:C:510:PRO:CA	2.31	0.77
1:C:407:CYS:O	1:C:451:ASP:CB	2.32	0.77
1:E:407:CYS:O	1:E:451:ASP:HB2	1.85	0.77
1:A:178:LEU:H	1:A:178:LEU:CD2	1.98	0.77
1:A:178:LEU:H	1:A:178:LEU:HD23	1.48	0.77
1:B:178:LEU:HD23	1:B:178:LEU:H	1.48	0.77
1:B:407:CYS:O	1:B:451:ASP:HB2	1.85	0.77
1:F:379:ALA:HB2	1:F:454:TYR:CZ	2.11	0.77
1:A:407:CYS:O	1:A:451:ASP:CB	2.32	0.77
1:E:84:VAL:HG13	1:E:85:ASP:O	1.85	0.77
1:A:171:ILE:HG22	1:A:172:SER:H	1.50	0.77
1:A:23:SER:HB3	1:A:483:ASN:HB3	1.64	0.77
1:A:407:CYS:O	1:A:451:ASP:HB2	1.84	0.77
1:C:178:LEU:H	1:C:178:LEU:HD23	1.48	0.76
1:E:178:LEU:H	1:E:178:LEU:CD2	1.98	0.76
1:E:454:TYR:CE2	1:E:469:PRO:CA	2.67	0.76
1:F:407:CYS:O	1:F:451:ASP:HB2	1.85	0.76
1:D:451:ASP:OD1	1:D:474:ILE:HD13	1.86	0.76
1:B:171:ILE:HG22	1:B:172:SER:H	1.50	0.76
1:B:407:CYS:O	1:B:451:ASP:CB	2.32	0.76
1:E:171:ILE:HG22	1:E:172:SER:H	1.50	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:451:ASP:OD1	1:E:474:ILE:HD13	1.86	0.76
1:F:178:LEU:CD2	1:F:178:LEU:H	1.98	0.76
1:F:454:TYR:CE2	1:F:469:PRO:CA	2.67	0.76
1:C:391:LYS:HZ3	1:C:440:ASN:HD21	1.33	0.76
1:C:451:ASP:OD1	1:C:474:ILE:HD13	1.86	0.76
1:D:24:THR:O	1:D:371:GLN:OE1	2.04	0.76
1:F:451:ASP:OD1	1:F:474:ILE:HD13	1.85	0.76
1:F:84:VAL:HG13	1:F:85:ASP:O	1.85	0.76
1:B:451:ASP:OD1	1:B:474:ILE:HD13	1.86	0.76
1:C:171:ILE:HG22	1:C:172:SER:H	1.50	0.76
1:D:84:VAL:HG13	1:D:85:ASP:O	1.85	0.76
1:E:24:THR:O	1:E:371:GLN:OE1	2.04	0.76
1:D:171:ILE:HG22	1:D:172:SER:H	1.50	0.76
1:F:110:TYR:HE1	1:F:178:LEU:O	1.69	0.76
1:B:84:VAL:HG13	1:B:85:ASP:O	1.85	0.75
1:B:454:TYR:CE2	1:B:469:PRO:CA	2.67	0.75
1:F:171:ILE:HG22	1:F:172:SER:H	1.50	0.75
1:A:454:TYR:CE2	1:A:469:PRO:CA	2.67	0.75
1:B:22:ASN:O	1:B:23:SER:OG	2.04	0.75
1:A:451:ASP:OD1	1:A:474:ILE:HD13	1.86	0.75
1:E:110:TYR:HE1	1:E:178:LEU:O	1.69	0.75
1:A:84:VAL:HG13	1:A:85:ASP:O	1.85	0.75
1:B:110:TYR:HE1	1:B:178:LEU:O	1.69	0.75
1:C:178:LEU:CD2	1:C:178:LEU:H	1.98	0.75
1:C:24:THR:O	1:C:371:GLN:OE1	2.04	0.75
1:A:509:THR:OG1	1:A:510:PRO:HA	1.87	0.75
1:B:509:THR:OG1	1:B:510:PRO:HA	1.87	0.75
1:D:112:VAL:O	1:D:131:ILE:O	2.04	0.75
1:D:110:TYR:HE1	1:D:178:LEU:O	1.69	0.75
1:B:178:LEU:CD2	1:B:178:LEU:H	1.98	0.75
1:C:454:TYR:CE2	1:C:469:PRO:CA	2.67	0.75
1:A:110:TYR:HE1	1:A:178:LEU:O	1.69	0.75
1:C:84:VAL:HG13	1:C:85:ASP:O	1.85	0.75
1:D:379:ALA:HB1	1:D:454:TYR:OH	1.73	0.75
1:F:112:VAL:O	1:F:131:ILE:O	2.04	0.75
1:F:509:THR:OG1	1:F:510:PRO:HA	1.87	0.75
1:C:26:THR:HA	1:C:77:ASP:OD1	1.87	0.75
1:F:391:LYS:HZ3	1:F:440:ASN:HD21	1.33	0.75
1:A:112:VAL:O	1:A:131:ILE:O	2.04	0.74
1:C:112:VAL:O	1:C:131:ILE:O	2.04	0.74
1:C:509:THR:OG1	1:C:510:PRO:HA	1.87	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:24:THR:O	1:F:371:GLN:OE1	2.04	0.74
1:B:379:ALA:HB2	1:B:454:TYR:CZ	2.11	0.74
1:E:26:THR:HA	1:E:77:ASP:OD1	1.87	0.74
1:A:24:THR:O	1:A:371:GLN:OE1	2.04	0.74
1:A:26:THR:HA	1:A:77:ASP:OD1	1.87	0.74
1:B:24:THR:O	1:B:371:GLN:OE1	2.04	0.74
1:B:509:THR:H	1:B:510:PRO:HA	1.52	0.74
1:D:178:LEU:CD2	1:D:178:LEU:H	1.98	0.74
1:D:509:THR:OG1	1:D:510:PRO:HA	1.87	0.74
1:E:112:VAL:O	1:E:131:ILE:O	2.04	0.74
1:E:509:THR:OG1	1:E:510:PRO:HA	1.87	0.74
1:F:26:THR:HA	1:F:77:ASP:OD1	1.87	0.74
1:A:379:ALA:HB2	1:A:454:TYR:CZ	2.11	0.74
1:A:409:PRO:O	1:A:454:TYR:OH	2.06	0.74
1:B:26:THR:HA	1:B:77:ASP:OD1	1.87	0.74
1:B:409:PRO:O	1:B:454:TYR:OH	2.06	0.74
1:C:110:TYR:HE1	1:C:178:LEU:O	1.69	0.74
1:B:112:VAL:O	1:B:131:ILE:O	2.04	0.74
1:D:22:ASN:O	1:D:23:SER:OG	2.04	0.74
1:B:112:VAL:HG13	1:B:112:VAL:O	1.88	0.74
1:E:22:ASN:O	1:E:23:SER:OG	2.04	0.73
1:A:112:VAL:O	1:A:112:VAL:HG13	1.88	0.73
1:C:509:THR:H	1:C:510:PRO:HA	1.53	0.73
1:F:409:PRO:O	1:F:454:TYR:OH	2.06	0.73
1:F:379:ALA:HB1	1:F:454:TYR:OH	1.73	0.73
1:A:509:THR:H	1:A:510:PRO:HA	1.52	0.73
1:E:409:PRO:O	1:E:454:TYR:OH	2.06	0.73
1:A:51:VAL:HG13	1:A:55:GLY:O	1.89	0.73
1:C:409:PRO:O	1:C:454:TYR:OH	2.06	0.73
1:C:51:VAL:HG13	1:C:55:GLY:O	1.89	0.73
1:D:410:PRO:O	1:D:413:THR:HG22	1.89	0.73
1:D:509:THR:H	1:D:510:PRO:HA	1.52	0.73
1:D:26:THR:HA	1:D:77:ASP:OD1	1.87	0.73
1:E:509:THR:H	1:E:510:PRO:HA	1.52	0.73
1:F:51:VAL:HG13	1:F:55:GLY:O	1.89	0.73
1:B:409:PRO:HD2	1:B:451:ASP:O	1.88	0.72
1:B:172:SER:C	1:B:174:SER:HA	2.09	0.72
1:C:409:PRO:HD2	1:C:451:ASP:O	1.88	0.72
1:E:410:PRO:O	1:E:413:THR:HG22	1.89	0.72
1:F:112:VAL:HG13	1:F:112:VAL:O	1.88	0.72
1:A:172:SER:C	1:A:174:SER:HA	2.09	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:454:TYR:HE2	1:A:469:PRO:HA	1.43	0.72
1:B:51:VAL:HG13	1:B:55:GLY:O	1.89	0.72
1:E:112:VAL:O	1:E:112:VAL:HG13	1.88	0.72
1:E:382:SER:HB2	1:E:385:THR:HG22	1.72	0.72
1:B:410:PRO:O	1:B:413:THR:HG22	1.89	0.72
1:C:410:PRO:O	1:C:413:THR:HG22	1.89	0.72
1:D:172:SER:C	1:D:174:SER:HA	2.09	0.72
1:D:409:PRO:O	1:D:454:TYR:OH	2.06	0.72
1:F:413:THR:HG23	1:F:414:VAL:HG23	1.72	0.72
1:C:112:VAL:O	1:C:112:VAL:HG13	1.88	0.72
1:D:51:VAL:HG13	1:D:55:GLY:O	1.89	0.72
1:D:112:VAL:HG13	1:D:112:VAL:O	1.88	0.72
1:E:413:THR:HG23	1:E:414:VAL:HG23	1.72	0.72
1:F:22:ASN:O	1:F:23:SER:OG	2.04	0.72
1:F:172:SER:C	1:F:174:SER:HA	2.09	0.72
1:A:410:PRO:O	1:A:413:THR:HG22	1.89	0.72
1:C:172:SER:C	1:C:174:SER:HA	2.09	0.72
1:C:454:TYR:HE2	1:C:469:PRO:CA	2.03	0.72
1:D:454:TYR:CE2	1:D:469:PRO:CA	2.67	0.72
1:D:382:SER:HB2	1:D:385:THR:HG22	1.72	0.72
1:D:409:PRO:HD2	1:D:451:ASP:O	1.88	0.72
1:D:36:GLY:HA2	1:D:82:ARG:HD2	1.72	0.71
1:E:172:SER:C	1:E:174:SER:HA	2.09	0.71
1:E:51:VAL:HG13	1:E:55:GLY:O	1.89	0.71
1:E:36:GLY:HA2	1:E:82:ARG:HD2	1.72	0.71
1:A:413:THR:HG23	1:A:414:VAL:HG23	1.72	0.71
1:D:454:TYR:HE2	1:D:469:PRO:CA	2.03	0.71
1:E:499:ILE:H	1:E:499:ILE:HD13	1.55	0.71
1:F:31:GLY:HA3	1:F:64:TYR:CD2	2.26	0.71
1:F:382:SER:HB2	1:F:385:THR:HG22	1.71	0.71
1:C:382:SER:HB2	1:C:385:THR:HG22	1.71	0.71
1:F:410:PRO:O	1:F:413:THR:HG22	1.89	0.71
1:C:36:GLY:HA2	1:C:82:ARG:HD2	1.72	0.71
1:B:454:TYR:HE2	1:B:469:PRO:CA	2.03	0.71
1:F:509:THR:H	1:F:510:PRO:HA	1.52	0.71
1:D:394:VAL:HG11	1:D:443:ILE:HD12	1.73	0.71
1:D:114:ASP:OD2	1:D:175:SER:HB2	1.91	0.71
1:D:31:GLY:HA3	1:D:64:TYR:CD2	2.26	0.71
1:A:31:GLY:HA3	1:A:64:TYR:CD2	2.26	0.71
1:F:23:SER:CB	1:F:483:ASN:HB2	2.21	0.71
1:D:406:LEU:HD11	1:D:475:ALA:HB2	1.73	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:31:GLY:HA3	1:E:64:TYR:CD2	2.25	0.71
1:B:36:GLY:HA2	1:B:82:ARG:HD2	1.72	0.70
1:D:413:THR:HG23	1:D:414:VAL:HG23	1.72	0.70
1:A:114:ASP:OD2	1:A:175:SER:HB2	1.91	0.70
1:A:499:ILE:H	1:A:499:ILE:HD13	1.55	0.70
1:C:114:ASP:OD2	1:C:175:SER:HB2	1.91	0.70
1:E:454:TYR:HE2	1:E:469:PRO:CA	2.03	0.70
1:C:454:TYR:HD2	1:C:469:PRO:HA	1.53	0.70
1:F:499:ILE:HD13	1:F:499:ILE:H	1.55	0.70
1:B:31:GLY:HA3	1:B:64:TYR:CD2	2.25	0.70
1:C:413:THR:HG23	1:C:414:VAL:HG23	1.72	0.70
1:E:454:TYR:HD2	1:E:469:PRO:HA	1.53	0.70
1:F:406:LEU:HD11	1:F:475:ALA:HB2	1.73	0.70
1:F:36:GLY:HA2	1:F:82:ARG:HD2	1.72	0.70
1:B:382:SER:HB2	1:B:385:THR:HG22	1.71	0.70
1:B:413:THR:HG23	1:B:414:VAL:HG23	1.72	0.70
1:C:406:LEU:HD11	1:C:475:ALA:HB2	1.73	0.70
1:F:454:TYR:HE2	1:F:469:PRO:CA	2.03	0.70
1:B:114:ASP:OD2	1:B:175:SER:HB2	1.91	0.70
1:C:499:ILE:HD13	1:C:499:ILE:H	1.55	0.70
1:E:23:SER:CB	1:E:483:ASN:HB2	2.21	0.70
1:E:406:LEU:HD11	1:E:475:ALA:HB2	1.73	0.70
1:A:382:SER:HB2	1:A:385:THR:HG22	1.72	0.70
1:A:454:TYR:HE2	1:A:469:PRO:CA	2.03	0.70
1:A:47:GLU:HG3	1:A:69:MET:HG3	1.74	0.70
1:A:23:SER:CB	1:A:483:ASN:HB2	2.21	0.70
1:E:450:ILE:CG1	1:E:451:ASP:H	1.89	0.70
1:A:22:ASN:O	1:A:23:SER:OG	2.04	0.70
1:A:394:VAL:HG11	1:A:443:ILE:HD12	1.73	0.70
1:A:36:GLY:HA2	1:A:82:ARG:HD2	1.72	0.70
1:C:31:GLY:HA3	1:C:64:TYR:CD2	2.25	0.70
1:E:114:ASP:OD2	1:E:175:SER:HB2	1.91	0.70
1:F:47:GLU:HG3	1:F:69:MET:HG3	1.74	0.70
1:C:51:VAL:CA	1:C:55:GLY:HA2	2.20	0.70
1:B:47:GLU:HG3	1:B:69:MET:HG3	1.74	0.69
1:E:394:VAL:HG11	1:E:443:ILE:HD12	1.73	0.69
1:D:23:SER:CB	1:D:483:ASN:HB2	2.21	0.69
1:D:499:ILE:H	1:D:499:ILE:HD13	1.55	0.69
1:B:406:LEU:HD11	1:B:475:ALA:HB2	1.73	0.69
1:A:406:LEU:HD11	1:A:475:ALA:HB2	1.73	0.69
1:B:394:VAL:HG11	1:B:443:ILE:HD12	1.73	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:23:SER:CB	1:C:483:ASN:HB2	2.21	0.69
1:E:379:ALA:HB1	1:E:454:TYR:OH	1.73	0.69
1:E:51:VAL:CA	1:E:55:GLY:HA2	2.20	0.69
1:F:114:ASP:OD2	1:F:175:SER:HB2	1.91	0.69
1:B:499:ILE:H	1:B:499:ILE:HD13	1.55	0.69
1:D:289:ILE:HD12	1:D:289:ILE:H	1.58	0.69
1:B:289:ILE:HD12	1:B:289:ILE:H	1.58	0.69
1:C:394:VAL:HG11	1:C:443:ILE:HD12	1.72	0.69
1:F:394:VAL:HG11	1:F:443:ILE:HD12	1.73	0.69
1:C:23:SER:HB3	1:C:483:ASN:CB	2.22	0.69
1:D:454:TYR:HD2	1:D:469:PRO:HA	1.53	0.69
1:D:47:GLU:HG3	1:D:69:MET:HG3	1.74	0.69
1:B:55:GLY:O	1:B:65:PHE:CE1	2.46	0.69
1:C:22:ASN:O	1:C:23:SER:OG	2.04	0.69
1:E:509:THR:OG1	1:E:510:PRO:C	2.32	0.69
1:F:55:GLY:O	1:F:65:PHE:CE1	2.46	0.69
1:B:215:LYS:HE3	1:B:329:ASN:HD21	1.58	0.69
1:B:23:SER:CB	1:B:483:ASN:HB2	2.21	0.69
1:C:289:ILE:H	1:C:289:ILE:HD12	1.58	0.69
1:E:55:GLY:O	1:E:65:PHE:CE1	2.46	0.69
1:A:509:THR:OG1	1:A:510:PRO:C	2.32	0.69
1:C:215:LYS:HE3	1:C:329:ASN:HD21	1.58	0.69
1:D:51:VAL:CA	1:D:55:GLY:HA2	2.20	0.68
1:D:55:GLY:O	1:D:65:PHE:CE1	2.46	0.68
1:B:454:TYR:HD2	1:B:469:PRO:HA	1.53	0.68
1:E:455:LYS:HG3	1:E:502:VAL:HG22	1.75	0.68
1:C:47:GLU:HG3	1:C:69:MET:HG3	1.74	0.68
1:E:409:PRO:HD2	1:E:451:ASP:O	1.88	0.68
1:F:289:ILE:H	1:F:289:ILE:HD12	1.57	0.68
1:C:509:THR:OG1	1:C:510:PRO:C	2.32	0.68
1:D:23:SER:HB3	1:D:483:ASN:CB	2.22	0.68
1:A:289:ILE:HD12	1:A:289:ILE:H	1.58	0.68
1:D:215:LYS:HE3	1:D:329:ASN:HD21	1.58	0.68
1:E:289:ILE:H	1:E:289:ILE:HD12	1.58	0.68
1:F:455:LYS:HG3	1:F:502:VAL:HG22	1.75	0.68
1:A:450:ILE:CG1	1:A:451:ASP:H	1.89	0.68
1:B:509:THR:OG1	1:B:510:PRO:C	2.32	0.68
1:C:55:GLY:O	1:C:65:PHE:CE1	2.46	0.68
1:E:23:SER:HB3	1:E:483:ASN:CB	2.22	0.68
1:E:215:LYS:HE3	1:E:329:ASN:HD21	1.58	0.68
1:A:55:GLY:O	1:A:65:PHE:CE1	2.46	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:171:ILE:HG22	1:C:172:SER:N	2.09	0.68
1:A:215:LYS:HE3	1:A:329:ASN:HD21	1.58	0.67
1:E:47:GLU:HG3	1:E:69:MET:HG3	1.74	0.67
1:F:427:VAL:O	1:F:431:THR:HG22	1.94	0.67
1:F:450:ILE:CG1	1:F:451:ASP:H	1.89	0.67
1:F:408:SER:HB2	1:F:471:ALA:HB2	1.77	0.67
1:F:509:THR:OG1	1:F:510:PRO:C	2.32	0.67
1:C:408:SER:HB2	1:C:471:ALA:HB2	1.77	0.67
1:D:500:LEU:HB2	1:D:501:ASN:OD1	1.95	0.67
1:F:171:ILE:HG22	1:F:172:SER:N	2.09	0.67
1:F:304:ILE:HG13	1:F:305:TYR:CE2	2.30	0.67
1:A:304:ILE:HG13	1:A:305:TYR:CE2	2.30	0.67
1:E:500:LEU:HB2	1:E:501:ASN:OD1	1.95	0.67
1:F:500:LEU:HB2	1:F:501:ASN:OD1	1.95	0.67
1:A:427:VAL:O	1:A:431:THR:HG22	1.95	0.67
1:A:500:LEU:HB2	1:A:501:ASN:OD1	1.95	0.67
1:B:171:ILE:HG22	1:B:172:SER:N	2.09	0.67
1:D:509:THR:OG1	1:D:510:PRO:C	2.32	0.67
1:E:427:VAL:O	1:E:431:THR:HG22	1.95	0.67
1:E:55:GLY:O	1:E:65:PHE:HE1	1.78	0.67
1:F:51:VAL:CA	1:F:55:GLY:HA2	2.20	0.67
1:F:55:GLY:O	1:F:65:PHE:HE1	1.78	0.67
1:D:171:ILE:HG22	1:D:172:SER:N	2.09	0.67
1:E:171:ILE:HG22	1:E:172:SER:N	2.09	0.67
1:E:304:ILE:HG13	1:E:305:TYR:CE2	2.30	0.67
1:F:215:LYS:HE3	1:F:329:ASN:HD21	1.58	0.67
1:A:391:LYS:NZ	1:A:440:ASN:HD21	1.92	0.67
1:A:55:GLY:O	1:A:65:PHE:HE1	1.78	0.67
1:D:408:SER:HB2	1:D:471:ALA:HB2	1.77	0.67
1:D:55:GLY:O	1:D:65:PHE:HE1	1.78	0.67
1:A:228:GLY:CA	1:A:345:SER:HB3	2.23	0.67
1:A:408:SER:HB2	1:A:471:ALA:HB2	1.77	0.67
1:C:304:ILE:HG13	1:C:305:TYR:CE2	2.30	0.67
1:D:351:THR:HG23	1:D:354:ASP:H	1.60	0.67
1:F:351:THR:HG23	1:F:354:ASP:H	1.60	0.67
1:F:409:PRO:HD2	1:F:451:ASP:O	1.88	0.67
1:B:455:LYS:HG3	1:B:502:VAL:HG22	1.75	0.67
1:C:500:LEU:HB2	1:C:501:ASN:OD1	1.95	0.67
1:E:96:ALA:HB2	1:E:191:SER:HA	1.77	0.67
1:B:304:ILE:HG13	1:B:305:TYR:CE2	2.30	0.66
1:F:454:TYR:HD2	1:F:469:PRO:HA	1.53	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:171:ILE:HG22	1:A:172:SER:N	2.09	0.66
1:A:455:LYS:HG3	1:A:502:VAL:HG22	1.75	0.66
1:B:228:GLY:CA	1:B:345:SER:HB3	2.23	0.66
1:B:427:VAL:O	1:B:431:THR:HG22	1.94	0.66
1:C:455:LYS:HG3	1:C:502:VAL:HG22	1.75	0.66
1:D:455:LYS:HG3	1:D:502:VAL:HG22	1.75	0.66
1:D:96:ALA:HB2	1:D:191:SER:HA	1.77	0.66
1:E:379:ALA:CB	1:E:454:TYR:CE2	2.79	0.66
1:C:351:THR:HG23	1:C:354:ASP:H	1.60	0.66
1:C:427:VAL:O	1:C:431:THR:HG22	1.95	0.66
1:C:228:GLY:CA	1:C:345:SER:HB3	2.23	0.66
1:D:379:ALA:CB	1:D:454:TYR:CE2	2.79	0.66
1:A:450:ILE:CG1	1:A:451:ASP:N	2.53	0.66
1:D:427:VAL:O	1:D:431:THR:HG22	1.94	0.66
1:A:351:THR:HG23	1:A:354:ASP:H	1.60	0.66
1:B:55:GLY:O	1:B:65:PHE:HE1	1.78	0.66
1:C:55:GLY:O	1:C:65:PHE:HE1	1.78	0.66
1:D:304:ILE:HG13	1:D:305:TYR:CE2	2.30	0.66
1:F:379:ALA:CB	1:F:454:TYR:CE2	2.79	0.66
1:B:500:LEU:HB2	1:B:501:ASN:OD1	1.95	0.66
1:B:96:ALA:HB2	1:B:191:SER:HA	1.77	0.66
1:E:408:SER:HB2	1:E:471:ALA:HB2	1.77	0.66
1:A:379:ALA:CB	1:A:454:TYR:CE2	2.78	0.66
1:B:408:SER:HB2	1:B:471:ALA:HB2	1.77	0.65
1:C:391:LYS:HZ1	1:C:440:ASN:ND2	1.93	0.65
1:C:409:PRO:C	1:C:454:TYR:HE1	1.98	0.65
1:F:391:LYS:HZ1	1:F:440:ASN:ND2	1.93	0.65
1:B:23:SER:HB3	1:B:483:ASN:CB	2.22	0.65
1:A:121:VAL:HG22	1:A:166:ASN:HB3	1.78	0.65
1:B:121:VAL:HG22	1:B:166:ASN:HB3	1.78	0.65
1:B:379:ALA:CB	1:B:454:TYR:CE2	2.79	0.65
1:E:228:GLY:CA	1:E:345:SER:HB3	2.23	0.65
1:F:96:ALA:HB2	1:F:191:SER:HA	1.77	0.65
1:C:450:ILE:CG1	1:C:451:ASP:H	1.89	0.65
1:C:96:ALA:HB2	1:C:191:SER:HA	1.77	0.65
1:D:228:GLY:CA	1:D:345:SER:HB3	2.23	0.65
1:D:409:PRO:C	1:D:454:TYR:HE1	1.98	0.65
1:C:121:VAL:HG22	1:C:166:ASN:HB3	1.78	0.65
1:C:379:ALA:CB	1:C:454:TYR:CE2	2.79	0.65
1:D:121:VAL:HG22	1:D:166:ASN:HB3	1.78	0.65
1:B:351:THR:HG23	1:B:354:ASP:H	1.60	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:96:ALA:HB2	1:A:191:SER:HA	1.77	0.65
1:B:51:VAL:CA	1:B:55:GLY:HA2	2.20	0.65
1:B:450:ILE:CG1	1:B:451:ASP:H	1.89	0.64
1:A:409:PRO:HD2	1:A:451:ASP:O	1.88	0.64
1:A:51:VAL:CA	1:A:55:GLY:HA2	2.20	0.64
1:B:409:PRO:C	1:B:454:TYR:HE1	1.98	0.64
1:C:100:GLU:HG3	1:C:186:LYS:H	1.63	0.64
1:C:66:MET:HG2	1:C:468:VAL:HG11	1.80	0.64
1:E:351:THR:HG23	1:E:354:ASP:H	1.60	0.64
1:E:409:PRO:C	1:E:454:TYR:HE1	1.98	0.64
1:E:66:MET:HG2	1:E:468:VAL:HG11	1.80	0.64
1:F:100:GLU:HG3	1:F:186:LYS:H	1.63	0.64
1:F:23:SER:HB3	1:F:483:ASN:CB	2.22	0.64
1:F:391:LYS:NZ	1:F:440:ASN:HD21	1.92	0.64
1:D:100:GLU:HG3	1:D:186:LYS:H	1.63	0.64
1:D:23:SER:HG	1:D:483:ASN:HB3	1.63	0.64
1:A:454:TYR:HD2	1:A:469:PRO:HA	1.53	0.64
1:B:215:LYS:HE3	1:B:329:ASN:ND2	2.13	0.64
1:F:66:MET:HG2	1:F:468:VAL:HG11	1.80	0.64
1:E:100:GLU:HG3	1:E:186:LYS:H	1.63	0.64
1:B:100:GLU:HG3	1:B:186:LYS:H	1.63	0.63
1:E:121:VAL:HG22	1:E:166:ASN:HB3	1.78	0.63
1:F:121:VAL:HG22	1:F:166:ASN:HB3	1.78	0.63
1:D:509:THR:H	1:D:510:PRO:CA	2.12	0.63
1:D:66:MET:HG2	1:D:468:VAL:HG11	1.80	0.63
1:A:66:MET:HG2	1:A:468:VAL:HG11	1.80	0.63
1:B:450:ILE:CG1	1:B:451:ASP:N	2.53	0.63
1:C:499:ILE:HG13	1:C:502:VAL:HG21	1.81	0.63
1:E:509:THR:H	1:E:510:PRO:CA	2.12	0.63
1:F:509:THR:H	1:F:510:PRO:CA	2.12	0.63
1:A:100:GLU:HG3	1:A:186:LYS:H	1.63	0.63
1:A:215:LYS:HE3	1:A:329:ASN:ND2	2.13	0.63
1:A:499:ILE:HG13	1:A:502:VAL:HG21	1.81	0.63
1:A:509:THR:H	1:A:510:PRO:CA	2.12	0.63
1:F:499:ILE:HG13	1:F:502:VAL:HG21	1.81	0.63
1:B:391:LYS:HZ1	1:B:440:ASN:ND2	1.96	0.63
1:B:509:THR:H	1:B:510:PRO:CA	2.12	0.63
1:C:215:LYS:HE3	1:C:329:ASN:ND2	2.13	0.63
1:D:499:ILE:HG13	1:D:502:VAL:HG21	1.81	0.63
1:E:23:SER:HG	1:E:483:ASN:HB3	1.64	0.63
1:C:509:THR:H	1:C:510:PRO:CA	2.12	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:23:SER:HB3	1:A:483:ASN:CB	2.22	0.63
1:F:409:PRO:C	1:F:454:TYR:HE1	1.98	0.63
1:A:409:PRO:C	1:A:454:TYR:HE1	1.98	0.63
1:B:499:ILE:HG13	1:B:502:VAL:HG21	1.81	0.62
1:E:215:LYS:HE3	1:E:329:ASN:ND2	2.13	0.62
1:F:215:LYS:HE3	1:F:329:ASN:ND2	2.13	0.62
1:B:66:MET:HG2	1:B:468:VAL:HG11	1.80	0.62
1:D:213:ASN:HD22	1:D:213:ASN:N	1.98	0.62
1:E:499:ILE:HG13	1:E:502:VAL:HG21	1.81	0.62
1:A:407:CYS:O	1:A:450:ILE:HA	2.00	0.62
1:B:107:GLY:HA3	1:B:110:TYR:CE1	2.35	0.62
1:C:213:ASN:N	1:C:213:ASN:HD22	1.98	0.62
1:E:213:ASN:HD22	1:E:213:ASN:N	1.98	0.62
1:C:107:GLY:HA3	1:C:110:TYR:CE1	2.35	0.62
1:D:391:LYS:HZ1	1:D:440:ASN:ND2	1.96	0.62
1:D:407:CYS:O	1:D:450:ILE:HA	2.00	0.62
1:F:213:ASN:N	1:F:213:ASN:HD22	1.98	0.62
1:B:23:SER:HG	1:B:483:ASN:HB3	1.63	0.62
1:A:213:ASN:HD22	1:A:213:ASN:N	1.98	0.62
1:D:107:GLY:HA3	1:D:110:TYR:CE1	2.35	0.62
1:E:407:CYS:O	1:E:450:ILE:HA	2.00	0.62
1:F:407:CYS:O	1:F:450:ILE:HA	2.00	0.62
1:A:107:GLY:HA3	1:A:110:TYR:CE1	2.35	0.62
1:B:407:CYS:O	1:B:450:ILE:HA	2.00	0.62
1:D:215:LYS:HE3	1:D:329:ASN:ND2	2.13	0.62
1:A:391:LYS:HZ3	1:A:440:ASN:HD21	1.48	0.62
1:B:107:GLY:HA3	1:B:110:TYR:HE1	1.65	0.62
1:E:391:LYS:HZ1	1:E:440:ASN:ND2	1.94	0.61
1:F:107:GLY:HA3	1:F:110:TYR:CE1	2.35	0.61
1:E:107:GLY:HA3	1:E:110:TYR:CE1	2.34	0.61
1:E:278:GLN:HG2	1:E:296:SER:HB2	1.83	0.61
1:B:213:ASN:HD22	1:B:213:ASN:N	1.98	0.61
1:C:407:CYS:O	1:C:450:ILE:HA	2.00	0.61
1:E:455:LYS:HE2	1:E:502:VAL:HG22	1.82	0.61
1:E:107:GLY:HA3	1:E:110:TYR:HE1	1.65	0.61
1:C:107:GLY:HA3	1:C:110:TYR:HE1	1.65	0.61
1:D:161:PRO:HB3	1:D:187:ILE:HB	1.83	0.61
1:D:455:LYS:HE2	1:D:502:VAL:HG22	1.82	0.61
1:F:228:GLY:CA	1:F:345:SER:HB3	2.23	0.61
1:D:278:GLN:HG2	1:D:296:SER:HB2	1.83	0.61
1:B:455:LYS:HE2	1:B:502:VAL:HG22	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:450:ILE:CG1	1:C:451:ASP:N	2.53	0.60
1:B:391:LYS:CE	1:B:440:ASN:O	2.49	0.60
1:F:107:GLY:HA3	1:F:110:TYR:HE1	1.65	0.60
1:F:97:GLY:HA3	1:F:256:PRO:HG2	1.84	0.60
1:A:107:GLY:HA3	1:A:110:TYR:HE1	1.65	0.60
1:A:391:LYS:CE	1:A:440:ASN:O	2.49	0.60
1:A:455:LYS:HE2	1:A:502:VAL:HG22	1.82	0.60
1:F:278:GLN:HG2	1:F:296:SER:HB2	1.83	0.60
1:B:97:GLY:HA3	1:B:256:PRO:HG2	1.84	0.60
1:A:97:GLY:HA3	1:A:256:PRO:HG2	1.84	0.60
1:A:278:GLN:HG2	1:A:296:SER:HB2	1.82	0.60
1:C:161:PRO:HB3	1:C:187:ILE:HB	1.83	0.60
1:B:419:VAL:HA	1:B:422:ALA:HB3	1.84	0.60
1:C:455:LYS:HE2	1:C:502:VAL:HG22	1.82	0.60
1:B:161:PRO:HB3	1:B:187:ILE:HB	1.83	0.60
1:D:107:GLY:HA3	1:D:110:TYR:HE1	1.65	0.60
1:E:419:VAL:HA	1:E:422:ALA:HB3	1.84	0.60
1:F:391:LYS:CE	1:F:440:ASN:O	2.49	0.60
1:C:278:GLN:HG2	1:C:296:SER:HB2	1.82	0.59
1:C:509:THR:N	1:C:510:PRO:HA	2.14	0.59
1:D:419:VAL:HA	1:D:422:ALA:HB3	1.84	0.59
1:F:455:LYS:HE2	1:F:502:VAL:HG22	1.82	0.59
1:C:419:VAL:HA	1:C:422:ALA:HB3	1.84	0.59
1:D:60:GLU:HG2	1:D:347:ASN:HB2	1.85	0.59
1:E:97:GLY:HA3	1:E:256:PRO:HG2	1.84	0.59
1:A:161:PRO:HB3	1:A:187:ILE:HB	1.83	0.59
1:E:161:PRO:HB3	1:E:187:ILE:HB	1.83	0.59
1:F:419:VAL:HA	1:F:422:ALA:HB3	1.84	0.59
1:A:419:VAL:HA	1:A:422:ALA:HB3	1.84	0.59
1:E:391:LYS:CE	1:E:440:ASN:O	2.49	0.59
1:F:161:PRO:HB3	1:F:187:ILE:HB	1.83	0.59
1:C:60:GLU:HG2	1:C:347:ASN:HB2	1.85	0.59
1:C:97:GLY:HA3	1:C:256:PRO:HG2	1.84	0.59
1:B:278:GLN:HG2	1:B:296:SER:HB2	1.82	0.59
1:F:509:THR:N	1:F:510:PRO:HA	2.14	0.59
1:A:456:TYR:HB3	1:A:504:LYS:HB3	1.85	0.59
1:B:509:THR:N	1:B:510:PRO:HA	2.14	0.58
1:E:60:GLU:HG2	1:E:347:ASN:HB2	1.85	0.58
1:A:501:ASN:N	1:A:501:ASN:OD1	2.36	0.58
1:F:501:ASN:N	1:F:501:ASN:OD1	2.37	0.58
1:B:178:LEU:CD2	1:B:178:LEU:N	2.66	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:97:GLY:HA3	1:D:256:PRO:HG2	1.84	0.58
1:A:60:GLU:HG2	1:A:347:ASN:HB2	1.85	0.58
1:E:398:ASP:O	1:E:401:GLN:HG3	2.04	0.58
1:F:429:TRP:CZ2	1:F:441:PHE:HB2	2.39	0.58
1:B:398:ASP:O	1:B:401:GLN:HG3	2.04	0.58
1:B:429:TRP:CZ2	1:B:441:PHE:HB2	2.39	0.58
1:C:398:ASP:O	1:C:401:GLN:HG3	2.04	0.58
1:E:456:TYR:HB3	1:E:504:LYS:HB3	1.85	0.58
1:A:133:GLU:HB3	1:A:142:LYS:HB3	1.86	0.58
1:B:456:TYR:O	1:B:503:ILE:HG12	2.04	0.58
1:D:178:LEU:N	1:D:178:LEU:CD2	2.66	0.58
1:E:450:ILE:CG1	1:E:451:ASP:N	2.53	0.58
1:D:398:ASP:O	1:D:401:GLN:HG3	2.04	0.58
1:F:398:ASP:O	1:F:401:GLN:HG3	2.04	0.58
1:A:373:PHE:HB2	1:A:405:VAL:HA	1.86	0.58
1:D:501:ASN:OD1	1:D:501:ASN:N	2.36	0.58
1:A:429:TRP:CZ2	1:A:441:PHE:HB2	2.39	0.57
1:B:373:PHE:HB2	1:B:405:VAL:HA	1.86	0.57
1:C:178:LEU:CD2	1:C:178:LEU:N	2.66	0.57
1:E:23:SER:OG	1:E:483:ASN:HB2	2.04	0.57
1:E:373:PHE:HB2	1:E:404:LEU:O	2.04	0.57
1:F:133:GLU:HB3	1:F:142:LYS:HB3	1.86	0.57
1:F:60:GLU:HG2	1:F:347:ASN:HB2	1.85	0.57
1:A:23:SER:OG	1:A:483:ASN:HB2	2.04	0.57
1:A:398:ASP:O	1:A:401:GLN:HG3	2.04	0.57
1:A:499:ILE:HG13	1:A:502:VAL:CG2	2.35	0.57
1:B:456:TYR:HB3	1:B:504:LYS:HB3	1.85	0.57
1:B:60:GLU:HG2	1:B:347:ASN:HB2	1.85	0.57
1:C:429:TRP:CZ2	1:C:441:PHE:HB2	2.39	0.57
1:C:499:ILE:HG13	1:C:502:VAL:CG2	2.35	0.57
1:B:133:GLU:HB3	1:B:142:LYS:HB3	1.86	0.57
1:E:499:ILE:HG13	1:E:502:VAL:CG2	2.35	0.57
1:C:391:LYS:CE	1:C:440:ASN:O	2.49	0.57
1:D:456:TYR:HB3	1:D:504:LYS:HB3	1.85	0.57
1:E:133:GLU:HB3	1:E:142:LYS:HB3	1.86	0.57
1:E:456:TYR:O	1:E:503:ILE:HG12	2.04	0.57
1:A:455:LYS:HG2	1:A:456:TYR:N	2.19	0.57
1:C:379:ALA:HB1	1:C:454:TYR:OH	1.73	0.57
1:F:456:TYR:HB3	1:F:504:LYS:HB3	1.86	0.57
1:A:456:TYR:O	1:A:503:ILE:HG12	2.04	0.57
1:B:23:SER:OG	1:B:483:ASN:HB2	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:499:ILE:HG13	1:D:502:VAL:CG2	2.35	0.57
1:F:373:PHE:HB2	1:F:404:LEU:O	2.04	0.57
1:D:373:PHE:HB2	1:D:404:LEU:O	2.04	0.57
1:D:429:TRP:CZ2	1:D:441:PHE:HB2	2.39	0.57
1:E:429:TRP:CZ2	1:E:441:PHE:HB2	2.39	0.57
1:A:509:THR:N	1:A:510:PRO:HA	2.14	0.57
1:C:456:TYR:O	1:C:503:ILE:HG12	2.04	0.57
1:D:455:LYS:HG2	1:D:456:TYR:N	2.19	0.57
1:D:456:TYR:O	1:D:503:ILE:HG12	2.04	0.57
1:F:499:ILE:HG13	1:F:502:VAL:CG2	2.35	0.57
1:A:373:PHE:HB2	1:A:404:LEU:O	2.04	0.57
1:C:373:PHE:HB2	1:C:405:VAL:HA	1.86	0.57
1:C:455:LYS:HG2	1:C:456:TYR:N	2.19	0.57
1:D:373:PHE:HB2	1:D:405:VAL:HA	1.86	0.57
1:E:373:PHE:HB2	1:E:405:VAL:HA	1.86	0.57
1:E:509:THR:N	1:E:510:PRO:HA	2.14	0.57
1:B:455:LYS:HG2	1:B:456:TYR:N	2.19	0.56
1:B:501:ASN:OD1	1:B:501:ASN:N	2.36	0.56
1:C:501:ASN:N	1:C:501:ASN:OD1	2.36	0.56
1:F:455:LYS:HG2	1:F:456:TYR:N	2.19	0.56
1:C:456:TYR:HB3	1:C:504:LYS:HB3	1.86	0.56
1:B:499:ILE:HG13	1:B:502:VAL:CG2	2.35	0.56
1:C:373:PHE:HB2	1:C:404:LEU:O	2.04	0.56
1:D:133:GLU:HB3	1:D:142:LYS:HB3	1.86	0.56
1:E:455:LYS:HG2	1:E:456:TYR:N	2.19	0.56
1:E:501:ASN:N	1:E:501:ASN:OD1	2.36	0.56
1:F:373:PHE:HB2	1:F:405:VAL:HA	1.86	0.56
1:A:454:TYR:HE2	1:A:469:PRO:CB	2.19	0.56
1:D:391:LYS:CE	1:D:440:ASN:O	2.49	0.56
1:D:50:LEU:C	1:D:50:LEU:HD12	2.26	0.56
1:F:456:TYR:O	1:F:503:ILE:HG12	2.04	0.56
1:A:431:THR:O	1:A:432:ALA:HB2	2.06	0.56
1:B:373:PHE:HB2	1:B:404:LEU:O	2.04	0.56
1:C:283:VAL:HG21	1:C:323:ILE:HD13	1.88	0.56
1:F:50:LEU:C	1:F:50:LEU:HD12	2.26	0.56
1:B:431:THR:O	1:B:432:ALA:HB2	2.06	0.56
1:D:23:SER:OG	1:D:483:ASN:HB2	2.04	0.56
1:D:283:VAL:HG21	1:D:323:ILE:HD13	1.88	0.56
1:C:133:GLU:HB3	1:C:142:LYS:HB3	1.86	0.56
1:F:454:TYR:HE2	1:F:469:PRO:CB	2.19	0.56
1:C:454:TYR:HE2	1:C:469:PRO:CB	2.19	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:454:TYR:HE2	1:D:469:PRO:CB	2.19	0.56
1:E:431:THR:O	1:E:432:ALA:HB2	2.06	0.56
1:C:302:LYS:HD3	1:C:306:ASP:HA	1.88	0.56
1:E:84:VAL:CG1	1:E:85:ASP:O	2.54	0.56
1:B:236:ILE:HD12	1:B:236:ILE:H	1.71	0.56
1:B:283:VAL:HG21	1:B:323:ILE:HD13	1.88	0.56
1:E:178:LEU:N	1:E:178:LEU:CD2	2.66	0.56
1:C:431:THR:O	1:C:432:ALA:HB2	2.06	0.55
1:E:283:VAL:HG21	1:E:323:ILE:HD13	1.88	0.55
1:A:23:SER:HG	1:A:483:ASN:HB3	1.69	0.55
1:C:50:LEU:HD12	1:C:50:LEU:C	2.26	0.55
1:A:50:LEU:C	1:A:50:LEU:HD12	2.26	0.55
1:B:302:LYS:HD3	1:B:306:ASP:HA	1.88	0.55
1:B:454:TYR:HE2	1:B:469:PRO:CB	2.19	0.55
1:B:50:LEU:C	1:B:50:LEU:HD12	2.26	0.55
1:F:84:VAL:CG1	1:F:85:ASP:O	2.54	0.55
1:A:178:LEU:N	1:A:178:LEU:CD2	2.66	0.55
1:A:236:ILE:HD12	1:A:236:ILE:H	1.72	0.55
1:D:84:VAL:CG1	1:D:85:ASP:O	2.54	0.55
1:D:302:LYS:HD3	1:D:306:ASP:HA	1.89	0.55
1:A:381:GLU:HB3	1:A:385:THR:HG23	1.89	0.55
1:E:454:TYR:HE2	1:E:469:PRO:CB	2.19	0.55
1:F:382:SER:O	1:F:383:LEU:C	2.45	0.55
1:F:498:GLN:HA	1:F:498:GLN:OE1	2.07	0.55
1:A:283:VAL:HG21	1:A:323:ILE:HD13	1.88	0.55
1:B:347:ASN:O	1:B:348:ALA:C	2.45	0.55
1:C:234:ILE:HB	1:C:340:LEU:HD12	1.89	0.55
1:D:498:GLN:HA	1:D:498:GLN:OE1	2.07	0.55
1:E:150:ILE:HG22	1:E:167:TRP:CZ3	2.42	0.55
1:F:236:ILE:H	1:F:236:ILE:HD12	1.71	0.55
1:F:431:THR:O	1:F:432:ALA:HB2	2.06	0.55
1:A:379:ALA:HB1	1:A:454:TYR:OH	1.73	0.55
1:A:84:VAL:CG1	1:A:85:ASP:O	2.54	0.55
1:B:206:THR:HG22	1:B:206:THR:O	2.07	0.55
1:C:206:THR:O	1:C:206:THR:HG22	2.07	0.55
1:D:150:ILE:HG22	1:D:167:TRP:CZ3	2.42	0.55
1:E:206:THR:HG22	1:E:206:THR:O	2.07	0.55
1:E:50:LEU:HD12	1:E:50:LEU:C	2.26	0.55
1:F:150:ILE:HG22	1:F:167:TRP:HZ3	1.72	0.55
1:A:150:ILE:HG22	1:A:167:TRP:HZ3	1.72	0.55
1:A:150:ILE:HG22	1:A:167:TRP:CZ3	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:455:LYS:HE2	1:A:502:VAL:CG2	2.37	0.55
1:E:236:ILE:HD12	1:E:236:ILE:H	1.71	0.55
1:E:498:GLN:HA	1:E:498:GLN:OE1	2.07	0.55
1:F:283:VAL:HG21	1:F:323:ILE:HD13	1.88	0.55
1:A:498:GLN:OE1	1:A:498:GLN:HA	2.07	0.55
1:B:274:GLN:H	1:B:278:GLN:NE2	2.05	0.55
1:C:150:ILE:HG22	1:C:167:TRP:HZ3	1.72	0.55
1:C:173:SER:N	1:C:174:SER:HA	2.22	0.55
1:C:274:GLN:H	1:C:278:GLN:NE2	2.05	0.55
1:C:381:GLU:HB3	1:C:385:THR:HG23	1.89	0.55
1:D:150:ILE:HG22	1:D:167:TRP:HZ3	1.72	0.55
1:D:234:ILE:HB	1:D:340:LEU:HD12	1.89	0.55
1:D:236:ILE:HD12	1:D:236:ILE:H	1.71	0.55
1:D:431:THR:O	1:D:432:ALA:HB2	2.06	0.55
1:F:503:ILE:O	1:F:504:LYS:HB2	2.06	0.55
1:A:46:ASN:HB2	1:A:49:ASP:HB2	1.89	0.54
1:B:498:GLN:OE1	1:B:498:GLN:HA	2.07	0.54
1:E:503:ILE:O	1:E:504:LYS:HB2	2.06	0.54
1:E:89:ALA:HB3	1:E:194:LEU:HD11	1.88	0.54
1:F:150:ILE:HG22	1:F:167:TRP:CZ3	2.42	0.54
1:F:381:GLU:HB3	1:F:385:THR:HG23	1.89	0.54
1:F:455:LYS:HE2	1:F:502:VAL:CG2	2.37	0.54
1:A:89:ALA:HB3	1:A:194:LEU:HD11	1.88	0.54
1:B:150:ILE:HG22	1:B:167:TRP:HZ3	1.72	0.54
1:E:150:ILE:HG22	1:E:167:TRP:HZ3	1.72	0.54
1:F:46:ASN:HB2	1:F:49:ASP:HB2	1.89	0.54
1:A:347:ASN:O	1:A:348:ALA:C	2.45	0.54
1:A:382:SER:O	1:A:383:LEU:C	2.45	0.54
1:C:51:VAL:HG22	1:C:65:PHE:HZ	1.73	0.54
1:C:89:ALA:HB3	1:C:194:LEU:HD11	1.88	0.54
1:D:206:THR:O	1:D:206:THR:HG22	2.07	0.54
1:D:381:GLU:HB3	1:D:385:THR:HG23	1.88	0.54
1:D:503:ILE:O	1:D:504:LYS:HB2	2.06	0.54
1:B:234:ILE:HB	1:B:340:LEU:HD12	1.89	0.54
1:B:51:VAL:HG22	1:B:65:PHE:HZ	1.73	0.54
1:C:236:ILE:H	1:C:236:ILE:HD12	1.71	0.54
1:D:46:ASN:HB2	1:D:49:ASP:HB2	1.89	0.54
1:E:302:LYS:HD3	1:E:306:ASP:HA	1.88	0.54
1:F:228:GLY:HA2	1:F:345:SER:CB	2.32	0.54
1:F:391:LYS:HZ3	1:F:440:ASN:ND2	1.94	0.54
1:A:234:ILE:HB	1:A:340:LEU:HD12	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:371:GLN:HB3	1:B:484:VAL:HG23	1.90	0.54
1:B:382:SER:O	1:B:383:LEU:C	2.45	0.54
1:C:347:ASN:O	1:C:348:ALA:C	2.45	0.54
1:C:498:GLN:OE1	1:C:498:GLN:HA	2.07	0.54
1:D:274:GLN:H	1:D:278:GLN:NE2	2.05	0.54
1:D:347:ASN:O	1:D:348:ALA:C	2.45	0.54
1:D:455:LYS:HE2	1:D:502:VAL:CG2	2.37	0.54
1:D:51:VAL:HG22	1:D:65:PHE:HZ	1.73	0.54
1:A:228:GLY:HA2	1:A:345:SER:CB	2.32	0.54
1:A:302:LYS:HD3	1:A:306:ASP:HA	1.89	0.54
1:B:381:GLU:HB3	1:B:385:THR:HG23	1.88	0.54
1:B:46:ASN:HB2	1:B:49:ASP:HB2	1.89	0.54
1:B:503:ILE:O	1:B:504:LYS:HB2	2.06	0.54
1:B:84:VAL:CG1	1:B:85:ASP:O	2.54	0.54
1:C:455:LYS:HE2	1:C:502:VAL:CG2	2.37	0.54
1:F:89:ALA:HB3	1:F:194:LEU:HD11	1.88	0.54
1:A:274:GLN:H	1:A:278:GLN:NE2	2.05	0.54
1:B:89:ALA:HB3	1:B:194:LEU:HD11	1.88	0.54
1:C:503:ILE:O	1:C:504:LYS:HB2	2.06	0.54
1:C:84:VAL:CG1	1:C:85:ASP:O	2.54	0.54
1:D:173:SER:N	1:D:174:SER:HA	2.22	0.54
1:D:371:GLN:HB3	1:D:484:VAL:HG23	1.90	0.54
1:F:347:ASN:O	1:F:348:ALA:C	2.45	0.54
1:C:150:ILE:HG22	1:C:167:TRP:CZ3	2.42	0.54
1:C:371:GLN:HB3	1:C:484:VAL:HG23	1.90	0.54
1:D:89:ALA:HB3	1:D:194:LEU:HD11	1.88	0.54
1:D:382:SER:O	1:D:383:LEU:C	2.45	0.54
1:E:347:ASN:O	1:E:348:ALA:C	2.45	0.54
1:E:46:ASN:HB2	1:E:49:ASP:HB2	1.89	0.54
1:E:455:LYS:HE2	1:E:502:VAL:CG2	2.37	0.54
1:E:51:VAL:HG22	1:E:65:PHE:HZ	1.73	0.54
1:F:90:LYS:HB2	1:F:344:LEU:HB3	1.90	0.54
1:A:51:VAL:HG22	1:A:65:PHE:HZ	1.73	0.54
1:E:382:SER:O	1:E:383:LEU:C	2.45	0.54
1:A:244:TYR:CD2	1:A:273:PRO:HD2	2.43	0.54
1:A:90:LYS:HB2	1:A:344:LEU:HB3	1.90	0.54
1:E:244:TYR:CD2	1:E:273:PRO:HD2	2.43	0.54
1:E:274:GLN:H	1:E:278:GLN:NE2	2.05	0.54
1:F:172:SER:O	1:F:174:SER:HA	2.08	0.54
1:F:244:TYR:CD2	1:F:273:PRO:HD2	2.43	0.54
1:F:302:LYS:HD3	1:F:306:ASP:HA	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:244:TYR:CD2	1:B:273:PRO:HD2	2.43	0.53
1:F:408:SER:CB	1:F:451:ASP:HB3	2.39	0.53
1:B:455:LYS:HE2	1:B:502:VAL:CG2	2.37	0.53
1:E:234:ILE:HB	1:E:340:LEU:HD12	1.89	0.53
1:F:234:ILE:HB	1:F:340:LEU:HD12	1.89	0.53
1:F:274:GLN:H	1:F:278:GLN:NE2	2.05	0.53
1:F:51:VAL:HG22	1:F:65:PHE:HZ	1.73	0.53
1:B:150:ILE:HG22	1:B:167:TRP:CZ3	2.42	0.53
1:B:90:LYS:HB2	1:B:344:LEU:HB3	1.90	0.53
1:C:23:SER:OG	1:C:483:ASN:HB2	2.04	0.53
1:C:46:ASN:HB2	1:C:49:ASP:HB2	1.89	0.53
1:A:172:SER:O	1:A:174:SER:HA	2.08	0.53
1:A:206:THR:O	1:A:206:THR:HG22	2.07	0.53
1:A:371:GLN:HB3	1:A:484:VAL:HG23	1.90	0.53
1:E:408:SER:CB	1:E:451:ASP:HB3	2.39	0.53
1:F:23:SER:HG	1:F:483:ASN:HB3	1.73	0.53
1:A:503:ILE:O	1:A:504:LYS:HB2	2.06	0.53
1:B:451:ASP:OD2	1:B:471:ALA:N	2.42	0.53
1:D:374:ILE:HG23	1:D:472:ALA:HA	1.91	0.53
1:F:178:LEU:CD2	1:F:178:LEU:N	2.66	0.53
1:A:173:SER:N	1:A:174:SER:HA	2.22	0.53
1:B:374:ILE:HG23	1:B:472:ALA:HA	1.91	0.53
1:D:244:TYR:CD2	1:D:273:PRO:HD2	2.43	0.53
1:F:206:THR:O	1:F:206:THR:HG22	2.07	0.53
1:F:397:GLY:HA2	1:F:403:CYS:SG	2.49	0.53
1:D:451:ASP:OD2	1:D:471:ALA:N	2.42	0.53
1:E:172:SER:O	1:E:174:SER:HA	2.08	0.53
1:B:397:GLY:HA2	1:B:403:CYS:SG	2.49	0.53
1:C:90:LYS:HB2	1:C:344:LEU:HB3	1.90	0.53
1:C:397:GLY:HA2	1:C:403:CYS:SG	2.49	0.53
1:C:374:ILE:HG23	1:C:472:ALA:HA	1.91	0.53
1:E:114:ASP:CG	1:E:175:SER:HB2	2.29	0.53
1:E:381:GLU:HB3	1:E:385:THR:HG23	1.89	0.53
1:A:397:GLY:HA2	1:A:403:CYS:SG	2.49	0.53
1:B:228:GLY:HA2	1:B:345:SER:CB	2.32	0.53
1:E:451:ASP:OD2	1:E:471:ALA:N	2.42	0.53
1:A:451:ASP:OD2	1:A:471:ALA:N	2.42	0.53
1:B:114:ASP:CG	1:B:175:SER:HB2	2.29	0.53
1:C:382:SER:O	1:C:383:LEU:C	2.45	0.53
1:C:399:VAL:O	1:C:399:VAL:HG12	2.09	0.53
1:F:451:ASP:OD2	1:F:471:ALA:N	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:399:VAL:O	1:B:399:VAL:HG12	2.09	0.52
1:C:172:SER:O	1:C:174:SER:HA	2.08	0.52
1:D:509:THR:N	1:D:510:PRO:HA	2.14	0.52
1:E:90:LYS:HB2	1:E:344:LEU:HB3	1.90	0.52
1:E:371:GLN:HB3	1:E:484:VAL:HG23	1.90	0.52
1:F:275:THR:OG1	1:F:278:GLN:HG3	2.10	0.52
1:A:228:GLY:HA2	1:A:345:SER:H	1.74	0.52
1:A:374:ILE:HG23	1:A:472:ALA:HA	1.91	0.52
1:A:408:SER:CB	1:A:451:ASP:HB3	2.39	0.52
1:B:275:THR:OG1	1:B:278:GLN:HG3	2.09	0.52
1:C:244:TYR:CD2	1:C:273:PRO:HD2	2.43	0.52
1:C:275:THR:OG1	1:C:278:GLN:HG3	2.10	0.52
1:C:228:GLY:HA2	1:C:345:SER:H	1.74	0.52
1:D:275:THR:OG1	1:D:278:GLN:HG3	2.09	0.52
1:F:173:SER:N	1:F:174:SER:HA	2.22	0.52
1:D:172:SER:O	1:D:174:SER:HA	2.08	0.52
1:D:397:GLY:HA2	1:D:403:CYS:SG	2.49	0.52
1:D:90:LYS:HB2	1:D:344:LEU:HB3	1.90	0.52
1:F:371:GLN:HB3	1:F:484:VAL:HG23	1.90	0.52
1:C:228:GLY:HA2	1:C:345:SER:CB	2.32	0.52
1:E:228:GLY:HA2	1:E:345:SER:CB	2.32	0.52
1:E:374:ILE:HG23	1:E:472:ALA:HA	1.91	0.52
1:B:198:ILE:HG23	1:B:201:ALA:HB2	1.92	0.52
1:C:114:ASP:CG	1:C:175:SER:HB2	2.29	0.52
1:C:451:ASP:OD2	1:C:471:ALA:N	2.42	0.52
1:F:114:ASP:CG	1:F:175:SER:HB2	2.29	0.52
1:F:374:ILE:HG23	1:F:472:ALA:HA	1.91	0.52
1:B:502:VAL:HG12	1:B:504:LYS:H	1.75	0.52
1:B:29:LEU:O	1:B:80:VAL:HA	2.10	0.52
1:C:198:ILE:HG23	1:C:201:ALA:HB2	1.92	0.52
1:C:408:SER:CB	1:C:451:ASP:HB3	2.39	0.52
1:E:397:GLY:HA2	1:E:403:CYS:SG	2.49	0.52
1:E:29:LEU:O	1:E:80:VAL:HA	2.10	0.52
1:F:453:ASN:HD22	1:F:453:ASN:H	1.58	0.52
1:B:228:GLY:HA2	1:B:345:SER:H	1.74	0.52
1:D:408:SER:CB	1:D:451:ASP:HB3	2.39	0.52
1:E:453:ASN:H	1:E:453:ASN:HD22	1.58	0.52
1:A:198:ILE:HG23	1:A:201:ALA:HB2	1.92	0.52
1:A:275:THR:OG1	1:A:278:GLN:HG3	2.09	0.52
1:B:408:SER:CB	1:B:451:ASP:HB3	2.38	0.52
1:D:399:VAL:O	1:D:399:VAL:HG12	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:51:VAL:HG22	1:F:65:PHE:CZ	2.45	0.52
1:B:172:SER:O	1:B:174:SER:HA	2.08	0.52
1:C:391:LYS:HE3	1:C:441:PHE:HA	1.92	0.52
1:C:391:LYS:NZ	1:C:440:ASN:HD21	1.92	0.52
1:D:198:ILE:HG23	1:D:201:ALA:HB2	1.92	0.52
1:F:228:GLY:HA2	1:F:345:SER:H	1.74	0.52
1:A:453:ASN:HD22	1:A:453:ASN:H	1.58	0.52
1:C:502:VAL:HG12	1:C:504:LYS:H	1.75	0.52
1:D:391:LYS:HE3	1:D:441:PHE:HA	1.92	0.52
1:D:453:ASN:H	1:D:453:ASN:HD22	1.58	0.52
1:E:84:VAL:HG13	1:E:89:ALA:HB2	1.92	0.52
1:B:391:LYS:HE3	1:B:441:PHE:HA	1.92	0.51
1:B:454:TYR:HE2	1:B:469:PRO:HB3	1.75	0.51
1:D:29:LEU:O	1:D:80:VAL:HA	2.10	0.51
1:F:84:VAL:HG13	1:F:89:ALA:HB2	1.92	0.51
1:A:114:ASP:CG	1:A:175:SER:HB2	2.29	0.51
1:A:399:VAL:HG12	1:A:399:VAL:O	2.09	0.51
1:A:51:VAL:HG22	1:A:65:PHE:CZ	2.45	0.51
1:C:508:GLU:CG	1:C:509:THR:HG22	2.36	0.51
1:A:454:TYR:HE2	1:A:469:PRO:HB3	1.75	0.51
1:A:25:GLY:HA2	1:A:484:VAL:HG21	1.93	0.51
1:A:84:VAL:HG13	1:A:89:ALA:HB2	1.92	0.51
1:B:453:ASN:H	1:B:453:ASN:HD22	1.58	0.51
1:C:51:VAL:HG22	1:C:65:PHE:CZ	2.45	0.51
1:D:51:VAL:HG22	1:D:65:PHE:CZ	2.45	0.51
1:D:84:VAL:HG13	1:D:89:ALA:HB2	1.92	0.51
1:E:275:THR:OG1	1:E:278:GLN:HG3	2.10	0.51
1:E:399:VAL:O	1:E:399:VAL:HG12	2.09	0.51
1:E:454:TYR:HE2	1:E:469:PRO:HB3	1.75	0.51
1:F:29:LEU:O	1:F:80:VAL:HA	2.10	0.51
1:F:399:VAL:HG12	1:F:399:VAL:O	2.09	0.51
1:A:502:VAL:HG12	1:A:504:LYS:H	1.75	0.51
1:B:237:GLU:HG3	1:B:337:ILE:CD1	2.41	0.51
1:D:161:PRO:O	1:D:186:LYS:HB3	2.11	0.51
1:D:228:GLY:HA2	1:D:345:SER:H	1.74	0.51
1:E:161:PRO:O	1:E:186:LYS:HB3	2.11	0.51
1:E:352:ALA:O	1:E:355:LEU:HB2	2.10	0.51
1:E:25:GLY:HA2	1:E:484:VAL:HG21	1.93	0.51
1:F:454:TYR:HE2	1:F:469:PRO:HB3	1.75	0.51
1:F:25:GLY:HA2	1:F:484:VAL:HG21	1.93	0.51
1:A:29:LEU:O	1:A:80:VAL:HA	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:173:SER:N	1:B:174:SER:HA	2.22	0.51
1:B:194:LEU:HD23	1:B:195:LEU:N	2.26	0.51
1:C:30:ALA:HB3	1:C:359:TRP:CD2	2.46	0.51
1:C:453:ASN:H	1:C:453:ASN:HD22	1.58	0.51
1:C:29:LEU:O	1:C:80:VAL:HA	2.10	0.51
1:E:194:LEU:HD23	1:E:195:LEU:N	2.26	0.51
1:E:228:GLY:HA2	1:E:345:SER:H	1.74	0.51
1:F:228:GLY:HA2	1:F:345:SER:N	2.25	0.51
1:A:30:ALA:HB3	1:A:359:TRP:CD2	2.46	0.51
1:B:161:PRO:O	1:B:186:LYS:HB3	2.11	0.51
1:C:161:PRO:O	1:C:186:LYS:HB3	2.11	0.51
1:D:30:ALA:HB3	1:D:359:TRP:CD2	2.46	0.51
1:E:502:VAL:HG12	1:E:504:LYS:H	1.75	0.51
1:F:198:ILE:HG23	1:F:201:ALA:HB2	1.92	0.51
1:A:237:GLU:HG3	1:A:337:ILE:CD1	2.41	0.51
1:D:454:TYR:HE2	1:D:469:PRO:HB3	1.75	0.51
1:D:509:THR:N	1:D:510:PRO:CA	2.73	0.51
1:E:237:GLU:HG3	1:E:337:ILE:CD1	2.41	0.51
1:F:30:ALA:HB3	1:F:359:TRP:CD2	2.46	0.51
1:B:30:ALA:HB3	1:B:359:TRP:CD2	2.46	0.51
1:B:379:ALA:HB2	1:B:454:TYR:CE2	2.46	0.51
1:D:114:ASP:CG	1:D:175:SER:HB2	2.29	0.51
1:D:194:LEU:HD23	1:D:195:LEU:N	2.26	0.51
1:E:198:ILE:HG23	1:E:201:ALA:HB2	1.92	0.51
1:E:391:LYS:HE3	1:E:441:PHE:HA	1.92	0.51
1:F:502:VAL:HG12	1:F:504:LYS:H	1.75	0.51
1:A:391:LYS:HE3	1:A:441:PHE:HA	1.92	0.51
1:A:70:ASN:HB3	1:A:457:GLN:HE22	1.76	0.51
1:B:228:GLY:HA2	1:B:345:SER:N	2.25	0.51
1:C:194:LEU:HD23	1:C:195:LEU:N	2.26	0.51
1:C:84:VAL:HG13	1:C:89:ALA:HB2	1.92	0.51
1:D:352:ALA:O	1:D:355:LEU:HB2	2.10	0.51
1:E:228:GLY:HA2	1:E:345:SER:N	2.25	0.51
1:E:51:VAL:HG22	1:E:65:PHE:CZ	2.45	0.51
1:A:352:ALA:O	1:A:355:LEU:HB2	2.10	0.51
1:B:407:CYS:N	1:B:449:ALA:O	2.44	0.51
1:B:84:VAL:HG13	1:B:89:ALA:HB2	1.92	0.51
1:C:352:ALA:O	1:C:355:LEU:HB2	2.10	0.51
1:D:300:GLY:O	1:D:302:LYS:HG3	2.11	0.51
1:D:228:GLY:HA2	1:D:345:SER:N	2.25	0.51
1:A:228:GLY:HA2	1:A:345:SER:N	2.25	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:254:ILE:HG12	1:A:337:ILE:HB	1.93	0.50
1:A:407:CYS:N	1:A:449:ALA:O	2.44	0.50
1:B:254:ILE:HG12	1:B:337:ILE:HB	1.93	0.50
1:B:25:GLY:HA2	1:B:484:VAL:HG21	1.93	0.50
1:C:228:GLY:HA2	1:C:345:SER:N	2.25	0.50
1:C:454:TYR:HE2	1:C:469:PRO:HB3	1.75	0.50
1:C:25:GLY:HA2	1:C:484:VAL:HG21	1.93	0.50
1:C:70:ASN:HB3	1:C:457:GLN:HE22	1.76	0.50
1:D:407:CYS:N	1:D:449:ALA:O	2.44	0.50
1:F:289:ILE:HD12	1:F:289:ILE:N	2.24	0.50
1:C:407:CYS:N	1:C:449:ALA:O	2.45	0.50
1:D:502:VAL:HG12	1:D:504:LYS:H	1.75	0.50
1:E:30:ALA:HB3	1:E:359:TRP:CD2	2.46	0.50
1:E:508:GLU:CG	1:E:509:THR:HG22	2.36	0.50
1:F:161:PRO:O	1:F:186:LYS:HB3	2.11	0.50
1:A:220:PRO:HD2	1:A:338:LEU:HD11	1.94	0.50
1:A:289:ILE:N	1:A:289:ILE:HD12	2.24	0.50
1:D:25:GLY:HA2	1:D:484:VAL:HG21	1.93	0.50
1:E:220:PRO:HD2	1:E:338:LEU:HD11	1.94	0.50
1:B:300:GLY:O	1:B:302:LYS:HG3	2.11	0.50
1:C:300:GLY:O	1:C:302:LYS:HG3	2.12	0.50
1:C:237:GLU:HG3	1:C:337:ILE:CD1	2.41	0.50
1:D:237:GLU:HG3	1:D:337:ILE:CD1	2.41	0.50
1:E:300:GLY:O	1:E:302:LYS:HG3	2.12	0.50
1:E:509:THR:N	1:E:510:PRO:CA	2.73	0.50
1:F:178:LEU:HD23	1:F:178:LEU:N	2.22	0.50
1:F:194:LEU:HD23	1:F:195:LEU:N	2.26	0.50
1:F:391:LYS:HE3	1:F:441:PHE:HA	1.92	0.50
1:A:161:PRO:O	1:A:186:LYS:HB3	2.11	0.50
1:A:194:LEU:HD23	1:A:195:LEU:N	2.26	0.50
1:B:352:ALA:O	1:B:355:LEU:HB2	2.11	0.50
1:D:228:GLY:HA2	1:D:345:SER:CB	2.32	0.50
1:F:237:GLU:HG3	1:F:337:ILE:CD1	2.41	0.50
1:F:70:ASN:HB3	1:F:457:GLN:HE22	1.76	0.50
1:F:71:PHE:C	1:F:71:PHE:CD2	2.85	0.50
1:A:71:PHE:CD2	1:A:71:PHE:C	2.85	0.50
1:B:51:VAL:HG22	1:B:65:PHE:CZ	2.45	0.50
1:E:289:ILE:N	1:E:289:ILE:HD12	2.24	0.50
1:D:220:PRO:HD2	1:D:338:LEU:HD11	1.94	0.50
1:A:300:GLY:O	1:A:302:LYS:HG3	2.11	0.50
1:B:236:ILE:HD12	1:B:236:ILE:N	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:254:ILE:HG12	1:C:337:ILE:HB	1.93	0.50
1:C:379:ALA:HB2	1:C:454:TYR:CE2	2.46	0.50
1:D:70:ASN:HB3	1:D:457:GLN:HE22	1.76	0.50
1:E:407:CYS:N	1:E:449:ALA:O	2.44	0.50
1:F:254:ILE:HG12	1:F:337:ILE:HB	1.93	0.50
1:F:352:ALA:O	1:F:355:LEU:HB2	2.10	0.50
1:B:304:ILE:HG13	1:B:305:TYR:CD2	2.47	0.50
1:C:236:ILE:HD12	1:C:236:ILE:N	2.27	0.50
1:D:236:ILE:N	1:D:236:ILE:HD12	2.27	0.50
1:E:70:ASN:HB3	1:E:457:GLN:HE22	1.76	0.50
1:F:300:GLY:O	1:F:302:LYS:HG3	2.12	0.50
1:D:245:ALA:C	1:D:247:GLY:H	2.15	0.49
1:A:236:ILE:N	1:A:236:ILE:HD12	2.27	0.49
1:D:362:PHE:HA	1:D:368:VAL:HG21	1.94	0.49
1:E:254:ILE:HG12	1:E:337:ILE:HB	1.93	0.49
1:E:362:PHE:HA	1:E:368:VAL:HG21	1.94	0.49
1:F:236:ILE:N	1:F:236:ILE:HD12	2.27	0.49
1:F:407:CYS:N	1:F:449:ALA:O	2.44	0.49
1:B:220:PRO:HD2	1:B:338:LEU:HD11	1.94	0.49
1:C:71:PHE:C	1:C:71:PHE:CD2	2.85	0.49
1:D:304:ILE:HG13	1:D:305:TYR:CD2	2.47	0.49
1:D:383:LEU:O	1:D:386:ALA:HB3	2.13	0.49
1:D:508:GLU:CG	1:D:509:THR:HG22	2.36	0.49
1:E:236:ILE:HD12	1:E:236:ILE:N	2.27	0.49
1:F:220:PRO:HD2	1:F:338:LEU:HD11	1.94	0.49
1:A:304:ILE:HG13	1:A:305:TYR:CD2	2.47	0.49
1:B:391:LYS:NZ	1:B:440:ASN:HD21	1.92	0.49
1:D:254:ILE:HG12	1:D:337:ILE:HB	1.93	0.49
1:E:109:ASN:O	1:E:177:GLY:HA3	2.13	0.49
1:E:173:SER:N	1:E:174:SER:HA	2.22	0.49
1:B:70:ASN:HB3	1:B:457:GLN:HE22	1.76	0.49
1:D:456:TYR:HB2	1:D:467:TRP:CZ3	2.48	0.49
1:E:71:PHE:CD2	1:E:71:PHE:C	2.85	0.49
1:F:245:ALA:C	1:F:247:GLY:H	2.15	0.49
1:F:456:TYR:HB2	1:F:467:TRP:CZ3	2.48	0.49
1:A:456:TYR:HB2	1:A:467:TRP:CZ3	2.48	0.49
1:B:71:PHE:CD2	1:B:71:PHE:C	2.85	0.49
1:C:362:PHE:HA	1:C:368:VAL:HG21	1.94	0.49
1:E:383:LEU:O	1:E:386:ALA:HB3	2.13	0.49
1:F:304:ILE:HG13	1:F:305:TYR:CD2	2.47	0.49
1:F:376:GLY:HA2	1:F:390:GLN:NE2	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:245:ALA:C	1:A:247:GLY:H	2.16	0.49
1:A:376:GLY:HA2	1:A:390:GLN:NE2	2.28	0.49
1:B:109:ASN:O	1:B:177:GLY:HA3	2.13	0.49
1:C:383:LEU:O	1:C:386:ALA:HB3	2.13	0.49
1:F:215:LYS:CE	1:F:329:ASN:HD21	2.25	0.49
1:F:379:ALA:HB2	1:F:454:TYR:CE2	2.46	0.49
1:B:376:GLY:HA2	1:B:390:GLN:NE2	2.28	0.49
1:B:445:SER:HB3	1:B:448:ALA:HB2	1.95	0.49
1:C:456:TYR:HB2	1:C:467:TRP:CZ3	2.48	0.49
1:B:383:LEU:O	1:B:386:ALA:HB3	2.13	0.49
1:C:220:PRO:HD2	1:C:338:LEU:HD11	1.94	0.49
1:E:456:TYR:HB2	1:E:467:TRP:CZ3	2.48	0.49
1:A:508:GLU:HA	1:A:509:THR:HA	1.59	0.48
1:A:63:ASP:O	1:A:67:SER:HB2	2.14	0.48
1:B:413:THR:OG1	1:B:425:ASN:HB3	2.14	0.48
1:D:109:ASN:O	1:D:177:GLY:HA3	2.13	0.48
1:D:289:ILE:HD12	1:D:289:ILE:N	2.24	0.48
1:D:71:PHE:CD2	1:D:71:PHE:C	2.85	0.48
1:F:383:LEU:O	1:F:386:ALA:HB3	2.13	0.48
1:C:23:SER:HG	1:C:483:ASN:HB3	1.76	0.48
1:D:379:ALA:HB2	1:D:454:TYR:CE2	2.46	0.48
1:E:304:ILE:HG13	1:E:305:TYR:CD2	2.47	0.48
1:E:445:SER:HB3	1:E:448:ALA:HB2	1.95	0.48
1:A:383:LEU:O	1:A:386:ALA:HB3	2.13	0.48
1:B:456:TYR:HB2	1:B:467:TRP:CZ3	2.48	0.48
1:C:304:ILE:HG13	1:C:305:TYR:CD2	2.47	0.48
1:C:408:SER:HA	1:C:451:ASP:O	2.14	0.48
1:C:63:ASP:O	1:C:67:SER:HB2	2.14	0.48
1:A:362:PHE:HA	1:A:368:VAL:HG21	1.94	0.48
1:A:413:THR:OG1	1:A:425:ASN:HB3	2.14	0.48
1:B:63:ASP:O	1:B:67:SER:HB2	2.14	0.48
1:C:289:ILE:N	1:C:289:ILE:HD12	2.24	0.48
1:C:376:GLY:HA2	1:C:390:GLN:NE2	2.28	0.48
1:D:376:GLY:HA2	1:D:390:GLN:NE2	2.28	0.48
1:D:408:SER:HA	1:D:451:ASP:O	2.14	0.48
1:E:382:SER:CB	1:E:385:THR:HG22	2.42	0.48
1:E:376:GLY:HA2	1:E:390:GLN:NE2	2.28	0.48
1:E:453:ASN:H	1:E:453:ASN:ND2	2.11	0.48
1:F:63:ASP:O	1:F:67:SER:HB2	2.14	0.48
1:A:109:ASN:O	1:A:177:GLY:HA3	2.13	0.48
1:B:245:ALA:C	1:B:247:GLY:H	2.16	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:289:ILE:HD12	1:B:289:ILE:N	2.24	0.48
1:D:445:SER:HB3	1:D:448:ALA:HB2	1.95	0.48
1:E:408:SER:HA	1:E:451:ASP:O	2.14	0.48
1:E:508:GLU:HA	1:E:509:THR:HA	1.59	0.48
1:A:456:TYR:CZ	1:A:465:ASN:HB3	2.49	0.48
1:C:245:ALA:C	1:C:247:GLY:H	2.15	0.48
1:D:413:THR:OG1	1:D:425:ASN:HB3	2.14	0.48
1:E:413:THR:OG1	1:E:425:ASN:HB3	2.14	0.48
1:F:362:PHE:HA	1:F:368:VAL:HG21	1.94	0.48
1:A:453:ASN:ND2	1:A:453:ASN:H	2.11	0.48
1:B:284:ARG:HA	1:B:288:ALA:O	2.14	0.48
1:F:445:SER:HB3	1:F:448:ALA:HB2	1.95	0.48
1:F:453:ASN:ND2	1:F:453:ASN:N	2.62	0.48
1:C:109:ASN:O	1:C:177:GLY:HA3	2.13	0.48
1:C:285:ARG:O	1:C:286:ASN:HB2	2.14	0.48
1:C:284:ARG:HA	1:C:288:ALA:O	2.14	0.48
1:C:409:PRO:C	1:C:454:TYR:CE1	2.71	0.48
1:F:413:THR:OG1	1:F:425:ASN:HB3	2.14	0.48
1:A:285:ARG:O	1:A:286:ASN:HB2	2.14	0.48
1:C:456:TYR:CZ	1:C:465:ASN:HB3	2.49	0.48
1:F:125:ILE:HD12	1:F:153:LYS:HG2	1.96	0.48
1:F:284:ARG:HA	1:F:288:ALA:O	2.14	0.48
1:F:450:ILE:CG1	1:F:451:ASP:N	2.53	0.48
1:A:445:SER:HB3	1:A:448:ALA:HB2	1.95	0.48
1:A:453:ASN:ND2	1:A:453:ASN:N	2.62	0.48
1:C:453:ASN:H	1:C:453:ASN:ND2	2.12	0.48
1:D:284:ARG:HA	1:D:288:ALA:O	2.14	0.48
1:E:171:ILE:CG2	1:E:172:SER:H	2.25	0.48
1:E:285:ARG:O	1:E:286:ASN:HB2	2.14	0.48
1:E:284:ARG:HA	1:E:288:ALA:O	2.14	0.48
1:F:453:ASN:ND2	1:F:453:ASN:H	2.11	0.48
1:A:125:ILE:HD12	1:A:153:LYS:HG2	1.96	0.47
1:B:125:ILE:HD12	1:B:153:LYS:HG2	1.96	0.47
1:B:362:PHE:HA	1:B:368:VAL:HG21	1.94	0.47
1:B:453:ASN:H	1:B:453:ASN:ND2	2.11	0.47
1:E:245:ALA:C	1:E:247:GLY:H	2.15	0.47
1:F:456:TYR:CZ	1:F:465:ASN:HB3	2.49	0.47
1:B:30:ALA:HB3	1:B:359:TRP:CE2	2.49	0.47
1:D:30:ALA:HB3	1:D:359:TRP:CE2	2.49	0.47
1:E:440:ASN:C	1:E:440:ASN:HD22	2.17	0.47
1:A:30:ALA:HB3	1:A:359:TRP:CE2	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:440:ASN:HD22	1:A:440:ASN:C	2.17	0.47
1:D:215:LYS:CE	1:D:329:ASN:HD21	2.25	0.47
1:D:453:ASN:H	1:D:453:ASN:ND2	2.11	0.47
1:D:409:PRO:C	1:D:454:TYR:CE1	2.71	0.47
1:D:63:ASP:O	1:D:67:SER:HB2	2.14	0.47
1:F:440:ASN:C	1:F:440:ASN:HD22	2.17	0.47
1:A:408:SER:HA	1:A:451:ASP:O	2.14	0.47
1:B:456:TYR:CZ	1:B:465:ASN:HB3	2.49	0.47
1:E:125:ILE:HD12	1:E:153:LYS:HG2	1.96	0.47
1:F:285:ARG:O	1:F:286:ASN:HB2	2.14	0.47
1:F:502:VAL:HG12	1:F:503:ILE:N	2.29	0.47
1:A:163:LEU:HB3	1:A:164:GLY:H	1.63	0.47
1:D:407:CYS:O	1:D:451:ASP:HB3	2.14	0.47
1:E:456:TYR:CZ	1:E:465:ASN:HB3	2.49	0.47
1:F:109:ASN:O	1:F:177:GLY:HA3	2.13	0.47
1:F:30:ALA:HB3	1:F:359:TRP:CE2	2.49	0.47
1:A:284:ARG:HA	1:A:288:ALA:O	2.14	0.47
1:C:30:ALA:HB3	1:C:359:TRP:CE2	2.49	0.47
1:C:413:THR:OG1	1:C:425:ASN:HB3	2.14	0.47
1:D:407:CYS:O	1:D:451:ASP:N	2.48	0.47
1:E:502:VAL:HG12	1:E:503:ILE:N	2.29	0.47
1:E:27:ALA:HB2	1:E:71:PHE:CZ	2.50	0.47
1:F:382:SER:CB	1:F:385:THR:HG22	2.42	0.47
1:F:508:GLU:CG	1:F:509:THR:HG22	2.36	0.47
1:A:37:PRO:HB2	1:A:40:GLN:HB2	1.97	0.47
1:A:58:THR:H	1:A:61:THR:HB	1.79	0.47
1:C:125:ILE:HD12	1:C:153:LYS:HG2	1.96	0.47
1:D:456:TYR:CZ	1:D:465:ASN:HB3	2.49	0.47
1:E:407:CYS:O	1:E:451:ASP:N	2.48	0.47
1:F:407:CYS:O	1:F:451:ASP:HB3	2.14	0.47
1:B:453:ASN:ND2	1:B:453:ASN:N	2.62	0.47
1:C:215:LYS:CE	1:C:329:ASN:HD21	2.25	0.47
1:D:125:ILE:HD12	1:D:153:LYS:HG2	1.96	0.47
1:A:407:CYS:O	1:A:451:ASP:N	2.48	0.47
1:B:151:ILE:HG13	1:B:152:ALA:N	2.30	0.47
1:C:37:PRO:HB2	1:C:40:GLN:HB2	1.97	0.47
1:C:445:SER:HB3	1:C:448:ALA:HB2	1.95	0.47
1:D:37:PRO:HB2	1:D:40:GLN:HB2	1.97	0.47
1:D:440:ASN:HD22	1:D:440:ASN:C	2.17	0.47
1:D:453:ASN:N	1:D:453:ASN:ND2	2.62	0.47
1:D:508:GLU:HA	1:D:509:THR:HA	1.59	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:63:ASP:O	1:E:67:SER:HB2	2.14	0.47
1:F:62:ALA:HB1	1:F:466:ARG:NE	2.30	0.47
1:F:58:THR:H	1:F:61:THR:HB	1.79	0.47
1:A:62:ALA:HB1	1:A:466:ARG:NE	2.30	0.47
1:B:215:LYS:CE	1:B:329:ASN:HD21	2.25	0.47
1:B:408:SER:HA	1:B:451:ASP:O	2.14	0.47
1:C:151:ILE:HG13	1:C:152:ALA:N	2.30	0.47
1:C:407:CYS:O	1:C:451:ASP:N	2.48	0.47
1:D:27:ALA:HB2	1:D:71:PHE:CZ	2.50	0.47
1:D:382:SER:CB	1:D:385:THR:HG22	2.42	0.47
1:E:215:LYS:CE	1:E:329:ASN:HD21	2.25	0.47
1:F:27:ALA:HB2	1:F:71:PHE:CZ	2.50	0.47
1:B:285:ARG:O	1:B:286:ASN:HB2	2.14	0.47
1:B:62:ALA:HB1	1:B:466:ARG:NE	2.30	0.47
1:C:440:ASN:HD22	1:C:440:ASN:C	2.17	0.47
1:C:453:ASN:N	1:C:453:ASN:ND2	2.62	0.47
1:E:151:ILE:HG13	1:E:152:ALA:N	2.30	0.47
1:E:30:ALA:HB3	1:E:359:TRP:CE2	2.49	0.47
1:E:407:CYS:O	1:E:451:ASP:HB3	2.14	0.47
1:A:411:ARG:O	1:A:412:GLU:C	2.54	0.46
1:B:350:VAL:HG13	1:B:354:ASP:HB2	1.97	0.46
1:B:411:ARG:O	1:B:412:GLU:C	2.54	0.46
1:B:407:CYS:O	1:B:451:ASP:N	2.48	0.46
1:C:411:ARG:O	1:C:412:GLU:C	2.54	0.46
1:C:58:THR:H	1:C:61:THR:HB	1.79	0.46
1:D:58:THR:H	1:D:61:THR:HB	1.80	0.46
1:F:411:ARG:O	1:F:412:GLU:C	2.54	0.46
1:A:379:ALA:HB2	1:A:454:TYR:CE2	2.46	0.46
1:B:171:ILE:CG2	1:B:172:SER:H	2.25	0.46
1:B:440:ASN:C	1:B:440:ASN:HD22	2.17	0.46
1:C:100:GLU:HG2	1:C:186:LYS:O	2.16	0.46
1:C:382:SER:CB	1:C:385:THR:HG22	2.42	0.46
1:C:502:VAL:HG12	1:C:503:ILE:N	2.29	0.46
1:D:411:ARG:O	1:D:412:GLU:C	2.54	0.46
1:F:100:GLU:HG2	1:F:186:LYS:O	2.16	0.46
1:A:215:LYS:CE	1:A:329:ASN:HD21	2.25	0.46
1:A:27:ALA:HB3	1:A:78:LEU:HD12	1.98	0.46
1:B:502:VAL:HG12	1:B:503:ILE:N	2.29	0.46
1:D:27:ALA:HB3	1:D:78:LEU:HD12	1.98	0.46
1:E:411:ARG:O	1:E:412:GLU:C	2.54	0.46
1:E:62:ALA:HB1	1:E:466:ARG:NE	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:37:PRO:HB2	1:F:40:GLN:HB2	1.97	0.46
1:A:290:VAL:HG11	1:A:322:TYR:CD1	2.50	0.46
1:A:350:VAL:HG13	1:A:354:ASP:HB2	1.97	0.46
1:C:293:VAL:HG22	1:C:294:VAL:N	2.30	0.46
1:C:62:ALA:HB1	1:C:466:ARG:NE	2.30	0.46
1:C:27:ALA:HB2	1:C:71:PHE:CZ	2.50	0.46
1:F:407:CYS:O	1:F:451:ASP:N	2.48	0.46
1:A:27:ALA:HB2	1:A:71:PHE:CZ	2.50	0.46
1:A:35:TRP:HB3	1:A:54:PHE:HA	1.98	0.46
1:B:293:VAL:HG22	1:B:294:VAL:N	2.30	0.46
1:B:58:THR:H	1:B:61:THR:HB	1.79	0.46
1:B:71:PHE:C	1:B:73:GLN:N	2.69	0.46
1:B:27:ALA:HB2	1:B:71:PHE:CZ	2.50	0.46
1:C:208:VAL:HG23	1:C:209:ASP:N	2.31	0.46
1:C:290:VAL:HG11	1:C:322:TYR:CD1	2.50	0.46
1:C:509:THR:CB	1:C:510:PRO:HA	2.43	0.46
1:E:58:THR:H	1:E:61:THR:HB	1.79	0.46
1:F:290:VAL:HG11	1:F:322:TYR:CD1	2.50	0.46
1:F:408:SER:HA	1:F:451:ASP:O	2.14	0.46
1:F:509:THR:CB	1:F:510:PRO:HA	2.44	0.46
1:A:458:TYR:CE2	1:A:460:LYS:HA	2.51	0.46
1:B:509:THR:CB	1:B:510:PRO:HA	2.44	0.46
1:C:173:SER:HA	1:C:174:SER:HB3	1.98	0.46
1:C:35:TRP:HB3	1:C:54:PHE:HA	1.98	0.46
1:D:285:ARG:O	1:D:286:ASN:HB2	2.14	0.46
1:D:35:TRP:HB3	1:D:54:PHE:HA	1.98	0.46
1:D:502:VAL:HG12	1:D:503:ILE:N	2.29	0.46
1:E:56:GLN:HA	1:E:57:PRO:HD3	1.81	0.46
1:F:508:GLU:HA	1:F:509:THR:HA	1.59	0.46
1:F:27:ALA:HB3	1:F:78:LEU:HD12	1.98	0.46
1:A:151:ILE:HG13	1:A:152:ALA:N	2.30	0.46
1:A:100:GLU:HG2	1:A:186:LYS:O	2.16	0.46
1:B:56:GLN:HA	1:B:57:PRO:HD3	1.81	0.46
1:C:350:VAL:HG13	1:C:354:ASP:HB2	1.97	0.46
1:C:71:PHE:C	1:C:73:GLN:N	2.69	0.46
1:D:100:GLU:HG2	1:D:186:LYS:O	2.16	0.46
1:D:290:VAL:HG11	1:D:322:TYR:CD1	2.50	0.46
1:E:208:VAL:HG23	1:E:209:ASP:N	2.31	0.46
1:E:27:ALA:HB3	1:E:78:LEU:HD12	1.98	0.46
1:E:290:VAL:HG11	1:E:322:TYR:CD1	2.50	0.46
1:F:458:TYR:CE2	1:F:460:LYS:HA	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:56:GLN:HA	1:A:57:PRO:HD3	1.81	0.46
1:B:208:VAL:HG23	1:B:209:ASP:N	2.31	0.46
1:B:35:TRP:HB3	1:B:54:PHE:HA	1.98	0.46
1:B:71:PHE:C	1:B:73:GLN:H	2.19	0.46
1:F:71:PHE:C	1:F:73:GLN:H	2.19	0.46
1:A:71:PHE:C	1:A:73:GLN:N	2.69	0.46
1:B:27:ALA:HB3	1:B:78:LEU:HD12	1.98	0.46
1:C:508:GLU:HA	1:C:509:THR:HA	1.59	0.46
1:C:27:ALA:HB3	1:C:78:LEU:HD12	1.98	0.46
1:D:73:GLN:HB3	1:D:500:LEU:HD12	1.98	0.46
1:E:100:GLU:HG2	1:E:186:LYS:O	2.16	0.46
1:E:211:GLN:OE1	1:E:328:GLN:HG2	2.16	0.46
1:F:171:ILE:CG2	1:F:172:SER:H	2.25	0.46
1:A:293:VAL:HG22	1:A:294:VAL:N	2.30	0.46
1:A:502:VAL:HG12	1:A:503:ILE:N	2.29	0.46
1:B:37:PRO:HB2	1:B:40:GLN:HB2	1.97	0.46
1:B:508:GLU:HA	1:B:509:THR:HA	1.59	0.46
1:B:508:GLU:CG	1:B:509:THR:HG22	2.36	0.46
1:C:419:VAL:HA	1:C:422:ALA:CB	2.46	0.46
1:E:73:GLN:HB3	1:E:500:LEU:HD12	1.98	0.46
1:F:293:VAL:HG22	1:F:294:VAL:N	2.30	0.46
1:A:130:LYS:O	1:A:132:THR:HG23	2.16	0.45
1:A:71:PHE:C	1:A:73:GLN:H	2.19	0.45
1:B:171:ILE:CG2	1:B:172:SER:N	2.79	0.45
1:D:307:SER:O	1:D:309:ILE:HG23	2.16	0.45
1:D:350:VAL:HG13	1:D:354:ASP:HB2	1.97	0.45
1:D:71:PHE:C	1:D:73:GLN:N	2.69	0.45
1:F:208:VAL:HG23	1:F:209:ASP:N	2.31	0.45
1:F:71:PHE:C	1:F:73:GLN:N	2.69	0.45
1:A:171:ILE:CG2	1:A:172:SER:H	2.25	0.45
1:B:100:GLU:HG2	1:B:186:LYS:O	2.16	0.45
1:B:73:GLN:HB3	1:B:500:LEU:HD12	1.98	0.45
1:D:173:SER:HA	1:D:174:SER:HB3	1.98	0.45
1:D:419:VAL:HA	1:D:422:ALA:CB	2.46	0.45
1:E:350:VAL:HG13	1:E:354:ASP:HB2	1.97	0.45
1:E:35:TRP:HB3	1:E:54:PHE:HA	1.98	0.45
1:F:23:SER:OG	1:F:483:ASN:HB2	2.04	0.45
1:F:35:TRP:HB3	1:F:54:PHE:HA	1.98	0.45
1:B:130:LYS:O	1:B:132:THR:HG23	2.16	0.45
1:B:173:SER:HA	1:B:174:SER:HB3	1.98	0.45
1:B:307:SER:O	1:B:309:ILE:HG23	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:50:LEU:HD12	1:C:51:VAL:N	2.32	0.45
1:D:151:ILE:HG13	1:D:152:ALA:N	2.30	0.45
1:D:293:VAL:HG22	1:D:294:VAL:N	2.30	0.45
1:E:37:PRO:HB2	1:E:40:GLN:HB2	1.97	0.45
1:E:453:ASN:ND2	1:E:453:ASN:N	2.62	0.45
1:E:509:THR:HG1	1:E:510:PRO:HA	1.81	0.45
1:A:509:THR:CB	1:A:510:PRO:HA	2.44	0.45
1:B:290:VAL:HG11	1:B:322:TYR:CD1	2.50	0.45
1:B:458:TYR:CE2	1:B:460:LYS:HA	2.51	0.45
1:C:130:LYS:O	1:C:132:THR:HG23	2.16	0.45
1:C:73:GLN:HB3	1:C:500:LEU:HD12	1.98	0.45
1:D:208:VAL:HG23	1:D:209:ASP:N	2.31	0.45
1:E:293:VAL:HG22	1:E:294:VAL:N	2.30	0.45
1:E:307:SER:O	1:E:309:ILE:HG23	2.16	0.45
1:F:350:VAL:HG13	1:F:354:ASP:HB2	1.97	0.45
1:B:382:SER:CB	1:B:385:THR:HG22	2.42	0.45
1:D:456:TYR:CE2	1:D:503:ILE:HD11	2.52	0.45
1:E:458:TYR:CE2	1:E:460:LYS:HA	2.51	0.45
1:E:71:PHE:C	1:E:73:GLN:N	2.69	0.45
1:A:173:SER:HA	1:A:174:SER:HB3	1.98	0.45
1:A:211:GLN:OE1	1:A:328:GLN:HG2	2.16	0.45
1:C:307:SER:O	1:C:309:ILE:HG23	2.16	0.45
1:C:458:TYR:CE2	1:C:460:LYS:HA	2.51	0.45
1:D:211:GLN:OE1	1:D:328:GLN:HG2	2.16	0.45
1:E:379:ALA:HB2	1:E:454:TYR:CE2	2.46	0.45
1:A:208:VAL:HG23	1:A:209:ASP:N	2.31	0.45
1:B:211:GLN:OE1	1:B:328:GLN:HG2	2.16	0.45
1:C:390:GLN:HE22	1:C:408:SER:H	1.65	0.45
1:D:283:VAL:CG2	1:D:323:ILE:HD13	2.47	0.45
1:E:50:LEU:HD12	1:E:51:VAL:N	2.32	0.45
1:A:153:LYS:O	1:A:157:VAL:HG22	2.17	0.45
1:B:153:LYS:O	1:B:157:VAL:HG22	2.17	0.45
1:B:390:GLN:HE22	1:B:408:SER:H	1.65	0.45
1:C:211:GLN:OE1	1:C:328:GLN:HG2	2.16	0.45
1:C:71:PHE:C	1:C:73:GLN:H	2.19	0.45
1:D:153:LYS:O	1:D:157:VAL:HG22	2.17	0.45
1:D:50:LEU:HD12	1:D:51:VAL:N	2.32	0.45
1:D:62:ALA:HB1	1:D:466:ARG:NE	2.30	0.45
1:E:173:SER:HA	1:E:174:SER:HB3	1.98	0.45
1:E:71:PHE:C	1:E:73:GLN:H	2.19	0.45
1:D:71:PHE:C	1:D:73:GLN:H	2.19	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:153:LYS:O	1:F:157:VAL:HG22	2.17	0.45
1:F:173:SER:HA	1:F:174:SER:HB3	1.98	0.45
1:F:456:TYR:CE2	1:F:503:ILE:HD11	2.52	0.45
1:A:90:LYS:N	1:A:344:LEU:O	2.48	0.45
1:A:382:SER:CB	1:A:385:THR:HG22	2.42	0.45
1:C:283:VAL:CG2	1:C:323:ILE:HD13	2.47	0.45
1:C:385:THR:HA	1:C:388:THR:HG23	1.98	0.45
1:C:56:GLN:HA	1:C:57:PRO:HD3	1.81	0.45
1:D:178:LEU:N	1:D:178:LEU:HD23	2.22	0.45
1:D:390:GLN:HE22	1:D:408:SER:H	1.65	0.45
1:E:130:LYS:O	1:E:132:THR:HG23	2.16	0.45
1:E:283:VAL:CG2	1:E:323:ILE:HD13	2.47	0.45
1:F:375:ALA:HB3	1:F:406:LEU:O	2.17	0.45
1:A:73:GLN:HB3	1:A:500:LEU:HD12	1.98	0.44
1:B:160:TYR:HA	1:B:161:PRO:HA	1.82	0.44
1:B:283:VAL:CG2	1:B:323:ILE:HD13	2.47	0.44
1:B:50:LEU:HD12	1:B:51:VAL:N	2.31	0.44
1:C:364:ASP:OD1	1:C:364:ASP:N	2.51	0.44
1:D:130:LYS:O	1:D:132:THR:HG23	2.16	0.44
1:D:147:THR:O	1:D:151:ILE:HG23	2.17	0.44
1:D:458:TYR:CE2	1:D:460:LYS:HA	2.51	0.44
1:E:456:TYR:CE2	1:E:503:ILE:HD11	2.52	0.44
1:A:456:TYR:CE2	1:A:503:ILE:HD11	2.52	0.44
1:B:385:THR:HA	1:B:388:THR:HG23	1.98	0.44
1:C:375:ALA:HB3	1:C:406:LEU:O	2.17	0.44
1:D:44:VAL:HG11	1:D:50:LEU:HB3	1.99	0.44
1:D:454:TYR:O	1:D:467:TRP:CZ3	2.71	0.44
1:E:364:ASP:N	1:E:364:ASP:OD1	2.51	0.44
1:E:385:THR:HA	1:E:388:THR:HG23	1.98	0.44
1:E:454:TYR:O	1:E:467:TRP:CZ3	2.71	0.44
1:F:307:SER:O	1:F:309:ILE:HG23	2.16	0.44
1:C:153:LYS:O	1:C:157:VAL:HG22	2.17	0.44
1:C:456:TYR:CE2	1:C:503:ILE:HD11	2.52	0.44
1:E:147:THR:O	1:E:151:ILE:HG23	2.17	0.44
1:E:375:ALA:HB3	1:E:406:LEU:O	2.17	0.44
1:A:307:SER:O	1:A:309:ILE:HG23	2.16	0.44
1:A:283:VAL:CG2	1:A:323:ILE:HD13	2.47	0.44
1:A:419:VAL:HA	1:A:422:ALA:CB	2.46	0.44
1:A:508:GLU:CG	1:A:509:THR:HG22	2.36	0.44
1:C:160:TYR:HA	1:C:161:PRO:HA	1.82	0.44
1:F:73:GLN:HB3	1:F:500:LEU:HD12	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:147:THR:O	1:A:151:ILE:HG23	2.17	0.44
1:C:253:PRO:HD2	1:C:336:GLY:HA2	2.00	0.44
1:F:130:LYS:O	1:F:132:THR:HG23	2.16	0.44
1:F:147:THR:O	1:F:151:ILE:HG23	2.17	0.44
1:A:222:VAL:HG11	1:A:236:ILE:HG12	2.00	0.44
1:A:364:ASP:N	1:A:364:ASP:OD1	2.50	0.44
1:B:253:PRO:HD2	1:B:336:GLY:HA2	2.00	0.44
1:B:456:TYR:CE2	1:B:503:ILE:HD11	2.52	0.44
1:C:147:THR:O	1:C:151:ILE:HG23	2.17	0.44
1:D:385:THR:HA	1:D:388:THR:HG23	1.99	0.44
1:E:153:LYS:O	1:E:157:VAL:HG22	2.17	0.44
1:E:419:VAL:HA	1:E:422:ALA:CB	2.46	0.44
1:F:211:GLN:OE1	1:F:328:GLN:HG2	2.16	0.44
1:F:222:VAL:HG11	1:F:236:ILE:HG12	2.00	0.44
1:F:454:TYR:O	1:F:467:TRP:CZ3	2.71	0.44
1:A:390:GLN:HE22	1:A:408:SER:H	1.65	0.44
1:A:44:VAL:HG11	1:A:50:LEU:HB3	1.99	0.44
1:B:454:TYR:O	1:B:467:TRP:CZ3	2.71	0.44
1:C:44:VAL:HG11	1:C:50:LEU:HB3	1.99	0.44
1:D:62:ALA:HB1	1:D:466:ARG:HE	1.83	0.44
1:F:283:VAL:CG2	1:F:323:ILE:HD13	2.47	0.44
1:A:171:ILE:CG2	1:A:172:SER:N	2.79	0.44
1:D:163:LEU:HB3	1:D:164:GLY:H	1.63	0.44
1:F:419:VAL:HA	1:F:422:ALA:CB	2.46	0.44
1:B:222:VAL:HG11	1:B:236:ILE:HG12	2.00	0.44
1:A:100:GLU:HB2	1:A:185:GLY:CA	2.48	0.43
1:B:147:THR:O	1:B:151:ILE:HG23	2.17	0.43
1:B:375:ALA:HB3	1:B:406:LEU:O	2.17	0.43
1:E:222:VAL:HG11	1:E:236:ILE:HG12	2.00	0.43
1:F:151:ILE:HG13	1:F:152:ALA:N	2.30	0.43
1:F:364:ASP:OD1	1:F:364:ASP:N	2.50	0.43
1:F:390:GLN:HE22	1:F:408:SER:H	1.65	0.43
1:F:44:VAL:HG11	1:F:50:LEU:HB3	1.99	0.43
1:A:454:TYR:O	1:A:467:TRP:CZ3	2.71	0.43
1:B:100:GLU:HB2	1:B:185:GLY:CA	2.48	0.43
1:C:453:ASN:HD22	1:C:453:ASN:N	2.16	0.43
1:D:100:GLU:HB2	1:D:185:GLY:CA	2.48	0.43
1:D:375:ALA:HB3	1:D:406:LEU:O	2.17	0.43
1:D:499:ILE:N	1:D:499:ILE:HD13	2.28	0.43
1:E:254:ILE:HB	1:E:258:GLY:O	2.18	0.43
1:E:62:ALA:HB1	1:E:466:ARG:HE	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:377:SER:HA	1:F:469:PRO:HG3	2.00	0.43
1:A:295:LEU:HD11	1:A:314:PHE:CD2	2.54	0.43
1:A:385:THR:HA	1:A:388:THR:HG23	1.98	0.43
1:E:44:VAL:HG11	1:E:50:LEU:HB3	1.99	0.43
1:F:100:GLU:HB2	1:F:185:GLY:CA	2.48	0.43
1:F:254:ILE:HB	1:F:258:GLY:O	2.19	0.43
1:F:385:THR:HA	1:F:388:THR:HG23	1.98	0.43
1:A:254:ILE:HB	1:A:258:GLY:O	2.18	0.43
1:B:377:SER:HA	1:B:469:PRO:HG3	2.00	0.43
1:C:222:VAL:HG11	1:C:236:ILE:HG12	2.00	0.43
1:C:304:ILE:HG13	1:C:305:TYR:HE2	1.81	0.43
1:C:62:ALA:HB1	1:C:466:ARG:HE	1.83	0.43
1:D:295:LEU:HD11	1:D:314:PHE:CD2	2.54	0.43
1:D:74:TYR:OH	1:D:473:ASP:OD2	2.35	0.43
1:E:100:GLU:HB2	1:E:185:GLY:CA	2.48	0.43
1:E:377:SER:HA	1:E:469:PRO:HG3	2.00	0.43
1:E:499:ILE:N	1:E:499:ILE:HD13	2.28	0.43
1:A:253:PRO:HD2	1:A:336:GLY:HA2	2.00	0.43
1:A:377:SER:HA	1:A:469:PRO:HG3	2.00	0.43
1:C:100:GLU:HB2	1:C:185:GLY:CA	2.48	0.43
1:C:454:TYR:O	1:C:467:TRP:CZ3	2.71	0.43
1:C:377:SER:HA	1:C:469:PRO:HG3	2.00	0.43
1:E:100:GLU:HG3	1:E:186:LYS:N	2.32	0.43
1:E:409:PRO:C	1:E:454:TYR:CE1	2.71	0.43
1:F:240:SER:HB3	1:F:279:TYR:CE1	2.53	0.43
1:F:453:ASN:HD22	1:F:453:ASN:N	2.15	0.43
1:A:502:VAL:CG1	1:A:504:LYS:H	2.31	0.43
1:C:295:LEU:HD11	1:C:314:PHE:CD2	2.54	0.43
1:D:222:VAL:HG11	1:D:236:ILE:HG12	2.00	0.43
1:D:253:PRO:HD2	1:D:336:GLY:HA2	2.00	0.43
1:D:502:VAL:CG1	1:D:504:LYS:H	2.31	0.43
1:E:390:GLN:HE22	1:E:408:SER:H	1.65	0.43
1:B:254:ILE:HB	1:B:258:GLY:O	2.18	0.43
1:B:304:ILE:HG13	1:B:305:TYR:HE2	1.81	0.43
1:B:409:PRO:C	1:B:454:TYR:CE1	2.71	0.43
1:C:215:LYS:HE3	1:C:329:ASN:OD1	2.19	0.43
1:C:502:VAL:CG1	1:C:504:LYS:H	2.31	0.43
1:E:48:VAL:O	1:E:48:VAL:HG12	2.19	0.43
1:F:34:GLN:OE1	1:F:230:LEU:HD11	2.19	0.43
1:F:50:LEU:HD12	1:F:51:VAL:N	2.32	0.43
1:A:215:LYS:HE3	1:A:329:ASN:OD1	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:34:GLN:OE1	1:A:230:LEU:HD11	2.19	0.43
1:A:50:LEU:HD12	1:A:51:VAL:N	2.32	0.43
1:A:97:GLY:O	1:A:98:ASN:O	2.37	0.43
1:C:478:CYS:C	1:C:480:ARG:N	2.72	0.43
1:D:254:ILE:HB	1:D:258:GLY:O	2.18	0.43
1:E:215:LYS:HE3	1:E:329:ASN:OD1	2.19	0.43
1:E:34:GLN:OE1	1:E:230:LEU:HD11	2.19	0.43
1:F:253:PRO:HD2	1:F:336:GLY:HA2	2.00	0.43
1:A:252:LEU:HA	1:A:253:PRO:HD3	1.80	0.43
1:A:240:SER:HB3	1:A:279:TYR:CE1	2.54	0.43
1:A:375:ALA:HB3	1:A:406:LEU:O	2.17	0.43
1:B:97:GLY:O	1:B:98:ASN:O	2.37	0.43
1:D:364:ASP:OD1	1:D:364:ASP:N	2.50	0.43
1:D:460:LYS:HB3	1:D:460:LYS:HE3	1.82	0.43
1:E:163:LEU:HB3	1:E:164:GLY:H	1.63	0.43
1:E:295:LEU:HD11	1:E:314:PHE:CD2	2.54	0.43
1:E:502:VAL:CG1	1:E:504:LYS:H	2.31	0.43
1:F:295:LEU:HD11	1:F:314:PHE:CD2	2.54	0.43
1:A:407:CYS:O	1:A:451:ASP:HB3	2.14	0.43
1:A:62:ALA:HB1	1:A:466:ARG:HE	1.83	0.43
1:A:48:VAL:O	1:A:48:VAL:HG12	2.19	0.43
1:B:215:LYS:HE3	1:B:329:ASN:OD1	2.19	0.43
1:B:240:SER:HB3	1:B:279:TYR:CE1	2.53	0.43
1:B:34:GLN:OE1	1:B:230:LEU:HD11	2.19	0.43
1:C:48:VAL:O	1:C:48:VAL:HG12	2.19	0.43
1:E:502:VAL:CG1	1:E:503:ILE:N	2.82	0.43
1:E:89:ALA:HB3	1:E:194:LEU:CD1	2.49	0.43
1:F:89:ALA:HB3	1:F:194:LEU:CD1	2.49	0.43
1:A:312:ASP:O	1:A:316:ALA:HB2	2.19	0.42
1:A:502:VAL:CG1	1:A:503:ILE:N	2.82	0.42
1:B:295:LEU:HD11	1:B:314:PHE:CD2	2.54	0.42
1:B:404:LEU:HD23	1:B:404:LEU:HA	1.90	0.42
1:B:419:VAL:HA	1:B:422:ALA:CB	2.46	0.42
1:B:453:ASN:N	1:B:453:ASN:HD22	2.16	0.42
1:B:67:SER:OG	1:B:472:ALA:HB2	2.19	0.42
1:C:34:GLN:OE1	1:C:230:LEU:HD11	2.19	0.42
1:C:77:ASP:O	1:C:77:ASP:OD1	2.37	0.42
1:D:502:VAL:CG1	1:D:503:ILE:N	2.82	0.42
1:E:197:GLU:H	1:E:197:GLU:CD	2.23	0.42
1:E:240:SER:HB3	1:E:279:TYR:CE1	2.54	0.42
1:F:312:ASP:O	1:F:316:ALA:HB2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:502:VAL:CG1	1:F:503:ILE:N	2.82	0.42
1:A:236:ILE:HD11	1:A:340:LEU:HD11	2.01	0.42
1:A:24:THR:O	1:A:26:THR:N	2.52	0.42
1:B:44:VAL:HG11	1:B:50:LEU:HB3	1.99	0.42
1:C:252:LEU:HA	1:C:253:PRO:HD3	1.80	0.42
1:C:254:ILE:HB	1:C:258:GLY:O	2.18	0.42
1:C:240:SER:HB3	1:C:279:TYR:CE1	2.54	0.42
1:C:407:CYS:O	1:C:451:ASP:HB3	2.14	0.42
1:D:377:SER:HA	1:D:469:PRO:HG3	2.01	0.42
1:D:478:CYS:C	1:D:480:ARG:N	2.72	0.42
1:E:24:THR:O	1:E:26:THR:N	2.52	0.42
1:F:100:GLU:HG3	1:F:186:LYS:N	2.32	0.42
1:F:197:GLU:H	1:F:197:GLU:CD	2.23	0.42
1:F:502:VAL:CG1	1:F:504:LYS:H	2.31	0.42
1:B:24:THR:O	1:B:26:THR:N	2.52	0.42
1:B:62:ALA:HB1	1:B:466:ARG:HE	1.83	0.42
1:B:77:ASP:O	1:B:77:ASP:OD1	2.38	0.42
1:C:404:LEU:HD23	1:C:404:LEU:HA	1.90	0.42
1:C:499:ILE:HD13	1:C:499:ILE:N	2.28	0.42
1:D:215:LYS:HE3	1:D:329:ASN:OD1	2.19	0.42
1:D:90:LYS:N	1:D:344:LEU:O	2.48	0.42
1:E:253:PRO:HD2	1:E:336:GLY:HA2	2.00	0.42
1:E:67:SER:OG	1:E:472:ALA:HB2	2.19	0.42
1:F:460:LYS:HE3	1:F:460:LYS:HB3	1.82	0.42
1:F:62:ALA:HB1	1:F:466:ARG:HE	1.83	0.42
1:F:68:ALA:O	1:F:69:MET:C	2.58	0.42
1:F:77:ASP:OD1	1:F:77:ASP:O	2.37	0.42
1:A:509:THR:N	1:A:510:PRO:CA	2.73	0.42
1:B:502:VAL:CG1	1:B:504:LYS:H	2.31	0.42
1:C:74:TYR:OH	1:C:473:ASP:OD2	2.35	0.42
1:D:89:ALA:HB3	1:D:194:LEU:CD1	2.49	0.42
1:E:74:TYR:OH	1:E:473:ASP:OD2	2.35	0.42
1:A:77:ASP:O	1:A:77:ASP:OD1	2.37	0.42
1:C:24:THR:O	1:C:26:THR:N	2.52	0.42
1:C:97:GLY:O	1:C:98:ASN:O	2.37	0.42
1:D:197:GLU:CD	1:D:197:GLU:H	2.23	0.42
1:D:67:SER:OG	1:D:472:ALA:HB2	2.19	0.42
1:D:77:ASP:O	1:D:77:ASP:OD1	2.37	0.42
1:E:252:LEU:HA	1:E:253:PRO:HD3	1.80	0.42
1:E:68:ALA:O	1:E:69:MET:C	2.58	0.42
1:F:67:SER:OG	1:F:472:ALA:HB2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:97:GLY:O	1:F:98:ASN:O	2.37	0.42
1:A:197:GLU:H	1:A:197:GLU:CD	2.23	0.42
1:A:453:ASN:HD22	1:A:453:ASN:N	2.16	0.42
1:A:67:SER:OG	1:A:472:ALA:HB2	2.19	0.42
1:B:312:ASP:O	1:B:316:ALA:HB2	2.19	0.42
1:B:364:ASP:N	1:B:364:ASP:OD1	2.50	0.42
1:C:371:GLN:O	1:C:403:CYS:HA	2.20	0.42
1:D:150:ILE:HG12	1:D:150:ILE:H	1.63	0.42
1:F:48:VAL:O	1:F:48:VAL:HG12	2.19	0.42
1:A:68:ALA:O	1:A:69:MET:C	2.58	0.42
1:C:67:SER:OG	1:C:472:ALA:HB2	2.19	0.42
1:D:48:VAL:HG12	1:D:48:VAL:O	2.19	0.42
1:D:97:GLY:O	1:D:98:ASN:O	2.37	0.42
1:E:77:ASP:O	1:E:77:ASP:OD1	2.37	0.42
1:F:215:LYS:HE3	1:F:329:ASN:OD1	2.19	0.42
1:F:236:ILE:HD11	1:F:340:LEU:HD11	2.01	0.42
1:F:406:LEU:HA	1:F:449:ALA:O	2.20	0.42
1:B:197:GLU:CD	1:B:197:GLU:H	2.23	0.42
1:B:48:VAL:HG12	1:B:48:VAL:O	2.19	0.42
1:C:312:ASP:O	1:C:316:ALA:HB2	2.19	0.42
1:C:502:VAL:CG1	1:C:503:ILE:N	2.82	0.42
1:D:100:GLU:HG3	1:D:186:LYS:N	2.32	0.42
1:D:24:THR:O	1:D:26:THR:N	2.52	0.42
1:F:171:ILE:CG2	1:F:172:SER:N	2.79	0.42
1:F:90:LYS:N	1:F:344:LEU:O	2.48	0.42
1:A:371:GLN:O	1:A:403:CYS:HA	2.20	0.42
1:B:252:LEU:HA	1:B:253:PRO:HD3	1.80	0.42
1:B:502:VAL:CG1	1:B:503:ILE:N	2.82	0.42
1:C:197:GLU:CD	1:C:197:GLU:H	2.23	0.42
1:C:236:ILE:HD11	1:C:340:LEU:HD11	2.01	0.42
1:D:46:ASN:HB2	1:D:49:ASP:CB	2.50	0.42
1:E:478:CYS:C	1:E:480:ARG:N	2.72	0.42
1:F:371:GLN:O	1:F:403:CYS:HA	2.20	0.42
1:F:509:THR:N	1:F:510:PRO:CA	2.73	0.42
1:A:370:VAL:O	1:A:370:VAL:HG23	2.20	0.42
1:C:171:ILE:CG2	1:C:172:SER:N	2.79	0.42
1:C:370:VAL:O	1:C:370:VAL:HG23	2.20	0.42
1:D:34:GLN:OE1	1:D:230:LEU:HD11	2.19	0.42
1:D:236:ILE:HD11	1:D:340:LEU:HD11	2.01	0.42
1:D:370:VAL:O	1:D:370:VAL:HG23	2.20	0.42
1:D:56:GLN:HA	1:D:57:PRO:HD3	1.81	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:68:ALA:O	1:D:69:MET:C	2.58	0.42
1:E:312:ASP:O	1:E:316:ALA:HB2	2.19	0.42
1:F:24:THR:O	1:F:26:THR:N	2.52	0.42
1:A:406:LEU:HA	1:A:449:ALA:O	2.20	0.41
1:A:409:PRO:HG2	1:A:454:TYR:CE1	2.55	0.41
1:B:119:LYS:HE3	1:B:124:ASP:OD1	2.20	0.41
1:B:407:CYS:O	1:B:451:ASP:HB3	2.14	0.41
1:C:171:ILE:CG2	1:C:172:SER:H	2.25	0.41
1:D:252:LEU:HA	1:D:253:PRO:HD3	1.80	0.41
1:D:240:SER:HB3	1:D:279:TYR:CE1	2.54	0.41
1:D:312:ASP:O	1:D:316:ALA:HB2	2.19	0.41
1:E:406:LEU:HA	1:E:449:ALA:O	2.20	0.41
1:B:68:ALA:O	1:B:69:MET:C	2.58	0.41
1:C:119:LYS:HE3	1:C:124:ASP:OD1	2.20	0.41
1:C:150:ILE:H	1:C:150:ILE:HG12	1.63	0.41
1:C:163:LEU:HB3	1:C:164:GLY:H	1.63	0.41
1:C:460:LYS:HE3	1:C:460:LYS:HB3	1.82	0.41
1:D:200:ASN:O	1:D:201:ALA:C	2.59	0.41
1:D:406:LEU:HA	1:D:449:ALA:O	2.20	0.41
1:E:119:LYS:HE3	1:E:124:ASP:OD1	2.20	0.41
1:E:46:ASN:HB2	1:E:49:ASP:CB	2.50	0.41
1:F:478:CYS:C	1:F:480:ARG:N	2.72	0.41
1:B:371:GLN:O	1:B:403:CYS:HA	2.19	0.41
1:C:100:GLU:HG3	1:C:186:LYS:N	2.32	0.41
1:C:89:ALA:HB3	1:C:194:LEU:CD1	2.49	0.41
1:D:409:PRO:HG2	1:D:454:TYR:CE1	2.55	0.41
1:E:402:ASP:O	1:E:402:ASP:CG	2.59	0.41
1:F:119:LYS:HE3	1:F:124:ASP:OD1	2.20	0.41
1:F:56:GLN:HA	1:F:57:PRO:HD3	1.81	0.41
1:A:391:LYS:CE	1:A:440:ASN:ND2	2.84	0.41
1:B:236:ILE:HD11	1:B:340:LEU:HD11	2.01	0.41
1:B:370:VAL:HG23	1:B:370:VAL:O	2.20	0.41
1:B:423:VAL:O	1:B:424:ASP:C	2.59	0.41
1:C:50:LEU:HD11	1:C:65:PHE:CE1	2.56	0.41
1:D:427:VAL:O	1:D:431:THR:CG2	2.68	0.41
1:E:200:ASN:O	1:E:201:ALA:C	2.59	0.41
1:E:370:VAL:HG23	1:E:370:VAL:O	2.20	0.41
1:F:391:LYS:CE	1:F:440:ASN:ND2	2.84	0.41
1:B:409:PRO:HG2	1:B:454:TYR:CE1	2.55	0.41
1:C:406:LEU:HA	1:C:449:ALA:O	2.20	0.41
1:D:371:GLN:O	1:D:403:CYS:HA	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:408:SER:OG	1:D:409:PRO:HD2	2.21	0.41
1:E:236:ILE:HD11	1:E:340:LEU:HD11	2.01	0.41
1:E:371:GLN:O	1:E:403:CYS:HA	2.20	0.41
1:E:409:PRO:HG2	1:E:454:TYR:CE1	2.55	0.41
1:E:97:GLY:O	1:E:98:ASN:O	2.37	0.41
1:F:408:SER:OG	1:F:409:PRO:HD2	2.21	0.41
1:F:46:ASN:HB2	1:F:49:ASP:CB	2.50	0.41
1:A:46:ASN:HB2	1:A:49:ASP:CB	2.50	0.41
1:F:50:LEU:HD11	1:F:65:PHE:CE1	2.56	0.41
1:A:100:GLU:HG3	1:A:186:LYS:N	2.32	0.41
1:A:304:ILE:HG13	1:A:305:TYR:HE2	1.81	0.41
1:A:61:THR:O	1:A:62:ALA:C	2.59	0.41
1:B:100:GLU:HB2	1:B:185:GLY:HA3	2.03	0.41
1:B:23:SER:OG	1:B:483:ASN:CA	2.69	0.41
1:C:409:PRO:HG2	1:C:454:TYR:CE1	2.55	0.41
1:C:46:ASN:HB2	1:C:49:ASP:CB	2.50	0.41
1:C:68:ALA:O	1:C:69:MET:C	2.58	0.41
1:D:73:GLN:HB3	1:D:500:LEU:CD1	2.51	0.41
1:E:408:SER:OG	1:E:409:PRO:HD2	2.21	0.41
1:F:370:VAL:HG23	1:F:370:VAL:O	2.20	0.41
1:F:381:GLU:O	1:F:382:SER:C	2.59	0.41
1:A:119:LYS:HE3	1:A:124:ASP:OD1	2.20	0.41
1:A:381:GLU:O	1:A:382:SER:C	2.59	0.41
1:A:408:SER:OG	1:A:409:PRO:HD2	2.21	0.41
1:B:73:GLN:HB3	1:B:500:LEU:CD1	2.51	0.41
1:C:200:ASN:O	1:C:201:ALA:C	2.59	0.41
1:C:73:GLN:HB3	1:C:500:LEU:CD1	2.51	0.41
1:D:23:SER:OG	1:D:483:ASN:CA	2.69	0.41
1:F:61:THR:O	1:F:62:ALA:C	2.59	0.41
1:A:423:VAL:O	1:A:424:ASP:C	2.59	0.41
1:B:308:ASN:HD21	1:B:313:ASP:CB	2.34	0.41
1:D:119:LYS:HE3	1:D:124:ASP:OD1	2.20	0.41
1:D:304:ILE:HG13	1:D:305:TYR:HE2	1.81	0.41
1:D:50:LEU:HD11	1:D:65:PHE:CE1	2.56	0.41
1:E:23:SER:OG	1:E:483:ASN:CA	2.69	0.41
1:F:163:LEU:HB3	1:F:164:GLY:H	1.63	0.41
1:F:308:ASN:HD21	1:F:313:ASP:CB	2.34	0.41
1:B:50:LEU:HD11	1:B:65:PHE:CE1	2.56	0.41
1:B:89:ALA:HB3	1:B:194:LEU:CD1	2.49	0.41
1:C:90:LYS:N	1:C:344:LEU:O	2.48	0.41
1:E:290:VAL:HG11	1:E:322:TYR:CE1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:423:VAL:O	1:E:424:ASP:C	2.59	0.41
1:F:409:PRO:HG2	1:F:454:TYR:CE1	2.55	0.41
1:A:200:ASN:O	1:A:201:ALA:C	2.59	0.41
1:A:402:ASP:O	1:A:402:ASP:CG	2.59	0.41
1:B:200:ASN:O	1:B:201:ALA:C	2.58	0.41
1:C:100:GLU:HB2	1:C:185:GLY:HA3	2.03	0.41
1:C:408:SER:OG	1:C:409:PRO:HD2	2.21	0.41
1:D:453:ASN:N	1:D:453:ASN:HD22	2.15	0.41
1:D:61:THR:O	1:D:62:ALA:C	2.59	0.41
1:E:50:LEU:HD11	1:E:65:PHE:CE1	2.56	0.41
1:E:61:THR:O	1:E:62:ALA:C	2.59	0.41
1:E:73:GLN:HB3	1:E:500:LEU:CD1	2.51	0.41
1:B:163:LEU:HB3	1:B:164:GLY:H	1.63	0.40
1:B:90:LYS:N	1:B:344:LEU:O	2.48	0.40
1:B:391:LYS:CE	1:B:440:ASN:ND2	2.84	0.40
1:B:61:THR:O	1:B:62:ALA:C	2.59	0.40
1:C:92:SER:OG	1:C:343:GLY:HA3	2.21	0.40
1:E:43:GLN:NE2	1:E:77:ASP:HB2	2.36	0.40
1:F:90:LYS:HA	1:F:90:LYS:HD3	1.93	0.40
1:A:160:TYR:HA	1:A:161:PRO:HA	1.82	0.40
1:A:215:LYS:HE3	1:A:329:ASN:CG	2.42	0.40
1:A:50:LEU:HD11	1:A:65:PHE:CE1	2.56	0.40
1:B:100:GLU:HG3	1:B:186:LYS:N	2.32	0.40
1:B:290:VAL:HG11	1:B:322:TYR:CE1	2.56	0.40
1:B:406:LEU:HA	1:B:449:ALA:O	2.20	0.40
1:C:66:MET:O	1:C:67:SER:C	2.60	0.40
1:D:290:VAL:HG11	1:D:322:TYR:CE1	2.56	0.40
1:E:90:LYS:N	1:E:344:LEU:O	2.48	0.40
1:A:92:SER:OG	1:A:343:GLY:HA3	2.22	0.40
1:B:51:VAL:HG13	1:B:55:GLY:C	2.42	0.40
1:C:51:VAL:HG13	1:C:55:GLY:C	2.42	0.40
1:D:43:GLN:NE2	1:D:77:ASP:HB2	2.36	0.40
1:E:213:ASN:ND2	1:E:213:ASN:N	2.68	0.40
1:E:408:SER:HB2	1:E:471:ALA:CB	2.50	0.40
1:E:509:THR:CB	1:E:510:PRO:HA	2.44	0.40
1:F:304:ILE:HG13	1:F:305:TYR:HE2	1.81	0.40
1:F:92:SER:OG	1:F:343:GLY:HA3	2.21	0.40
1:A:100:GLU:HB2	1:A:185:GLY:HA3	2.03	0.40
1:B:43:GLN:NE2	1:B:77:ASP:HB2	2.36	0.40
1:D:423:VAL:O	1:D:424:ASP:C	2.59	0.40
1:E:391:LYS:CE	1:E:440:ASN:ND2	2.84	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:252:LEU:HA	1:F:253:PRO:HD3	1.80	0.40
1:A:104:SER:HB2	1:A:181:VAL:HG12	2.04	0.40
1:A:478:CYS:C	1:A:480:ARG:N	2.72	0.40
1:B:402:ASP:O	1:B:402:ASP:CG	2.59	0.40
1:B:499:ILE:N	1:B:499:ILE:HD13	2.28	0.40
1:B:66:MET:O	1:B:67:SER:C	2.60	0.40
1:C:43:GLN:NE2	1:C:77:ASP:HB2	2.36	0.40
1:D:308:ASN:HD21	1:D:313:ASP:CB	2.34	0.40
1:D:381:GLU:O	1:D:382:SER:C	2.59	0.40
1:E:215:LYS:HE3	1:E:329:ASN:CG	2.42	0.40
1:F:290:VAL:HG11	1:F:322:TYR:CE1	2.56	0.40
1:F:453:ASN:HB2	1:F:454:TYR:H	1.70	0.40
1:F:74:TYR:OH	1:F:473:ASP:OD2	2.35	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 PDB entries followed by that with respect to all EM entries.

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	475/510 (93%)	371 (78%)	87 (18%)	17 (4%)	4	33
1	B	475/510 (93%)	371 (78%)	87 (18%)	17 (4%)	4	33
1	C	475/510 (93%)	371 (78%)	87 (18%)	17 (4%)	4	33
1	D	475/510 (93%)	371 (78%)	87 (18%)	17 (4%)	4	33
1	E	475/510 (93%)	371 (78%)	87 (18%)	17 (4%)	4	33
1	F	475/510 (93%)	370 (78%)	88 (18%)	17 (4%)	4	33
All	All	2850/3060 (93%)	2225 (78%)	523 (18%)	102 (4%)	7	33

All (102) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	98	ASN
1	A	201	ALA
1	A	432	ALA
1	B	98	ASN
1	B	201	ALA
1	B	432	ALA
1	C	98	ASN
1	C	201	ALA
1	C	432	ALA
1	D	98	ASN
1	D	201	ALA
1	D	432	ALA
1	E	98	ASN
1	E	201	ALA
1	E	432	ALA
1	F	98	ASN
1	F	201	ALA
1	F	432	ALA
1	A	403	CYS
1	A	480	ARG
1	A	504	LYS
1	B	403	CYS
1	B	480	ARG
1	B	504	LYS
1	C	403	CYS
1	C	480	ARG
1	C	504	LYS
1	D	403	CYS
1	D	480	ARG
1	D	504	LYS
1	E	403	CYS
1	E	480	ARG
1	E	504	LYS
1	F	403	CYS
1	F	480	ARG
1	F	504	LYS
1	A	62	ALA
1	A	311	ILE
1	A	348	ALA
1	A	482	ASP
1	B	62	ALA
1	B	311	ILE
1	B	348	ALA

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Mol	Chain	Res	Type
1	B	482	ASP
1	C	62	ALA
1	C	311	ILE
1	C	348	ALA
1	C	482	ASP
1	D	62	ALA
1	D	311	ILE
1	D	348	ALA
1	D	482	ASP
1	E	62	ALA
1	E	311	ILE
1	E	348	ALA
1	E	482	ASP
1	F	62	ALA
1	F	311	ILE
1	F	348	ALA
1	F	482	ASP
1	A	509	THR
1	B	509	THR
1	C	509	THR
1	D	509	THR
1	E	509	THR
1	F	509	THR
1	A	25	GLY
1	A	304	ILE
1	B	25	GLY
1	B	304	ILE
1	C	25	GLY
1	C	304	ILE
1	D	25	GLY
1	D	304	ILE
1	E	25	GLY
1	E	304	ILE
1	F	25	GLY
1	F	304	ILE
1	A	247	GLY
1	A	434	GLY
1	B	247	GLY
1	B	434	GLY
1	C	247	GLY
1	C	434	GLY
1	D	247	GLY

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Mol	Chain	Res	Type
1	D	434	GLY
1	E	247	GLY
1	E	434	GLY
1	F	247	GLY
1	F	434	GLY
1	A	121	VAL
1	A	318	GLY
1	B	121	VAL
1	B	318	GLY
1	C	121	VAL
1	C	318	GLY
1	D	121	VAL
1	D	318	GLY
1	E	121	VAL
1	E	318	GLY
1	F	121	VAL
1	F	318	GLY

### 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 PDB entries followed by that with respect to all EM entries.

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	383/411 (93%)	341 (89%)	42 (11%)	7	30
1	B	383/411 (93%)	341 (89%)	42 (11%)	7	30
1	C	383/411 (93%)	340 (89%)	43 (11%)	7	29
1	D	383/411 (93%)	340 (89%)	43 (11%)	7	29
1	E	383/411 (93%)	340 (89%)	43 (11%)	7	29
1	F	383/411 (93%)	340 (89%)	43 (11%)	7	29
All	All	2298/2466 (93%)	2042 (89%)	256 (11%)	11	29

All (256) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	50	LEU

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Mol	Chain	Res	Type
1	A	58	THR
1	A	66	MET
1	A	67	SER
1	A	71	PHE
1	A	74	TYR
1	A	77	ASP
1	A	80	VAL
1	A	86	ARG
1	A	95	ILE
1	A	102	THR
1	A	150	ILE
1	A	162	THR
1	A	178	LEU
1	A	188	ILE
1	A	189	THR
1	A	202	GLU
1	A	213	ASN
1	A	290	VAL
1	A	345	SER
1	A	347	ASN
1	A	349	GLU
1	A	354	ASP
1	A	367	SER
1	A	368	VAL
1	A	371	GLN
1	A	382	SER
1	A	383	LEU
1	A	388	THR
1	A	395	SER
1	A	404	LEU
1	A	431	THR
1	A	436	TYR
1	A	438	ASP
1	A	440	ASN
1	A	446	THR
1	A	450	ILE
1	A	453	ASN
1	A	460	LYS
1	A	483	ASN
1	A	499	ILE
1	A	501	ASN
1	B	50	LEU

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Mol	Chain	Res	Type
1	B	58	THR
1	B	66	MET
1	B	67	SER
1	B	71	PHE
1	B	74	TYR
1	B	77	ASP
1	B	80	VAL
1	B	86	ARG
1	B	95	ILE
1	B	102	THR
1	B	150	ILE
1	B	162	THR
1	B	178	LEU
1	B	188	ILE
1	B	189	THR
1	B	202	GLU
1	B	213	ASN
1	B	290	VAL
1	B	345	SER
1	B	347	ASN
1	B	349	GLU
1	B	354	ASP
1	B	367	SER
1	B	368	VAL
1	B	371	GLN
1	B	382	SER
1	B	383	LEU
1	B	388	THR
1	B	395	SER
1	B	404	LEU
1	B	431	THR
1	B	436	TYR
1	B	438	ASP
1	B	440	ASN
1	B	446	THR
1	B	450	ILE
1	B	453	ASN
1	B	460	LYS
1	B	483	ASN
1	B	499	ILE
1	B	501	ASN
1	C	50	LEU

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Mol	Chain	Res	Type
1	C	58	THR
1	C	66	MET
1	C	67	SER
1	C	71	PHE
1	C	74	TYR
1	C	77	ASP
1	C	80	VAL
1	C	86	ARG
1	C	95	ILE
1	C	102	THR
1	C	150	ILE
1	C	162	THR
1	C	178	LEU
1	C	188	ILE
1	C	189	THR
1	C	202	GLU
1	C	213	ASN
1	C	290	VAL
1	C	345	SER
1	C	347	ASN
1	C	349	GLU
1	C	354	ASP
1	C	367	SER
1	C	368	VAL
1	C	371	GLN
1	C	382	SER
1	C	383	LEU
1	C	388	THR
1	C	395	SER
1	C	404	LEU
1	C	431	THR
1	C	436	TYR
1	C	437	THR
1	C	438	ASP
1	C	440	ASN
1	C	446	THR
1	C	450	ILE
1	C	453	ASN
1	C	460	LYS
1	C	483	ASN
1	C	499	ILE
1	C	501	ASN

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Mol	Chain	Res	Type
1	D	50	LEU
1	D	58	THR
1	D	66	MET
1	D	67	SER
1	D	71	PHE
1	D	74	TYR
1	D	77	ASP
1	D	80	VAL
1	D	86	ARG
1	D	95	ILE
1	D	102	THR
1	D	150	ILE
1	D	162	THR
1	D	178	LEU
1	D	188	ILE
1	D	189	THR
1	D	202	GLU
1	D	213	ASN
1	D	290	VAL
1	D	345	SER
1	D	347	ASN
1	D	349	GLU
1	D	354	ASP
1	D	367	SER
1	D	368	VAL
1	D	371	GLN
1	D	382	SER
1	D	383	LEU
1	D	388	THR
1	D	395	SER
1	D	404	LEU
1	D	431	THR
1	D	436	TYR
1	D	437	THR
1	D	438	ASP
1	D	440	ASN
1	D	446	THR
1	D	450	ILE
1	D	453	ASN
1	D	460	LYS
1	D	483	ASN
1	D	499	ILE

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Mol	Chain	Res	Type
1	D	501	ASN
1	E	50	LEU
1	E	58	THR
1	E	66	MET
1	E	67	SER
1	E	71	PHE
1	E	74	TYR
1	E	77	ASP
1	E	80	VAL
1	E	86	ARG
1	E	95	ILE
1	E	102	THR
1	E	150	ILE
1	E	162	THR
1	E	178	LEU
1	E	188	ILE
1	E	189	THR
1	E	202	GLU
1	E	213	ASN
1	E	290	VAL
1	E	345	SER
1	E	347	ASN
1	E	349	GLU
1	E	354	ASP
1	E	367	SER
1	E	368	VAL
1	E	371	GLN
1	E	382	SER
1	E	383	LEU
1	E	388	THR
1	E	395	SER
1	E	404	LEU
1	E	431	THR
1	E	436	TYR
1	E	437	THR
1	E	438	ASP
1	E	440	ASN
1	E	446	THR
1	E	450	ILE
1	E	453	ASN
1	E	460	LYS
1	E	483	ASN

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Mol	Chain	Res	Type
1	E	499	ILE
1	E	501	ASN
1	F	50	LEU
1	F	58	THR
1	F	66	MET
1	F	67	SER
1	F	71	PHE
1	F	74	TYR
1	F	77	ASP
1	F	80	VAL
1	F	86	ARG
1	F	95	ILE
1	F	102	THR
1	F	150	ILE
1	F	162	THR
1	F	178	LEU
1	F	188	ILE
1	F	189	THR
1	F	202	GLU
1	F	213	ASN
1	F	290	VAL
1	F	345	SER
1	F	347	ASN
1	F	349	GLU
1	F	354	ASP
1	F	367	SER
1	F	368	VAL
1	F	371	GLN
1	F	382	SER
1	F	383	LEU
1	F	388	THR
1	F	395	SER
1	F	404	LEU
1	F	431	THR
1	F	436	TYR
1	F	437	THR
1	F	438	ASP
1	F	440	ASN
1	F	446	THR
1	F	450	ILE
1	F	453	ASN
1	F	460	LYS

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Mol	Chain	Res	Type
1	F	483	ASN
1	F	499	ILE
1	F	501	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (48) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	43	GLN
1	A	70	ASN
1	A	213	ASN
1	A	278	GLN
1	A	390	GLN
1	A	440	ASN
1	A	453	ASN
1	A	457	GLN
1	B	43	GLN
1	B	70	ASN
1	B	213	ASN
1	B	278	GLN
1	B	390	GLN
1	B	440	ASN
1	B	453	ASN
1	B	457	GLN
1	C	43	GLN
1	C	70	ASN
1	C	213	ASN
1	C	278	GLN
1	C	390	GLN
1	C	440	ASN
1	C	453	ASN
1	C	457	GLN
1	D	43	GLN
1	D	70	ASN
1	D	213	ASN
1	D	278	GLN
1	D	390	GLN
1	D	440	ASN
1	D	453	ASN
1	D	457	GLN
1	E	43	GLN
1	E	70	ASN
1	E	213	ASN

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Mol	Chain	Res	Type
1	E	278	GLN
1	E	390	GLN
1	E	440	ASN
1	E	453	ASN
1	E	457	GLN
1	F	43	GLN
1	F	70	ASN
1	F	213	ASN
1	F	278	GLN
1	F	390	GLN
1	F	440	ASN
1	F	453	ASN
1	F	457	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

### 5.7 Other polymers [i](#)

There are no such residues in this entry.

### 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.